

T-ALL vs. AML complex	samples: 9 / 36			
accuracy	0.977777777777778			
confidence	1			
failed:	8			
gene	signal-to-noise	p	decision limit	gene symbol
242292_at	1.76638958058548	0		
233569_x_at	-1.72473600410199	0		
201200_at	-1.67373612904555	0		CREG
221188_s_at	-1.58025708973943	0		CIDEB
214430_at	-1.57548239699241	0		GLA
203370_s_at	-1.49153229697191	0		ENIGMA
213101_s_at	-1.48624142663186	0		IL27
207543_s_at	-1.47703523852874	0*	244.15	P4HA1
200996_at	-1.46058173493331	0		ACTR3
228242_at	1.42599890928864	0		
200625_s_at	-1.41869234255251	0		CAP
212271_at	-1.41675681954144	0		MAPK1
213798_s_at	-1.3995900667655	0		CAP
218341_at	-1.38917958617976	0		FLJ11838
207809_s_at	-1.38033524444329	0		ATP6IP1
201416_at	1.36993537921948	0		SOX4
214017_s_at	-1.36371429454275	0		DDX34
210145_at	-1.35854949316142	0		PLA2G4A
221006_s_at	-1.35518233243855	0		MY014

T-ALL vs. AML normal		samples: 9 / 62		
accuracy	1	p	decision limit	gene symbol
confidence	0.957860143913647			
gene	signal-to-noise	p	decision limit	gene symbol
230292_at	1.88640079114873	0*	209.2	
201200_at	-1.83242104341312	0		CREG
202479_s_at	1.72124560429389	0*	139	GS3955
213539_at	1.67079068669821	0		CD3D
224918_x_at	-1.58916954867569	0		MGST1
227999_at	-1.50019492619142	0		LOC170394
219812_at	1.47878284715341	0		MGC2463
228007_at	1.4773281277912	0		
231736_x_at	-1.46304321667415	0		MGST1
219079_at	-1.46035185202908	0		b5&b5R
204484_at	1.43138015243683	0		PIK3C2B
201537_s_at	-1.41942605715997	0		DUSP3
210613_s_at	-1.41293569747837	0		SYNGR1
217989_at	-1.41116959479258	0		LOC51170
207996_s_at	1.40679076628897	0		C18orf1
200765_x_at	-1.40654043227196	0		CTNNA1
205382_s_at	-1.40167577220905	0		DF
201463_s_at	-1.39170471415992	0		TALDO1
233589_x_at	-1.39076513944045	0		
39650_s_at	1.23989100884988	0		KIAA0435

T-ALL vs. AML t(8;21)	samples: 9 / 13			
accuracy	1.	p	decision limit	gene symbol
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
242292_at	3.53231266693437	0*	19.4	
203949_at	-3.12642743394317	0		MPO
203948_s_at	-2.45792853300794	0		MPO
217989_at	-2.43298080062421	0		LOC51170
223482_at	-2.33409794008859	0		TMPIT
203795_s_at	2.1853673808492	0		BCL7A
218224_at	2.09498423445912	0		PNMA1
217080_s_at	-2.03866301670049	0		HOMER-2B
236019_at	2.02213343587896	0		
219477_s_at	2.01911441063646	0		LOC55901
228988_at	2.01251275923737	0		ZNF6
201486_at	1.99987326641982	0		RCN2
219478_at	-1.99876002437156	0		WFDC1
228266_s_at	1.98746817521137	0		CGI-142
207996_s_at	1.96448548584508	0		C18orf1
222203_s_at	1.94383192684329	0		
205640_at	-1.93350841183487	0		ALDH3B1
210613_s_at	-1.93015512462768	0		SYNGR1
228174_at	1.9244800134633	0		
223474_at	1.91826574900603	0		C14orf4

AML +8 vs. all other		samples: 10 / 259		
accuracy		0.966542750929368		
confidence		1		
failed:		1,2,3,5,6,7,8,9,10		
gene	signal-to-noise	p	decision limit	gene symbol
212250_at	1.00891676230186	0		
218549_s_at	0.942516384676453	0		LOC51115
212449_s_at	0.88821669704833	0		LYPLA1
205849_s_at	0.882097788580276	0		UQCRB
222166_at	-0.873718781745549	0		
203007_x_at	0.87144371195471	0		
242975_s_at	-0.862022087552992	0		GNAS
208697_s_at	0.80816796889713	0		EIF3S6
201592_at	0.794789783421717	0		EIF3S3
218482_at	0.794345693087361	0		DC6
201985_at	0.784318906218296	0		KIAA0196
231101_at	-0.7838812614223	0		PPP2R5E
218642_s_at	0.776600267973484	0		MGC2217
201652_at	0.761703817525426	0		COPS5
201433_s_at	0.761252302206581	0		PTDSS1
217916_s_at	0.757235902578392	0		BM-009
226165_at	0.738121051467492	0*	1969.6	E2F5
203110_at	0.736663801658822	0		PTK2B
224804_s_at	-0.734849706050297	0		FLJ00005

AML +8 vs. AML complex	samples: 10 / 36			
accuracy	1			
confidence	0.855027999708228			
gene	signal-to-noise	p	decision limit	gene symbol
222229_x_at	1.23332137897808	0		
208697_s_at	1.15066098039301	0		EIF3S6
205849_s_at	1.14869307530221	0		UQCRB
212586_at	1.11153173777253	0*	1231.4	ARTS-1
208646_at	1.07422424644875	0		
230795_at	-1.06732853628123	0		H4F2
202746_at	-1.03422849717783	0		
226545_at	-1.00972156245463	0*	100.15	
222166_at	-0.999828982909011	0*	1	
210715_s_at	-0.978857795907468	0*	573.3	SPINT2
228652_at	-0.974511468277957	0		
217979_at	-0.973647566321829	0*	234.35	NET-6
201548_s_at	-0.970651188910704	0*	289.85	PLU-1
202747_s_at	-0.952100249128964	0		ITM2A
201602_s_at	-0.951073671804128	0		PPP1R12A
205674_x_at	-0.945871996779656	0		FXYD2
244740_at	-0.942099475768156	0		
219518_s_at	-0.938970502867646	0		FLJ22637
227249_at	-0.931085853722028	0		NUDE1

AML +8 vs. AML normal	samples: 10 / 62			
accuracy	0.944444444444444			
confidence	1			
failed:	2,8,9,10			
gene	signal-to-noise	p	decision limit	gene symbol
214394_x_at	1.16987396866816	0		FLJ20897
203110_at	1.09167544137433	0		PTK2B
203007_x_at	1.00013993270134	0		
235124_at	-0.983829818030274	0		
212251_at	0.969996357896378	0*	4073.8	
242975_s_at	-0.968085578079267	0		GNAS
206781_at	-0.939680187764268	0		DNAJC4
225406_at	-0.924590937077397	0		TSG
218482_at	0.900623425034112	0		DC6
237291_at	-0.889981273455645	0.01		
235647_at	-0.87846991187601	0		
234726_s_at	-0.877362222213618	0		
225889_at	-0.85606834671728	0		
236837_x_at	-0.842273497900729	0		
222166_at	-0.840979666931678	0		
228092_at	-0.833074953827583	0		
212250_at	0.830552344097529	0		
226450_at	0.827753984186341	0		
238392_at	-0.812637849766076	0		
200655_s_at	0.811239676737242	0		CALM1

AML +8 vs. AML t(8;21)	samples: 10 / 13					
	accuracy	confidence	signal-to-noise	p	decision limit	gene symbol
228827_at	1	1	-2.03460798747208	0*	162.15	
203188_at			1.98171895993959	0		B3GNT6
209522_s_at			1.87499941760774	0		CRAT
50221_at			1.77237042593137	0		
212586_at			1.70313290894867	0		ARTS-1
217816_s_at			1.69811663165145	0		pcnp
219084_at			1.68534097481951	0		NSD1
241370_at			1.66453119103938	0		
221581_s_at			1.64609943226078	0		WBSCR5
205528_s_at			-1.64467496425566	0		CBFA2T1
211341_at			-1.63310072579237	0		POU4F1
212250_at			1.62854737716103	0		
206940_s_at			-1.60737424398258	0		POU4F1
205529_s_at			-1.591491111654	0		CBFA2T1
213150_at			1.57881564631984	0		HOXA10
214394_x_at			1.57039311243451	0		FLJ20897
212895_s_at			1.56878968456679	0		ABR
218341_at			1.53928870336148	0		FLJ11838
204249_s_at			1.52597204656408	0		LMO2
214651_s_at			1.52240931149048	0		HOXA9

AML complex vs. all other	samples: 36 / 233			
accuracy	0.940520446096654			
confidence	0.921791251652985			
failed:	1,3,4,7,9,11,13,17,19,22,26,29,30,31,36,159			
gene	signal-to-noise	p	decision limit	gene symbol
222229_x_at	-0.893099830348847	0		
200608_s_at	0.829215272839729	0*	1754.85	RAD21
219793_at	0.800006992121134	0*	82.35	SNX16
214700_x_at	0.78695642651388	0		
216652_s_at	0.767651877577316	0		
209523_at	0.752134816617307	0*	681.95	
203904_x_at	0.746250973896829	0		KAI1
209188_x_at	0.739903310934254	0		DR1
207654_x_at	0.732205254479051	0		DR1
223318_s_at	-0.730537441809073	0		MGC10974
201437_s_at	0.717807687112266	0		EIF4E
227056_at	-0.715710672900953	0		KIAA0141
209259_s_at	0.712514692902903	0		CSPG6
216304_x_at	0.711429386769807	0		
201263_at	0.705291260136426	0		TARS
213452_at	0.700628406937312	0		ZNF184
225344_at	0.690845684896899	0		
203133_at	0.686789233495541	0		SEC61B
203818_s_at	0.685434479377027	0		SF3A3
202413_s_at	0.684073197719258	0		USP1

AML complex vs. AML normal		samples: 36 / 62		
accuracy		0.959183673469388		
confidence		0.827538830649198		
failed:		4,17,26,95		
gene	signal-to-noise	p	decision limit	gene symbol
222229_x_at	-1.15282283406825	0		
227056_at	-1.01959539261157	0		KIAA0141
200093_s_at - HG-U133B	-0.981168516451417	0*	3052.25	HINT1
201922_at	-0.946723517280923	0*	3970.8	YR-29
239791_at	-0.927299942476145	0*	54	HOXB6
200608_s_at	0.881421230727578	0*	1566.2	RAD21
235502_at	-0.858356821521878	0		
200093_s_at - HG-U133A	-0.84958486306905	0		HINT1
205436_s_at	0.848914256281541	0		H2AFX
223318_s_at	-0.843205304716435	0		MGC10974
200023_s_at - HG-U133B	-0.834951347999649	0		EIF3S5
201164_s_at	0.825610572112667	0		PUM1
203345_s_at	0.823373110066695	0		M96
212251_at	0.821052485124022	0		
218645_at	-0.816440269243142	0		ZNF277
236728_at	-0.815324685029762	0		
214911_s_at	0.812703140158658	0		
236892_s_at	-0.810032594833065	0		HOXB6
211950_at	0.809875752517154	0*	1367.5	RBAF600
207983_s_at	0.808929428489603	0		STAG2

AML complex vs. AML t(8;21) samples: 36 / 13

accuracy	1	confidence	0.956366908409342	
gene	signal-to-noise	p	decision limit	gene symbol
201851_at	1.64654123030477	0		SH3GL1
228827_at	-1.63837794328364	0*	277.15	
214651_s_at	1.52618371146822	0		HOXA9
235521_at	1.52417126144756	0		HOXA3
204249_s_at	1.52365997713542	0*	1581.95	LMO2
203904_x_at	1.49494399498725	0		KAI1
206940_s_at	-1.48076766016125	0		POU4F1
211341_at	-1.47540487159533	0		POU4F1
209259_s_at	1.45032016623088	0		CSPG6
212058_at	1.43907164424644	0		KIAA0332
218577_at	1.42304726090167	0		FLJ20331
217963_s_at	1.41730181206619	0		HCS
206622_at	-1.41476408655437	0		TRH
200071_at - HG-U133A	1.4105258517176	0		SPF30
218933_at	1.38255573216414	0		MGC5347
205528_s_at	-1.38150242627303	0		CBFA2T1
218331_s_at	1.3810903886183	0		FLJ20360
202406_s_at	1.3795610685034	0		TIAL1
220796_x_at	1.36377544613334	0		FLJ14251
218582_at	1.35888148459997	0		FLJ20445

AML normal vs. all other	samples: 62 / 207		
accuracy	0.895910780669145		
confidence	0.964449931704009		
failed:	5,14,20,27,30,32,35,37,38,39,42,43,45,48,50,52,53,55,56,57,61,213, 215,217,219,227,230,254		
gene	signal-to-noise	p	decision limit
236892_s_at	0.883816204836633	0*	60.95
228904_at	0.842467327362967	0	
239791_at	0.82014114184115	0	
205601_s_at	0.78108191394345	0	
205600_x_at	0.763742762546178	0	
205366_s_at	0.755814747220724	0*	322.65
230743_at	0.685019971063637	0	
205453_at	0.673160741612025	0	
214651_s_at	0.668311761484385	0	
200679_x_at	-0.662124332081048	0	
225406_at	0.660717097117062	0	
200093_s_at - HG-U133B	0.660005840449192	0	
206295_at	0.640927517926634	0	
235753_at	0.637566839566103	0	
217768_at	0.632918049830813	0	
225553_at	0.62830766714963	0	
225175_s_at	-0.624292365035176	0	
200093_s_at - HG-U133A	0.621189010096421	0	
214911_s_at	-0.615055858265367	0	
241464_s_at	0.611746504394311	0	

AML normal vs. AML t(8;21)		samples: 62 / 13		
accuracy	1	p	decision limit	gene symbol
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
228827_at	-2.03460798747208	0*	162.15	
214651_s_at	1.87986749903764	0		HOXA9
205528_s_at	-1.64467496425566	0		CBFA2T1
235753_at	1.56101146788885	0		
205529_s_at	-1.4994140185132	0		CBFA2T1
211341_at	-1.4972813333234	0		POU4F1
206940_s_at	-1.48355335484551	0		POU4F1
209905_at	1.46906077761321	0		HOXA9
213150_at	1.46604197311664	0		HOXA10
217816_s_at	1.45253445141557	0		pcnp
219598_s_at	1.41726065845379	0		
205453_at	1.38558116676561	0		HOXB2
223498_at	1.33655832782001	0		
214000_s_at	-1.2765364955951	0		RGS10
235818_at	-1.27371437711255	0		
213844_at	1.25995066545668	0		HOXA5
235521_at	1.2540451261169	0		HOXA3
227279_at	1.2513845109424	0		MGC15737
222448_s_at	1.24728565933231	0		UMP-CMPK
213147_at	1.24192806323509	0		HOXA10

AML t(8;21) vs. all other	samples: 13 / 256			
accuracy	0.996282527881041			
confidence	1			
failed:	190			
gene	signal-to-noise	p	decision limit	gene symbol
228827_at	1.85657763737458	0		
205528_s_at	1.5282463620506	0		CBFA2T1
205529_s_at	1.44069436893782	0*	157.8	CBFA2T1
206622_at	1.31883260079515	0		TRH
206940_s_at	1.30418339343959	0		POU4F1
211341_at	1.2136561137121	0		POU4F1
212828_at	-1.0700055152284	0		SYNJ2
212480_at	-1.05079328033116	0		KIAA0376
219478_at	1.04231267665759	0		WFDC1
219598_s_at	-1.04225165555028	0		
204811_s_at	1.03799840690676	0		CACNA2D2
214000_s_at	1.01734079918989	0		RGS10
221581_s_at	-0.964830298373625	0		WBSCR5
224764_at	-0.954444787821262	0		ARHGAP10
34689_at	-0.942804241091645	0		TREX1
227279_at	-0.942193016486907	0		MGC15737
217816_s_at	-0.934103105967049	0		pcnp
207760_s_at	-0.925434637488157	0		NCOR2
238012_at	-0.924942905482366	0		
AFFX-r2-Hs28SrRNA-3_at				
HG-U133B	0.833222345890935	0		

Table 30: Analysis of 14 leukemia subgroups and normal bone marrow according to the method described by Westfall & Young. The 500 most significant genes are listed. The raw p value as well as the adjusted p value are shown. Furthermore it is indicated whether the genes were also identified as discriminative by the method described by Golub et al. (* most important gene in pairwise comparisons, + one of the top 20 significant genes)

5

geneID	Golub	rawp	adjp	Gene symbol
201497_x_at	*	0.0001	0.0001	MYH11
201998_at	+	0.0001	0.0001	SIAT1
204150_at	+	0.0001	0.0001	STAB1
204511_at		0.0001	0.0001	KIAA0793
205805_s_at	+	0.0001	0.0001	ROR1
206255_at	+	0.0001	0.0001	BLK
206337_at		0.0001	0.0001	CCR7
207802_at	+	0.0001	0.0001	SGP28
207819_s_at		0.0001	0.0001	ABCB4
208091_s_at	+	0.0001	0.0001	DKFZP564K0822
208456_s_at	+	0.0001	0.0001	RRAS2
209061_at		0.0001	0.0001	NCOA3
209374_s_at	+	0.0001	0.0001	IGHM
210244_at	+	0.0001	0.0001	CAMP
212313_at		0.0001	0.0001	
212531_at	*	0.0001	0.0001	LCN2
212590_at	+	0.0001	0.0001	
212827_at	+	0.0001	0.0001	IGHM
212953_x_at	*	0.0001	0.0001	CALR
214450_at	*	0.0001	0.0001	CTSW
214615_at	+	0.0001	0.0001	P2Y10
215925_s_at	+	0.0001	0.0001	
219471_at	+	0.0001	0.0001	FLJ21562
219837_s_at	+	0.0001	0.0001	C17
221268_s_at		0.0001	0.0001	LOC81537
221601_s_at		0.0001	0.0001	TOSO
221969_at	*	0.0001	0.0001	PAX5
223287_s_at	+	0.0001	0.0001	FOXP1
223391_at	+	0.0001	0.0001	LOC81537
223514_at	+	0.0001	0.0001	CARD11
224794_s_at	+	0.0001	0.0001	LOC51148
224837_at	+	0.0001	0.0001	FOXP1
224838_at	*	0.0001	0.0001	
227224_at		0.0001	0.0001	
228390_at	+	0.0001	0.0001	
228827_at	*	0.0001	0.0001	

229070_at		0.0001	0.0001 MGC12335
229072_at	+	0.0001	0.0001
229844_at	+	0.0001	0.0001
230768_at	+	0.0001	0.0001
232060_at		0.0001	0.0001
234725_s_at		0.0001	0.0001 SEMA4B
236226_at		0.0001	0.0001
236280_at	+	0.0001	0.0001
236854_at	+	0.0001	0.0001
239214_at	*	0.0001	0.0001
239287_at	*	0.0001	0.0001
243780_at	+	0.0001	0.0001
38487_at	*	0.0001	0.0001 FLJ12442
41660_at		0.0001	0.0001 CELSR1
44790_s_at	+	0.0001	0.0001 FLJ21562
202761_s_at		0.0001	0.0002 SYNE-2
203074_at	+	0.0001	0.0002 ANXA8
203936_s_at	+	0.0001	0.0002 MMP9
203948_s_at	*	0.0001	0.0002 MPO
204192_at	+	0.0001	0.0002 CD37
204215_at	*	0.0001	0.0002 MGC4175
205049_s_at	+	0.0001	0.0002 CD79A
205192_at	*	0.0001	0.0002 MAP3K14
205267_at		0.0001	0.0002 POU2AF1
205528_s_at	+	0.0001	0.0002 CBFA2T1
205901_at		0.0001	0.0002 PNOC
207700_s_at		0.0001	0.0002 NCOA3
207777_s_at		0.0001	0.0002 SP140
208195_at		0.0001	0.0002 TTN
209344_at	+	0.0001	0.0002 TPM4
211352_s_at		0.0001	0.0002 NCOA3
212386_at		0.0001	0.0002
212589_at	+	0.0001	0.0002 RRAS2
212914_at		0.0001	0.0002 PKP4
213142_x_at		0.0001	0.0002 LOC54103
213309_at		0.0001	0.0002 PLCL2
213689_x_at		0.0001	0.0002 RPL5
213927_at	+	0.0001	0.0002
218469_at	+	0.0001	0.0002 CKTSF1B1
219073_s_at		0.0001	0.0002 OSBPL10
221586_s_at		0.0001	0.0002 E2F5
225927_at	*	0.0001	0.0002 MAP3K1

226122_at		0.0001	0.0002
226147_s_at		0.0001	0.0002
226496_at	+	0.0001	0.0002
226713_at	+	0.0001	0.0002
226989_at	+	0.0001	0.0002
227030_at		0.0001	0.0002
227173_s_at	*	0.0001	0.0002 BACH2
227670_at		0.0001	0.0002
238604_at		0.0001	0.0002
239393_at	+	0.0001	0.0002
242458_at		0.0001	0.0002
202524_s_at		0.0001	0.0004 KIAA0275
203949_at	*	0.0001	0.0004 MPO
205382_s_at	*	0.0001	0.0004 DF
205529_s_at	*	0.0001	0.0004 CBFA2T1
206126_at		0.0001	0.0004 BLR1
206676_at	+	0.0001	0.0004 CEACAM8
207000_s_at	+	0.0001	0.0004 PPP3CC
209168_at	+	0.0001	0.0004 GPM6B
210997_at		0.0001	0.0004 HGF
212387_at		0.0001	0.0004
212956_at		0.0001	0.0004 KIAA0882
218090_s_at		0.0001	0.0004
218468_s_at		0.0001	0.0004 CKTSF1B1
219820_at		0.0001	0.0004 NTT5
226326_at	+	0.0001	0.0004
226454_at		0.0001	0.0004 LOC92979
227414_at		0.0001	0.0004 DKFZp547E052
229487_at	*	0.0001	0.0004
229659_s_at		0.0001	0.0004
230245_s_at		0.0001	0.0004
236301_at		0.0001	0.0004
41220_at	+	0.0001	0.0004 MSF
203373_at	+	0.0001	0.0005 STAT12
203753_at		0.0001	0.0005 TCF4
209060_x_at		0.0001	0.0005 NCOA3
210755_at		0.0001	0.0005 HGF
213891_s_at		0.0001	0.0005
216044_x_at		0.0001	0.0005
235674_at	+	0.0001	0.0005
236458_at		0.0001	0.0005
242104_at		0.0001	0.0005

200654_at	+	0.0001	0.0006 P4HB
203372_s_at	+	0.0001	0.0006 STAT12
204604_at		0.0001	0.0006 PFTK1
204951_at	*	0.0001	0.0006 ARHH
205933_at	+	0.0001	0.0006 SETBP1
206398_s_at	+	0.0001	0.0006 CD19
210356_x_at	+	0.0001	0.0006 MS4A2
217478_s_at	+	0.0001	0.0006
217504_at		0.0001	0.0006 ABCA6
221030_s_at		0.0001	0.0006 DKFZP564B1162
222146_s_at		0.0001	0.0006
222150_s_at		0.0001	0.0006
223422_s_at		0.0001	0.0006 DKFZP564B1162
225144_at		0.0001	0.0006
227198_at	*	0.0001	0.0006
228377_at	+	0.0001	0.0006 KIAA1384
228592_at		0.0001	0.0006
229194_at		0.0001	0.0006
230110_at		0.0001	0.0006
230648_at		0.0001	0.0006
232112_at		0.0001	0.0006
234140_s_at		0.0001	0.0006 STIM2
235444_at		0.0001	0.0006
243798_at		0.0001	0.0006
203217_s_at		0.0001	0.0007 SIAT9
204512_at		0.0001	0.0007 HIVEP1
205557_at	*	0.0001	0.0007 BPI
205997_at	+	0.0001	0.0007 ADAM28
206177_s_at		0.0001	0.0007 ARG1
206940_s_at	+	0.0001	0.0007 POU4F1
208914_at		0.0001	0.0007 GGA2
209101_at		0.0001	0.0007 CTGF
209169_at		0.0001	0.0007 GPM6B
209170_s_at	+	0.0001	0.0007 GPM6B
209765_at	+	0.0001	0.0007 ADAM19
212481_s_at		0.0001	0.0007 TPM4
213772_s_at	*	0.0001	0.0007 GGA2
214238_at		0.0001	0.0007
214315_x_at		0.0001	0.0007 CALR
217418_x_at		0.0001	0.0007 MS4A2
221004_s_at	+	0.0001	0.0007 ITM3
223828_s_at		0.0001	0.0007 LGALS12

224735_at		0.0001	0.0007
225246_at	+	0.0001	0.0007 STIM2
225563_at	+	0.0001	0.0007
226508_at		0.0001	0.0007
226635_at		0.0001	0.0007
227146_at		0.0001	0.0007
227243_s_at		0.0001	0.0007
227407_at	*	0.0001	0.0007
228555_at		0.0001	0.0007
229383_at		0.0001	0.0007
232950_s_at		0.0001	0.0007 NIR3
233955_x_at		0.0001	0.0007 HSPC195
235372_at		0.0001	0.0007 FREB
240572_s_at		0.0001	0.0007
34210_at	+	0.0001	0.0007 CDW52
AFFX-	+	0.0001	0.0007 GAPD
HUMGAPDH/M33197_3_at			
- HG-U133B			
203233_at		0.0001	0.0008 IL4R
204882_at		0.0001	0.0008 KIAA0053
206760_s_at		0.0001	0.0008 FCER2
209619_at	*	0.0001	0.0008 CD74
212285_s_at		0.0001	0.0008 AGRN
216095_x_at		0.0001	0.0008 MTMR1
221558_s_at	+	0.0001	0.0008 LEF1
222996_s_at		0.0001	0.0008 HSPC195
226538_at		0.0001	0.0008 MAN2A1
227152_at		0.0001	0.0008
230983_at		0.0001	0.0008
244261_at	+	0.0001	0.0008
64942_at	+	0.0001	0.0008
236787_at	+	0.0001	0.0009
205308_at		0.0001	0.001 LOC51101
208657_s_at		0.0001	0.001 MSF
209772_s_at	*	0.0001	0.001 CD24
209780_at		0.0001	0.001 DKFZP564F013
211126_s_at		0.0001	0.001 CSRP2
213511_s_at		0.0001	0.001
213539_at	+	0.0001	0.001 CD3D
213674_x_at		0.0001	0.001 IGHG3
214651_s_at	*	0.0001	0.001 HOXA9
214686_at		0.0001	0.001 ZNF266

214924_s_at		0.0001	0.001
216379_x_at	+	0.0001	0.001
218354_at		0.0001	0.001 LOC51693
224482_s_at		0.0001	0.001 MGC11316
224772_at	+	0.0001	0.001 MGC14961
227478_at		0.0001	0.001
227767_at		0.0001	0.001 CSNK1G3
228007_at	+	0.0001	0.001
228693_at		0.0001	0.001
230753_at		0.0001	0.001
230802_at		0.0001	0.001 DKFZP564B1162
231656_x_at		0.0001	0.001 OSBPL10
236341_at		0.0001	0.001 CTLA4
239122_at		0.0001	0.001 IL24
38149_at		0.0001	0.001 KIAA0053
200656_s_at	+	0.0001	0.0011 P4HB
204000_at		0.0001	0.0011 GNB5
208623_s_at		0.0001	0.0011 VIL2
210487_at	+	0.0001	0.0011 DNNT
201012_at		0.0001	0.0012 ANXA1
201069_at		0.0001	0.0012 MMP2
201200_at	+	0.0001	0.0012 CREG
201496_x_at	+	0.0001	0.0012 MYH11
201540_at	+	0.0001	0.0012 FHL1
201889_at		0.0001	0.0012 GS3786
202018_s_at	+	0.0001	0.0012 LTF
202709_at		0.0001	0.0012 FMOD
202880_s_at	+	0.0001	0.0012 PSCD1
203020_at		0.0001	0.0012 KIAA0471
203385_at		0.0001	0.0012 DGKA
203556_at		0.0001	0.0012 KIAA0854
203607_at		0.0001	0.0012 SAC2
203757_s_at	+	0.0001	0.0012 CEACAM6
203795_s_at	+	0.0001	0.0012 BCL7A
204199_at		0.0001	0.0012 RALGPS1A
204401_at		0.0001	0.0012 KCNN4
204661_at	*	0.0001	0.0012 CDW52
204674_at		0.0001	0.0012 LRMP
205383_s_at		0.0001	0.0012 ZNF288
205671_s_at		0.0001	0.0012 HLA-DOB
205790_at		0.0001	0.0012 SCAP1
206150_at		0.0001	0.0012 TNFRSF7

206515_at		0.0001	0.0012 CYP4F3
206759_at		0.0001	0.0012 FCER2
206871_at	+	0.0001	0.0012 ELA2
207030_s_at		0.0001	0.0012 CSRP2
207384_at		0.0001	0.0012 PGLYRP
207641_at		0.0001	0.0012 TACI
207957_s_at		0.0001	0.0012 PRKCB1
208852_s_at	+	0.0001	0.0012 CANX
209307_at		0.0001	0.0012 SWAP70
209686_at		0.0001	0.0012 S100B
209771_x_at	*	0.0001	0.0012 CD24
210279_at		0.0001	0.0012 GPR18
210788_s_at	+	0.0001	0.0012 LOC51635
211105_s_at		0.0001	0.0012 NFATC1
211341_at	+	0.0001	0.0012 POU4F1
211657_at	+	0.0001	0.0012
212074_at		0.0001	0.0012 KIAA0810
212314_at		0.0001	0.0012 KIAA0746
212400_at	*	0.0001	0.0012
212509_s_at	+	0.0001	0.0012
212614_at		0.0001	0.0012
212838_at		0.0001	0.0012 KIAA1010
214203_s_at		0.0001	0.0012 PRODH
214786_at	+	0.0001	0.0012 MAP3K1
215785_s_at	+	0.0001	0.0012 CYFIP2
216320_x_at	+	0.0001	0.0012
217838_s_at		0.0001	0.0012 RNB6
217979_at	*	0.0001	0.0012 NET-6
219574_at		0.0001	0.0012 FLJ20668
220001_at		0.0001	0.0012 PAD15
220118_at		0.0001	0.0012 TZFP
220999_s_at		0.0001	0.0012 PRO1331
221602_s_at		0.0001	0.0012 TOSO
223522_at		0.0001	0.0012 GL012
224406_s_at	+	0.0001	0.0012 IRTA2
224516_s_at		0.0001	0.0012 HSPC195
224833_at	+	0.0001	0.0012 ETS1
224918_x_at	+	0.0001	0.0012 MGST1
224994_at		0.0001	0.0012 CAMK2D
225230_at		0.0001	0.0012 CEPT1
225327_at		0.0001	0.0012 FLJ10980
225512_at		0.0001	0.0012

225592_at	+	0.0001	0.0012 NRM
225629_s_at		0.0001	0.0012 KIAA1538
226008_at		0.0001	0.0012 HCA4
226244_at	+	0.0001	0.0012
226408_at		0.0001	0.0012 TEAD2
226550_at		0.0001	0.0012
226878_at	+	0.0001	0.0012
226905_at		0.0001	0.0012
227046_at		0.0001	0.0012 C17orf26
227167_s_at		0.0001	0.0012
227189_at		0.0001	0.0012 KIAA1599
227261_at		0.0001	0.0012 KLF12
227408_s_at		0.0001	0.0012 MSTP043
227533_at		0.0001	0.0012
227607_at		0.0001	0.0012 KIAA1373
227646_at		0.0001	0.0012 EBF
228471_at		0.0001	0.0012
229513_at		0.0001	0.0012
229934_at	+	0.0001	0.0012
231736_x_at	+	0.0001	0.0012 MGST1
231873_at		0.0001	0.0012
232204_at		0.0001	0.0012 EBF
232210_at		0.0001	0.0012
232614_at		0.0001	0.0012
233072_at	+	0.0001	0.0012 KIAA1857
233261_at		0.0001	0.0012
234032_at		0.0001	0.0012
235061_at		0.0001	0.0012
235278_at		0.0001	0.0012
235385_at		0.0001	0.0012 FLJ20668
236190_at		0.0001	0.0012
236265_at		0.0001	0.0012
238057_at		0.0001	0.0012
238376_at		0.0001	0.0012
238587_at		0.0001	0.0012 MGC15437
238790_at		0.0001	0.0012
239231_at		0.0001	0.0012
239278_at	+	0.0001	0.0012
239442_at		0.0001	0.0012
241383_at	+	0.0001	0.0012
241525_at	+	0.0001	0.0012
32541_at		0.0001	0.0012 PPP3CC

74694_s_at		0.0001	0.0012 FLJ23282
AFFX-HUMGAPDH/M33197_3_at	-	0.0001	0.0012 GAPD
HG-U133A			
AFFX-HUMGAPDH/M33197_M_at	-	0.0001	0.0012 GAPD
HG-U133A			
201189_s_at		0.0001	0.0013 ITPR3
201811_x_at	+	0.0001	0.0013 SH3BP5
201853_s_at		0.0001	0.0013 CDC25B
202822_at		0.0001	0.0013 LPP
203288_at		0.0001	0.0013 KIAA0355
203685_at		0.0001	0.0013 BCL2
203932_at	+	0.0001	0.0013 HLA-DMB
205513_at	+	0.0001	0.0013 TCN1
205614_x_at	+	0.0001	0.0013 MST1
205863_at	+	0.0001	0.0013 S100A12
208268_at		0.0001	0.0013 ADAM28
208306_x_at	+	0.0001	0.0013 HLA-DRB4
209075_s_at		0.0001	0.0013 NIFU
209167_at	+	0.0001	0.0013 GPM6B
209306_s_at		0.0001	0.0013 SWAP70
210004_at	+	0.0001	0.0013 OLR1
210448_s_at		0.0001	0.0013 P2RX5
210658_s_at		0.0001	0.0013 GGA2
210982_s_at	+	0.0001	0.0013 HLA-DRA
212382_at		0.0001	0.0013
212385_at		0.0001	0.0013
212579_at		0.0001	0.0013 KIAA0650
212970_at		0.0001	0.0013
212985_at	+	0.0001	0.0013
213353_at	+	0.0001	0.0013 ABCA5
213453_x_at	+	0.0001	0.0013 GAPD
215346_at		0.0001	0.0013 TNFRSF5
216218_s_at		0.0001	0.0013 PLCL2
218100_s_at		0.0001	0.0013 ESRRBL1
219734_at		0.0001	0.0013 FLJ20174
225065_x_at	+	0.0001	0.0013
225635_s_at		0.0001	0.0013
225640_at		0.0001	0.0013
226641_at		0.0001	0.0013
227817_at		0.0001	0.0013
228029_at		0.0001	0.0013 KIAA1982
229681_at		0.0001	0.0013

230803_s_at		0.0001	0.0013 DKFZP564B1162
230917_at		0.0001	0.0013
231793_s_at		0.0001	0.0013 CAMK2D
232739_at		0.0001	0.0013
235401_s_at		0.0001	0.0013 FREB
235753_at	+	0.0001	0.0013
237411_at		0.0001	0.0013 LOC153516
238516_at		0.0001	0.0013 BMPR2
242866_x_at		0.0001	0.0013
243030_at		0.0001	0.0013
266_s_at	+	0.0001	0.0013 CD24
35974_at	+	0.0001	0.0013 LRMP
203057_s_at		0.0001	0.0014 PRDM2
205105_at		0.0001	0.0014 MAN2A1
210763_x_at		0.0001	0.0014 LY117
212569_at		0.0001	0.0014 KIAA0650
212886_at		0.0001	0.0014 DKFZP434C171
221331_x_at		0.0001	0.0014 CTLA4
239292_at		0.0001	0.0014
202052_s_at	+	0.0001	0.0015 RAI14
207734_at		0.0001	0.0015 FLJ20340
209822_s_at		0.0001	0.0015 VLDLR
210299_s_at	+	0.0001	0.0015 FHL1
211771_s_at		0.0001	0.0015 POU2F2
219090_at		0.0001	0.0015 SLC24A3
219667_s_at		0.0001	0.0015 BANK
226258_at		0.0001	0.0015
227584_at	+	0.0001	0.0015
201061_s_at		0.0001	0.0017 EPB72
202863_at	+	0.0001	0.0017 SP100
204069_at	*	0.0001	0.0017 MEIS1
204118_at		0.0001	0.0017 CD48
204163_at		0.0001	0.0017 EMILIN
206245_s_at		0.0001	0.0017 NS1-BP
208651_x_at	+	0.0001	0.0017 CD24
209236_at		0.0001	0.0017
211796_s_at		0.0001	0.0017 TRB
212231_at		0.0001	0.0017 FBXO21
213600_at		0.0001	0.0017 KIAA0545
218237_s_at	+	0.0001	0.0017 SLC38A1
218614_at		0.0001	0.0017 FLJ10652
227606_s_at		0.0001	0.0017 KIAA1373

230877_at		0.0001	0.0018 IGHG3
231794_at		0.0001	0.0017 CTLA4
200068_s_at - HG-U133B		0.0001	0.0018 CANX
200953_s_at	+	0.0001	0.0018 CCND2
201810_s_at		0.0001	0.0018 SH3BP5
202421_at		0.0001	0.0018 IGSF3
203143_s_at		0.0001	0.0018 KIAA0040
203355_s_at	+	0.0001	0.0018 KIAA0942
203796_s_at	+	0.0001	0.0018 BCL7A
204670_x_at	+	0.0001	0.0018 HLA-DRB5
204891_s_at		0.0001	0.0018 LCK
207168_s_at	+	0.0001	0.0018 H2AFY
207269_at	+	0.0001	0.0018 DEFA4
208894_at	+	0.0001	0.0018 HLA-DRA
209827_s_at		0.0001	0.0018 IL16
211138_s_at		0.0001	0.0018 KMO
212311_at		0.0001	0.0018 KIAA0746
214575_s_at	+	0.0001	0.0018 AZU1
220059_at		0.0001	0.0018 BRDG1
221234_s_at		0.0001	0.0018 BACh2
221778_at		0.0001	0.0018 KIAA1718
221865_at		0.0001	0.0018
222477_s_at		0.0001	0.0018 TM7SF3
224609_at		0.0001	0.0018 CTL2
225136_at		0.0001	0.0018
227242_s_at		0.0001	0.0018
228083_at	+	0.0001	0.0018
228343_at		0.0001	0.0018 POU2F2
228551_at		0.0001	0.0018
229168_at		0.0001	0.0018
230551_at		0.0001	0.0018
231332_at		0.0001	0.0018
242774_at	+	0.0001	0.0018 SYNE-2
243154_at	+	0.0001	0.0018
243932_at		0.0001	0.0018
38269_at	+	0.0001	0.0018 PKD2
200650_s_at		0.0001	0.0019 LDHA
201825_s_at		0.0001	0.0019 LOC51097
205599_at		0.0001	0.0019 TRAF1
212660_at		0.0001	0.0019 KIAA0239
219029_at		0.0001	0.0019 FLJ21657
222520_s_at		0.0001	0.0019 ESRRBL1

222915_s_at	+	0.0001	0.0019 BANK
224520_s_at		0.0001	0.0019 MGC13168
227900_at	+	0.0001	0.0019
236796_at		0.0001	0.0019
236979_at	+	0.0001	0.0019
242388_x_at		0.0001	0.0019
242520_s_at		0.0001	0.0019
37831_at		0.0001	0.0019 KIAA0545
AFFX-HUMGAPDH/M33197_M_at	-	0.0001	0.0019 GAPD
HG-U133B			
205624_at	*	0.0001	0.002 CPA3
209369_at		0.0001	0.002 ANXA3
214761_at	+	0.0001	0.002 OAZ
218531_at		0.0001	0.002 FLJ21749
227568_at		0.0001	0.002
230834_at		0.0001	- 0.002
230986_at		0.0001	0.002
235023_at		0.0001	0.002
235982_at		0.0001	0.002 FCRH1
201362_at		0.0001	0.0021 NS1-BP
202080_s_at	+	0.0001	0.0021 KIAA1042
202606_s_at		0.0001	0.0021 TLK1
204205_at		0.0001	0.0021 MDS019
204351_at	+	0.0001	0.0021 S100P
205223_at		0.0001	0.0021 KIAA0645
205414_s_at		0.0001	0.0021 KIAA0672
208302_at		0.0001	0.0021 HB-1
209365_s_at	*	0.0001	0.0021 ECM1
211502_s_at		0.0001	0.0021 PFTK1
211883_x_at		0.0001	0.0021 CEACAM1
211889_x_at		0.0001	0.0021 CEACAM1
212012_at	+	0.0001	0.0021 D2S448
213370_s_at		0.0001	0.0021 DKFZP434L243
218589_at	+	0.0001	0.0021 P2Y5
219221_at		0.0001	0.0021 FLJ22332
223321_s_at		0.0001	0.0021 FGFR1
223894_s_at	+	0.0001	0.0021 FTS
224811_at		0.0001	0.0021
225019_at		0.0001	0.0021 CAMK2D
225917_at		0.0001	0.0021 DKFZp762B226
226043_at	+	0.0001	0.0021 AGS3
226252_at		0.0001	0.0021

226560_at		0.0001	0.0021
227998_at	*	0.0001	0.0021 MGC17528
229001_at		0.0001	0.0021
230689_at		0.0001	0.0021
231418_at		0.0001	0.0021 MS4A2
239054_at		0.0001	0.0021
243362_s_at	+	0.0001	0.0021 LEF1

Table 31a: In total 46 cases of ALL were analyzed. 44 of 46 cases (95.7%) were assigned to the correct ALL subtype in all pairwise comparisons. The sensitivity indicated for each subgroup indicates the percentage of cases of the specific subgroup identified correctly in all pairwise comparisons. The specificity indicates for each subgroup the percentage of correct assignments to this subgroup.

5

	ALL t(4;11)	ALL t(8;14)	ALL B not Ph	ALL Ph	T-ALL	total	sensitivity %	specificity %
ALL t(4;11)	9					9	100.00	100.00
ALL t(8;14)		4				4	100.00	100.00
ALL B not Ph			6	1		9	88.89	88.89
ALL Ph			1	14		15	93.33	93.33
T-ALL					9	9	100.00	100.00
total	9	4	9	15	9	46		

10

Table 31b: In total 184 individual assignments of ALL were analyzed. 182 of 184 assignments (98.9%) were correct. The sensitivity indicated for each subgroup indicates the percentage of correct assignments for cases of the specific subgroup in pairwise comparisons. The specificity indicates for each subgroup the percentage of correct assignments to this subgroup.

5

	ALL t(4;11)	ALL t(8;14)	ALL Ph	B	not ALL	Ph	T-ALL	total	sensitivity %	Specificity %
ALL t(4;11)	36							36	100.00	100.00
ALL t(8;14)		16						16	100.00	100.00
ALL B not Ph			35	1			36	97.22	97.22	
ALL Ph			1	59	60	1	60	98.33	98.33	
T-ALL					36	36	36	100.00	100.00	
total	36	16	36	60	36	36	184			

Table 32: Analysis of 5 ALL subtypes according to the method described by Golub et al.

ALL

	n
ALL t(4;11)	9
ALL t(8;14)	4
ALL B not Ph	9
ALL Ph	15
T-ALL	9

ALL t(4;11) vs. all other

samples: 9 / 37

Accuracy	1	p	decision limit	gene symbol
Confidence	1			
Gene	signal-to-noise	p	decision limit	gene symbol
219033_at	3.20704240055607	0*	2553.55	FLJ21308
219463_at	2.92935553285382	0		C20orf103
204069_at	2.82114201903624	0		MEIS1
237431_at	2.55145965416011	0		
205899_at	2.08001706361176	0		CCNA1
221969_at	2.05226504657001	0		PAX5
225592_at	1.98551092155834	0		NRM
242414_at	1.90103345468382	0		
225563_at	1.85734510779608	0		
201105_at	1.84845429911833	0		LGALS1
243756_at	1.82938790694615	0		
213894_at	1.79258061939732	0		KIAA0960
215925_s_at	1.74909667158721	0		
228083_at	1.74681828228852	0		
204044_at	1.72555848313614	0		QPRT
209170_s_at	1.69865585409382	0		GPM6B
209168_at	1.67497314565832	0		GPM6B
210934_at	1.66143224232084	0		BLK
238750_at	1.59639718466905	0		
224681_at	1.58202928459614	0		GNA12

ALL t(4;11) vs. ALL t(8;14)	samples: 9 / 4			
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
210045_at	6.76734853184964	0*	142.15	IDH2
240106_at	6.10571301118426	0		
202853_s_at	-5.88804457870992	0		RYK
242434_at	-5.60754470569171	0		
237431_at	5.31661820706767	0		
201540_at	4.94655082712075	0		FHL1
215855_s_at	4.71299810202736	0		
212357_at	4.18767818184794	0		KIAA0280
204798_at	4.12313508850913	0		MYB
226795_at	4.12248256776444	0		
77508_r_at	4.0317985345148	0		FLJ23282
46142_at	3.95748459279267	0		FLJ12681
225277_at	3.7552029934786	0		
210934_at	3.72127171897839	0		BLK
215537_x_at	3.53324247477066	0		
232201_at	3.50091671488931	0		NKD2
214505_s_at	3.42260996379197	0		FHL1
244261_at	3.40910490910101	0		
208614_s_at	3.34565043119022	0		FLNB
210298_x_at	3.30171221592859	0		FHL1

ALL t(4;11) vs. ALL B not Ph	samples: 9 / 9			
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
237431_at	5.31661820706767	0*	49	
219033_at	3.19032095561144	0		FLJ21308
219463_at	2.69567768562793	0		C20orf103
204069_at	2.54127866831197	0		MEIS1
201105_at	2.30596776500018	0		LGALS1
200907_s_at	2.19034049161844	0		KIAA0992
242414_at	2.08870062415486	0		
222492_at	-2.04226084466602	0		FLJ21324
230441_at	-2.03717805375485	0		
235291_s_at	2.0210425168076	0		
225592_at	2.01329642963674	0		NRM
200906_s_at	1.9632986862999	0		
201153_s_at	1.93254941630797	0		MBNL
201152_s_at	1.93227192981893	0		MBNL
241985_at	-1.91875000661653	0		
213894_at	1.89533012552966	0		KIAA0960
243756_at	1.82938790694615	0		
225563_at	1.82046495626766	0		
232231_at	1.8138577510169	0		
240581_at	1.80942575017411	0		

ALL t(4;11) vs. ALL Ph	samples: 9 / 15			
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
204069_at	3.31118886883646	0*	482.55	MEIS1
219033_at	3.24786485857293	0		FLJ21308
219463_at	2.78353259146178	0		C20orf103
221969_at	2.4416835946504	0		PAX5
201874_at	2.38057857279198	0		FLJ21047
209170_s_at	2.31526351178702	0		GPM6B
233500_x_at	2.23629715560156	0		LLT1
205899_at	2.23375311954146	0		CCNA1
242414_at	2.21567202901383	0		
205821_at	2.10144186601662	0		D12S2489E
205055_at	2.04951650013049	0		ITGAE
209168_at	2.02899949049115	0		GPM6B
226939_at	1.99568402107224	0		
209354_at	-1.9938191217443	0		TNFRSF14
200906_s_at	1.9632986862999	0		
225563_at	1.88712595721941	0		
237431_at	1.87880985981148	0		
34210_at	-1.86187594200254	0		CDW52
202853_s_at	-1.84984316383277	0		RYK
209167_at	1.84829764568262	0		GPM6B

ALL t(4;11) vs. T-ALL	samples: 9 / 9			
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
221969_at	5.83664657385464	0*	1301	PAX5
237431_at	5.31661820706767	0		
213772_s_at	4.80540935532116	0		GGA2
219463_at	3.9253737114322	0		C20orf103
210934_at	3.72127171897839	0		BLK
242292_at	-3.53231266693437	0		
226496_at	3.49024496949904	0		
244261_at	3.40910490910101	0		
205640_at	3.04306419050975	0		ALDH3B1
219033_at	3.03434195473282	0		FLJ21308
209168_at	3.02932118514235	0		GPM6B
205821_at	2.9956567374574	0		D12S2489E
235706_at	2.99518505957364	0		CPM
225592_at	2.98114633774562	0		NRM
225314_at	-2.87525509857994	0		
209170_s_at	2.832580891342	0		GPM6B
215925_s_at	2.79328349720245	0		
204069_at	2.67025815490556	0		MEIS1
210192_at	2.63764031456982	0		ATP8A1
217080_s_at	2.60699026264913	0		HOMER-2B

ALL t(8;14) vs. all other	samples: 4 / 42			
accuracy	1	p	decision limit	gene symbol
confidence	0.920758831240362			
gene	signal-to-noise	p	decision limit	gene symbol
225277_at	-2.57998811180236	0		
228211_at	-2.14623380341388	0*	20.8	
202249_s_at	-1.96332308011424	0*	1	H326
221834_at	-1.9031437121116	0		
202262_x_at	-1.89325979398387	0		DDAH2
215537_x_at	-1.86843810729553	0		
209253_at	-1.83062488265555	0		SCAM-1
218836_at	1.75015142111032	0*	431.25	FLJ22638
201540_at	-1.7433648326086	0		FHL1
203373_at	-1.73135591115253	0		STATI2
212357_at	-1.70867340748188	0		KIAA0280
229061_s_at	1.637709601518	0		SLC25A13
211540_s_at	-1.62480264702951	0		RB1
213639_s_at	-1.6005915843515	0		KIAA0557
207971_s_at	-1.60022833182646	0		KIAA0582
202328_s_at	-1.58949139934067	0		PKD1
236019_at	-1.57756633888103	0		
36612_at	-1.57219062906198	0		KIAA0280
211031_s_at	-1.56936126526028	0		CYLN2

ALL t(8;14) vs. ALL B not Ph		samples: 4 / 9		
accuracy	1	p	decision limit	gene symbol
confidence	1,			
gene	signal-to-noise	p	decision limit	gene symbol
231567_s_at	-2.72106559758946	0*	34.3	TSP-NY
225277_at	-2.51129165288142	0		
236019_at	-2.39137207272003	0		
239835_at	2.1931044914088	0		KIAA1842
235287_at	-2.11679606735121	0.01		
221834_at	-2.07908926017389	0.01		
224221_s_at	-2.01560021968657	0.01		VAV3
202249_s_at	-2.00760725399781	0		H326
222275_at	-1.99241461922196	0.01		
231181_at	1.9495774287402	0		
202137_s_at	-1.92788330147706	0.01		BS69
212535_at	-1.92074458469524	0.01		
244230_at	-1.90852603079528	0		
215622_x_at	1.89164878686732	0.01		HSPC226
233813_at	-1.8799760260639	0.01		
209891_at	1.87886429835728	0		AD024
203373_at	-1.86193326506748	0		STAT12
213504_at	1.8188709452285	0		MOV34-34KD
237006_at	-1.7948046900018	0.02		
AFFX-r2-Hs18SrRNA-M_x_at - HG-	1.2766621379286	0.01		
U133B				

ALL t(8;14) vs. ALL Ph	samples: 4 / 15			
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
204663_at	-3.923285216392	0*	80.55	ME3
203373_at	-3.79361888147031	0		STATI2
207971_s_at	-3.75632756767036	0		KIAA0582
221634_at	-3.73210732395713	0		
212535_at	-3.35180803492209	0		
210487_at	-2.66400596339357	0		DNTT
226607_at	-2.65303285070543	0		L3MBTL
214505_s_at	-2.30002142127038	0		FHL1
226545_at	-2.26350222846019	0		
201540_at	-2.21889045310099	0		FHL1
209253_at	-2.17983750831107	0		SCAM-1
228496_s_at	-2.17784383479245	0		CRIM1
213854_at	-2.14963630962421	0		SYNGR1
228211_at	-2.14770747938169	0		
212012_at	-2.10857376713896	0		D2S448
208217_at	-2.10769716540219	0		GABRR2
202519_at	-2.05798709970069	0		MONDOA
218836_at	2.05747195088222	0		FLJ22638
211031_s_at	-2.05686503189171	0		CYLN2
50277_at	1.4804958933411	0		GGA1

ALL t(8;14) vs. T-ALL		samples: 4 / 9		
accuracy	1	p	decision limit	gene symbol
confidence	,1			
gene	signal-to-noise	p	decision limit	gene symbol
213772_s_at	4.99941703918842	0*	105.35	GGA2
236019_at	-4.8835710129593	0.01		
225277_at	-4.63399536600695	0		
40148_at	3.56542456382539	0.01		APBB2
228211_at	-3.35861431980337	0.01		
201334_s_at	3.32612092220108	0		ARHGEF12
201417_at	-2.74359054965603	0		
206241_at	-2.66958809534806	0		KPNA5
208918_s_at	2.59071326340578	0		FLJ13052
210038_at	-2.55792113825771	0		
225735_at	-2.54773299400117	0		
209253_at	-2.33749346955264	0		SCAM-1
202262_x_at	-2.29867528817227	0		DDAH2
225129_at	2.29232308514395	0.01		MDS026
221969_at	2.278395672233	0		PAX5
225080_at	2.24115131588386	0.01		MYO1C
218338_at	-2.22116851483018	0.01		EDR1
208664_s_at	-2.20362132175544	0.01		TTC3
201029_s_at	-2.14618908100153	0		MIC2
56256_at	1.43796973813133	0		LOC51092

ALL_B not Ph vs. all other	samples: 9 / 37			
accuracy	0.934782608695652			
confidence	0.902657186900126			
failed:	5,7,8			
gene	signal-to-noise	p	decision limit	gene symbol
219358_s_at	-1.04393215326702	0.01*	1	CENTA2
220744_s_at	-1.00349163214942	0*	1	WDR10
203808_at	-0.907795727801968	0		AKT2
243228_at	0.879849065993121	0		
218517_at	-0.867959639957627	0		FLJ22479
226646_at	0.864565503015451	0*	490.45	KLF2
224739_at	0.839978529078003	0		MG61
219036_at	-0.833911794382181	0		BITE
218464_s_at	-0.832082954669612	0.01		FLJ10700
211953_s_at	-0.830459962940188	0		KPNB3
241383_at	-0.819553908934904	0		
207403_at	-0.812859958493534	0		IRS4
210519_s_at	-0.8016666674223177	0		
214144_at	-0.796475066163317	0		POLR2D
209135_at	-0.787608359617365	0		ASPH
218543_s_at	0.773154455437408	0*	765.05	FLJ22693
34210_at	0.555729083194618	0		CDW52

ALL B not Ph vs. ALL Ph	samples: 9 / 15		
accuracy	0.9166666666666667		
confidence	1		
failed:	3,18		
gene	signal-to-noise	p	decision limit
219358_s_at	-1.52735607926994	0	CENTA2
241383_at	-1.07499870203752	0.01	
213895_at	-1.05505220750298	0	EMP1
202123_s_at	-1.02481061931947	0*	753.7
205911_at	-1.0236634987836	0.01	PTHR1
242223_at	1.02343172223498	0.01	
211709_s_at	-1.01491744255679	0	SCGF
234839_at	-1.00185285072786	0	
212150_at	-0.996731200580515	0	KIAA0143
221991_at	-0.987741661696868	0	NXPH3
218543_s_at	0.973909033712243	0	FLJ22693
201874_at	0.966766364385792	0	FLJ21047
212188_at	-0.947998533949464	0	LOC115207
207520_at	-0.936622132674122	0	
213979_s_at	-0.935519171149617	0	CTBP1
229745_x_at	-0.93424475879621	0	
216680_s_at	-0.934196756237652	0.01	EPHB4
202572_s_at	0.924395823520243	0	KIAA0964
243228_at	0.916138491705783	0	

ALL B not Ph vs. T-ALL		samples: 9 / 9		
accuracy	1	p	decision limit	gene symbol
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
242292_at	-3.53231266693437	0*	19.4	
36566_at	2.04687603382912	0		CTNS
230636_s_at	1.96129371358941	0		BTEB1
266_s_at	1.95685220231101	0		CD24
209771_x_at	1.95325312023269	0		CD24
219631_at	-1.90940390225071	0		FLJ12929
202113_s_at	1.86969444770264	0		SNX2
216379_x_at	1.84446878357139	0		
221969_at	1.82924887172424	0		PAX5
229487_at	1.78170685853126	0		
208650_s_at	1.77571318786079	0		CD24
218464_s_at	-1.71465707824422	0		FLJ10700
213944_x_at	1.69297405468728	0		
226496_at	1.65125933296341	0		
202206_at	-1.58502966518677	0		ARL7
205504_at	1.58481348793145	0		BTK
213539_at	-1.56405807954932	0		CD3D
211101_x_at	1.55958748994576	0		LILRA2
244876_at	1.55727218904507	0		
209772_s_at	1.54041193817483	0		CD24

ALL Ph vs. all other	samples: 15 / 31			
accuracy	0.934782608695652			
confidence	0.864155721068077			
failed:	5,11,37			
gene	signal-to-noise	p	decision limit	gene symbol [*]
202123_s_at	1.03184989278993	0		ABL1
201874_at	-0.922781388634418	0		FLJ21047
204501_at	0.896802057215648	0		NOV
212998_x_at	0.86615498180542	0		HLA-DQB1
224833_at	-0.858830478869203	0*	396.95	ETS1
222154_s_at	0.853355151564312	0		DKFZP564A2416
222237_s_at	0.842490839365056	0		
231887_s_at	0.818989313012035	0		KIAA1274
206995_x_at	0.814915994355934	0		SREC
206940_s_at	0.805187827741759	0		POU4F1
228737_at	-0.794850815744375	0		C20orf100
214321_at	0.787185980142624	0		NOV
212365_at	0.782772195022069	0		MYO1B
204030_s_at	0.779040391109499	0		SCHIP1
207971_s_at	0.777645713400436	0		KIAA0582
224772_at	0.777324945979331	0		MGC14961
230659_at	0.775582345606179	0		KIAA0212
214051_at	-0.763853883412362	0		TMSNB
231897_at	0.756283108145232	0		
206302_s_at	0.754443263514809	0		NUDT4

ALL Ph vs. T-ALL	samples: 15 / 9			
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
218224_at	-2.4418494296856	0		PNMA1
213854_at	2.14963630962421	0		SYNGR1
221969_at	2.06978634038245	0*	152.35	PAX5
205101_at	1.84182814954198	0		MHC2TA
213539_at	-1.83994967875006	0		CD3D
228988_at	-1.79658055608971	0		ZNF6
208894_at	1.79489847703276	0		HLA-DRA
209604_s_at	-1.75648531255811	0		GATA3
209619_at	1.72743796589982	0		CD74
209771_x_at	1.69086499548436	0		CD24
210982_s_at	1.68104679025052	0		HLA-DRA
229487_at	1.66237077940113	0		
235706_at	1.65050775066494	0		CPM
226878_at	1.64629305544324	0		
219631_at	-1.6447182870532	0		FLJ12929
216379_x_at	1.61950446576807	0		
232234_at	-1.6009007845449	0		C20orf24
210116_at	-1.58593866198308	0		SH2D1A
224772_at	1.58464619249453	0		MGC14961
213944_x_at	1.58085800202538	0		

T-ALL vs. all other	samples: 9 / 37			
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
218224_at	1.9746486763803	0		PNMA1
219631_at	1.74096689257481	0		FLJ12929
213539_at	1.72260640123424	0		CD3D
209771_x_at	-1.54682027770245	0		CD24
216379_x_at	-1.50086383881878	0		HLA-DRA
208894_at	-1.4723749670674	0		CD3G
206804_at	1.44192284369386	0		CD24
266_s_at	-1.41281622043848	0		C20orf24
232234_at	1.4114153057648	0		HLA-DRA
210982_s_at	-1.40110964085237	0		GGA2
213772_s_at	-1.38475219732458	0		CPM
235706_at	-1.37948942896001	0		CD19
206398_s_at	-1.37387052076155	0		ZNF6
242292_at	1.3716037079612	0		PAX5
228988_at	1.36889729345744	0		SNX2
221969_at	-1.35174546838558	0*	149.65	
202113_s_at	-1.32897344000246	0		
202746_at	1.32364323412114	0		
226496_at	-1.30740184360227	0		

Table 33: Analysis of 5 ALL subgroups according to the method described by Westfall & Young. The 23 significant genes are listed. The raw p value as well as the adjusted p value are shown. Furthermore it is indicated whether the genes were also identified as discriminative by the method described by Golub et al. (* most important gene in pairwise comparisons, + one of the top 20 significant genes)

5

geneID	Golub	rawp	adjp	Gene symbol
219463_at	+	0.0001	0.0042	C20orf103
204069_at	*	0.0001	0.0046	MEIS1
219033_at	*	0.0001	0.0051	FLJ21308
221969_at	*	0.0001	0.0071	PAX5
205899_at	+	0.0001	0.0081	CCNA1
237431_at	*	0.0001	0.0088	
242414_at	+	0.0001	0.0091	
225563_at	+	0.0001	0.0122	
215925_s_at	+	0.0001	0.0157	
209168_at	+	0.0001	0.0168	GPM6B
204044_at	+	0.0001	0.0170	QPRT
225592_at	+	0.0001	0.0174	NRM
228083_at	+	0.0001	0.0179	
218224_at	+	0.0001	0.0190	PNMA1
213539_at	+	0.0001	0.0195	CD3D
213894_at	+	0.0001	0.0197	KIAA0960
201105_at	+	0.0001	0.0199	LGALS1
219631_at	+	0.0001	0.0199	FLJ12929
209170_s_at	+	0.0001	0.0201	GPM6B
243756_at	+	0.0001	0.0214	
209822_s_at		0.0001	0.0254	VLDLR
228988_at	+	0.0001	0.0454	ZNF6
235749_at		0.0002	0.0477	

Table 34a: In total 173 cases of AML were analyzed. 160 of 174 cases (92.5%) were assigned to the correct AML subtype in all pairwise comparisons. The sensitivity indicated for each subgroup indicates the percentage of cases of the specific subgroup identified correctly in all pairwise comparisons. The specificity indicates for each subgroup the percentage of correct assignments to this subgroup.

5

	+8	other	complex	normal	t(8;21)	t(15;17)	inv(16)	MLL	total	sensitivity %	specificity %
+8	6			4					10	60.00	100.00
other		3		1	1				5	60.00	100.00
complex			33	3					36	91.67	94.29
normal				1	59				2	62	95.16
t(8;21)						13			13	100.00	100.00
t(15;17)						20			20	100.00	100.00
inv(16)							12		12	100.00	100.00
MLL				2				13	15	86.67	86.67
total	6	3	35	69	13	20	12	15	173		

Table 34b: In total 1211 individual assignments of AML were analyzed. 1198 of 1211 assignments (98.9%) were correct. The sensitivity indicated for each subgroup indicates the percentage of correct assignments for cases of the specific subgroup in pairwise comparisons. The specificity indicates for each subgroup the percentage of correct assignments to this subgroup.

5

	+8	other	complex	normal	t(8;21)	t(15;17)	inv(16)	MLL	total	sensitivity %	specificity %
+8	66			4					70	94.29	100.00
other		33		1	1				35	94.29	100.00
complex			249	3					252	98.81	99.20
normal				1	132				2	434	99.54
t(8;21)					91				91	100.00	100.00
t(15;17)						140			140	100.00	100.00
inv(16)							84		84	100.00	100.00
MLL				2				105	105	98.10	98.10
total	66	33	251	442	91	140	84	105	1211		

Table 35: Analysis of 8 AML subtypes according to the method described by Golub et al.

AML subtype	n
trisomy 8	10
other aberrant	5
complex	36
normal	62
t(8;21)	13
t(15;17)	20
inv(16)	12
MLL	15

trisomy 8 vs. all other	samples: 10 / 163	accuracy	0.959537572254335	confidence	0.569726638054273	failed:	1,2,9,10,32,44,50	gene	signal-to-noise	p	decision limit	gene symbol
214394_x_at	1.01312549146188	0						FLJ20897				
222166_at	-0.966941507782627	0										
242975_s_at	-0.84543459151348	0						GNAS				
218549_s_at	0.837748897801293	0*	1095.85					LOC51115				
218642_s_at	0.837443970437429	0						MGC2217				
212250_at	0.837142769828465	0										
203110_at	0.812826558097073	0						PTK2B				
219518_s_at	-0.798960392573077	0.01						FLJ22637				
237068_at	-0.76378369742971	0										
206781_at	-0.759613817823006	0						DNAJC4				
224804_s_at	-0.756694932705637	0.01						FLJ00005				
235647_at	-0.746385695306755	0*	1									
203007_x_at	0.741371207542559	0										
212449_s_at	0.729872362915738	0						LYPLA1				
231981_at	0.722528507843912	0*	199.8									
218482_at	0.71984358195818	0						DC6				
224076_s_at	0.717538242394189	0						WHSC1L1				
231101_at	-0.7149698250145	0						PPP2R5E				

trisomy 8 vs. other aberrant	samples: 10 / 5				
accuracy	1				
confidence	1				
gene	signal-to-noise	p	decision limit	gene symbol	
229848_at	-2.61497492874017	0*	36.7	ZNF10	
239538_at	-2.22698957925109	0			
230713_at	-2.16807291296049	0			
209490_s_at	-2.08613392690798	0		PPT2	
229362_at	-2.0821284659189	0			
225073_at	-2.06488846603302	0		HSPC232	
239699_s_at	-2.02729155150144	0			
242363_at	-1.94643377690021	0			
201974_s_at	-1.88600099933531	0		LOC51622	
219027_s_at	-1.866639067868364	0		MYO9A	
234643_x_at	1.78480980429735	0			
236837_x_at	-1.7783166983573	0			
226783_at	-1.75409747751331	0			
238039_at	-1.74203897189399	0.01			
224044_at	-1.72117511206513	0.01		FLJ11040	
226324_s_at	-1.71772128724622	0		SLB	
227587_at	-1.71651011254536	0		MGC15906	
229637_at	-1.71361022272893	0.01			
227744_s_at	-1.70786273052662	0		HNRPD	
635_s_at	1.25062226167699	0		PPP2R5B	

trisomy 8 vs. complex accuracy confidence gene	samples: 10 / 36		p	decision limit	gene symbol
222229_x_at	1.23332137897808	0			
208697_s_at	1.15066098039301	0			EIF3S6
205849_s_at	1.14869307530221	0			UQCRB
212586_at	1.11153173777253	0*	1231.4		ARTS-1
208646_at	1.07422424644875	0			
230795_at	-1.06732853628123	0			H4F2
202746_at	-1.03422849717783	0			
226545_at	-1.00972156245463	0*	100.15		
222166_at	-0.999828982909011	0*	1		
210715_s_at	-0.978857795907469	0*	573.3		SPINT2
228652_at	-0.974511468277957	0			
217979_at	-0.973647566321829	0*	234.35		NET-6
201548_s_at	-0.970651188910704	0*	289.85		PLU-1
202747_s_at	-0.952100249128964	0			ITM2A
201602_s_at	-0.951073671804128	0			PPP1R12A
205674_x_at	-0.945871996779656	0			FXYD2
244740_at	-0.942099475768156	0			
219518_s_at	-0.938970502867646	0			FLJ22637
227249_at	-0.931085853722028	0			NUDE1

trisomy 8 vs. normal	samples: 10 / 62			
accuracy	0.9444444444444444			
confidence	1			
failed:	1,2,3,5			
gene	signal-to-noise	p.	decision limit	gene symbol
214394_x_at	1.16270137582694	0		FLJ20897
235124_at	-1.01432223685267	0		
203007_x_at	0.983414984588329	0		
206781_at	-0.970185909793454	0		DNAJC4
242975_s_at	-0.968085578079267	0		GNAS
203110_at	0.964568800558985	0		PTK2B
212251_at	0.940237396721025	0*	4073.8	
225406_at	-0.932943214378223	0		TSG
234726_s_at	-0.900642735364519	0		
218482_at	0.893526812115568	0		DC6
237291_at	-0.889981273455646	0		
235647_at	-0.884166779739501	0		
236837_x_at	-0.866101703732076	0.01		
222166_at	-0.864343877506541	0		
225889_at	-0.864142405574917	0		
217994_x_at	-0.85609014416877	0		
203602_s_at	-0.841071963439903	0		ZNF151
228092_at	-0.837138335753897	0		
224804_s_at	-0.83110664616695	0		FLJ00005
212250_at	0.827294640416809	0		

trisomy 8 vs. t(8;21)	samples: 10 / 13			
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
228827_at	-2.03460798747208	0*	162.15	
203188_at	1.98171895993959	0		B3GNT6
209522_s_at	1.87499941760774	0		CRAT
50221_at	1.77237042593137	0		
212586_at	1.70313290894867	0		ARTS-1
217816_s_at	1.69811663165145	0		pcnp
219084_at	1.68534097481951	0		NSD1
241370_at	1.66453119103938	0		
221581_s_at	1.64609943226078	0		WBSCR5
205528_s_at	-1.64467496425566	0		CBFA2T1
211341_at	-1.63310072579237	0		POU4F1
212250_at	1.62854737716103	0		
206940_s_at	-1.60737424398258	0		POU4F1
205529_s_at	-1.591491111654	0		CBFA2T1
213150_at	1.57881564631984	0		HOXA10
214394_x_at	1.57039311243451	0		FLJ20897
212895_s_at	1.56878968456679	0		ABR
218341_at	1.53928870336148	0		FLJ11838
204249_s_at	1.52597204656408	0		LMO2
214651_s_at	1.52240931149048	0		HOXA9

trisomy 8 vs. t(15;17)	samples: 10 / 20			
accuracy	1	p	decision limit	gene symbol
confidence	1			
gene	signal-to-noise			
214450_at	-3.0865086945171	0*	1926.7	CTSW
212953_x_at	-2.71319553382926	0		CALR
236787_at	-2.4273500798775	0		
200952_s_at	-2.39696270141848	0		CCND2
205624_at	-2.38480346275743	0		CPA3
38487_at	-2.38251622694176	0		FLJ12442
205614_x_at	-2.24846130719191	0		MST1
206761_at	-2.20501899975366	0		TACTILE
216320_x_at	-2.16690689445934	0		
224794_s_at	-2.14479331910386	0		LOC51148
233072_at	-2.07721746169547	0		KIAA1857
221004_s_at	-2.05892662897696	0		ITM3
227326_at	-2.04924504239987	0		
221980_at	-2.01752809990056	0		
225547_at	1.98126007880124	0		
210145_at	1.95455412087558	0		PLA2G4A
212509_s_at	-1.92046303571342	0		
209344_at	-1.90906303754685	0		TPM4
201029_s_at	-1.87538506046111	0		MIC2

trisomy 8 vs. inv(16)	samples: 10 / 12			
accuracy	1	p	decision limit	gene symbol
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
233138_at	-3.4735123827114	0*	54.25	
209365_s_at	-3.00986865470169	0		ECM1
202283_at	-2.6160707896185	0		SERPINF1
218942_at	2.45751904192227	0		FLJ22055
201828_x_at	2.21365274281998	0		CXX1
200951_s_at	-2.02357943949022	0		CCND2
226120_at	2.01082485261142	0		LOC123016
203188_at	1.9379696222037	0		B3GNT6
202085_at	1.9147903697218	0		TJP2
206135_at	-1.90877055638373	0		KIAA0535
210024_s_at	1.90335978018863	0		UBE2E3
204661_at	-1.83776082826379	0		CDW52
241525_at	-1.83006374766269	0		
208710_s_at	1.80896001968559	0		AP3D1
34210_at	-1.75572696362264	0		CDW52
201497_x_at	-1.74852845185764	0		MYH11
212236_x_at	-1.74679406476776	0		
213810_s_at	-1.69077455623534	0		FLJ10342
212250_at	1.62885302351785	0		
202370_s_at	1.61951331078439	0		CBFB

trisomy 8 vs. MLL	samples: 10 / 15			
accuracy	1	p	decision limit	gene symbol
confidence	0.8689072208975			
gene	signal-to-noise	p	decision limit	gene symbol
200056_s_at - HG-U133A	1.60303643777462	0		C1D
212250_at	1.47262825515036	0		
228024_at	1.43968630786794	0		PAK1
205355_at	1.39534301157978	0		ACADSB
225700_at	1.39419450937928	0		
234726_s_at	-1.36257922965513	0		
202619_s_at	1.34323877280623	0		PLOD2
205453_at	1.29520111839967	0		HOXB2
202823_at	1.28255326311509	0		TCEB1
210749_x_at	1.26893758929818	0		DDR1
227786_at	1.24020773870069	0		TRAP25
212479_s_at	1.23922427261637	0*	437.3	FLJ13910
219312_s_at	1.21983738431425	0		RINZF
218172_s_at	1.21403337241271	0*	285.95	PRO2577
200867_at	1.2110165320696	0*	531	
202956_at	1.21043821718201	0*	550.6	BIG1
213902_at	1.19710457307816	0		ASAII
239597_at	-1.19444081572455	0		
214789_x_at	1.19367799101574	0		SRP46
203053_at	1.18683041233911	0		BCAS2

other aberrant vs. all other	samples: 5 / 168			
accuracy	0.994219653179191			
confidence	0.899486235418654			
failed:	4			
gene	signal-to-noise	p	decision limit	gene symbol
233328_x_at	-1.52904798962408	0.01		
219156_at	1.27140814977495	0		FLJ11271
214310_s_at	-1.27139871979195	0		ZFPL1
229003_x_at	-1.20449873883071	0		
213725_x_at	1.1911680827765	0		
236648_at	1.15777539407154	0*	1	
226634_at	1.15695756502745	0		
224664_at	1.14829275512581	0		
219337_at	-1.09306764196133	0		FLJ20584
228660_x_at	1.09254562955252	0*	82	SEMA4F
217375_at	-1.08474018637782	0		
219027_s_at	1.0790791377144	0		MYO9A
239538_at	1.07873188809285	0		
203796_s_at	1.04936325547633	0		BCL7A
211918_x_at	-1.04651632950823	0.01		PLAC3
241795_at	-1.04488187252	0		
222147_s_at	-1.02048867081398	0.01		
227206_at	-1.01633702093738	0.01		
635_s_at	-1.01612668262432	0		PPP2R5B

other aberrant vs. complex	samples: 5 / 36		
accuracy	0.975609756097561		
confidence	0.990141898103344		
failed:	2		
gene	signal-to-noise	p	decision limit
225804_at	1.56382089574999	0	
211819_s_at	-1.45297162934509	0*	1
233328_x_at	-1.44097598487297	0*	1
229003_x_at	-1.40901327014506	0*	1
223712_at	1.36997409793585	0	
635_s_at	-1.34942029903122	0	
231002_s_at	1.3258291286036	0	
241734_at	1.32533459318655	0	
201530_x_at	1.3093371019822	0	
211918_x_at	-1.30264105037178	0.01	
222229_x_at	1.214222183319	0	
231945_at	-1.2091074222176	0.01	
202150_s_at	-1.2052224977219	0	
212171_x_at	-1.20353762848401	0	
214310_s_at	-1.19546833367549	0	
219337_at	-1.19331909893746	0	
235263_at	1.19244840508646	0	
233195_at	-1.19077762820993	0	
210817_s_at	1.17387606136153	0	

other aberrant vs. normal	samples: 5 / 62		
accuracy	0.985074626865672		
confidence	0.991986319540221		
failed:	4		
gene	signal-to-noise	p	decision limit
233328_x_at	-1.9106472582954	0*	1
220924_s_at	1.36395677335271	0	SLC38A2
213725_x_at	1.33852421412964	0*	1096.35
229003_x_at	-1.33766416205182	0	
207057_at	1.32428111403211	0	SLC16A7
239393_at	1.30248902092406	0	
218041_x_at	1.28800254801096	0	PRO1068
219156_at	1.27488096632736	0	FLJ11271
227206_at	-1.24583383572442	0	
217375_at	-1.22806408433652	0.01	
219337_at	-1.22223242666913	0.01	FLJ20584
214894_x_at	1.21435713598714	0	MACF1
225452_at	1.19358949672009	0	PPARBP
205316_at	1.18925500392873	0	SLC15A2
212469_at	1.17704907364629	0	IDN3
214310_s_at	-1.176580899867	0.01	ZFPL1
226634_at	1.15416325511173	0	
234132_at	-1.14588852496026	0.01	
215115_x_at	-1.14294381059057	0	NTRK3
45633_at	0.924726636126963	0	FLJ13912

other aberrant vs. t(8;21)	samples: 5 / 13			
accuracy	1	p	decision limit	gene symbol
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
221770_at	7.99150022255116	0*	55.8	RPE
205607_s_at	5.76670522441814	0		LOC57147
225670_at	3.48256305910835	0		
34689_at	3.47855359314813	0		TREX1
203796_s_at	3.25650613162099	0		BCL7A
226634_at	3.21064553321956	0		
232127_at	2.70698092772246	0.01		
200659_s_at	2.68716126436031	0		PHB
202288_at	2.6425819500005	0		FRAP1
234005_x_at	2.64219114616805	0		STK36
212309_at	2.52957598578167	0		CLASP2
221206_at	2.4774418396665	0		FLJ21459
222163_s_at	2.44259488401336	0		MGC5347
210128_s_at	2.40486023166818	0		LTB4R
242448_at	2.40485463677367	0		
212895_s_at	2.38453513890117	0		ABR
213313_at	2.35617502073221	0		GAPCENA
220796_x_at	2.33914050862301	0		FLJ14251
242363_at	2.29793881298951	0		
225902_at	2.28202551140514	0		

other aberrant vs. t(15;17)	samples: 5 / 20			
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
213716_s_at	5.68177086653034	0*	124.75	SECTM1
235483_at	3.71724867723655	0		
224664_at	3.45875495264879	0		
214310_s_at	-3.345175974803	0		ZFPL1
38487_at	-3.26848789132101	0		FLJ12442
210128_s_at	3.21387420114625	0		LTB4R
214450_at	-3.16199946091496	0		CTSW
209428_s_at	-2.91976796793381	0		ZFPL1
233328_x_at	-2.90760586187832	0		
201034_at	2.88463519708491	0		ADD3
212953_x_at	-2.71444362815032	0		CALR
201753_s_at	2.7070306360752	0		ADD3
208629_s_at	-2.67288815920275	0		HADHA
205668_at	2.67287531876386	0		LY75
229937_x_at	2.57076096076482	0		
227701_at	2.49972617912329	0		
203948_s_at	-2.49051133555807	0		MPO
219280_at	2.49000744284001	0		WDR9
227999_at	2.46891417509171	0		LOC170394

other aberrant vs. inv(16)	samples: 5 / 12			
accuracy	1	p	decision limit	gene symbol
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
227224_at	4.52730002135185	0*	67.25	
212469_at	4.42589960567721	0		IDN3
229003_x_at	-3.90005268853897	0		
239538_at	3.74361173339624	0		
216399_s_at	3.5206821287331	0		
223471_at	3.22276962259045	0		
201338_x_at	3.16855282128268	0		GTF3A
231926_at	3.15052042879849	0		
202370_s_at	3.09376701617797	0		CBFB
224664_at	3.04111626168471	0		
204858_s_at	-2.96720397750981	0		ECGF1
227701_at	2.92458695035083	0		
212686_at	2.82379160235424	0		KIAA1157
242525_at	2.80598603189029	0		
211824_x_at	-2.77113099215966	0		DEFCAP
218259_at	2.6673432505011	0		KIAA1243
229848_at	2.61497492874017	0		ZNF10
238791_at	2.55305211995074	0		
212287_at	2.52556127587716	0		JJAZ1
205055_at	2.49589801203404	0		ITGAE

other aberrant vs. MLL	samples: 5 / 15			
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
232125_at	2.83634822109321	0*	10.45	
222335_at	2.80079072544706	0		CD2AP
203593_at	2.50443810972067	0		SLC38A2
220924_s_at	2.44940338874045	0		ATE1
234584_s_at	2.36473818619324	0		
228328_at	2.2823093126082	0		TFAM
203177_x_at	2.20405255989013	0		PRO1068
218041_x_at	2.19960407203391	0		SLC38A2
222982_x_at	2.1705009156018	0		
240201_at	2.17038421694015	0		MDS006
223401_at	2.1574569971375	0		SLC16A7
207057_at	2.10339239461692	0		MST4
218499_at	2.08679728034545	0		NAG
231926_at	2.03322303603834	0		
202926_at	2.01182753157743	0		LOC57149
216399_s_at	1.98784990984825	0		LOC51234
212549_at	1.98266739917742	0		
203897_at	1.95412833774499	0		
226741_at	1.94025028754913	0		
243154_at	1.93816368688103	0		

complex vs. all other	samples: 36 / 137		
accuracy	0.936416184971098		
confidence	0.914058016154132		
failed:	2,5,9,12,14,19,23,26,30,32,36		
gene	signal-to-noise	p	decision limit
222229_x_at	-0.977113333847485	0	
223318_s_at	-0.871134323886282	0	MGC10974
200608_s_at	0.859861630456657	0*	1754.85
209085_x_at	0.827754504723174	0*	543.85
201377_at	0.821542753098708	0	KIAA0144
214700_x_at	0.816898518764863	0	
227056_at	-0.808158632738399	0	KIAA0141
201164_s_at	0.805491372224207	0	PUM1
202413_s_at	0.794856444512317	0	USP1
209523_at	0.794733968085209	0	
205382_s_at	-0.786501229240988	0	DF
213452_at	0.763286023547173	0	ZNF184
203904_x_at	0.761563303490256	0	KAI1
212629_s_at	0.758597736815579	0	PRKCL2
219793_at	0.753945856377937	0	SNX16
200093_s_at - HG-U133B	-0.7505050474584	0	HINT1
225065_x_at	-0.740661805635393	0	
210053_at	0.737429178254302	0	TAF5
209259_s_at	0.734770265079843	0	CSPG6
209023_s_at	0.732408586508097	0	STAG2

complex vs. normal	samples: 36 / 62			
accuracy	0.959183673469388			
confidence	0.816646490079598			
failed:	9,23,36,88			
gene	signal-to-noise	p	decision limit	gene symbol
222229_x_at	-1.12052810135302	0		
227056_at	-1.02600466720905	0		KIAA0141
201922_at	-0.972449400267713	0*	3970.8	YR-29
200093_s_at - HG-U133B	-0.968640220043115	0		HINT1
239791_at	-0.927299942476145	0*	54	HOXB6
200608_s_at	0.882207986996843	0*	1566.2	RAD21
235502_at	-0.870929654024877	0		
223318_s_at	-0.867424298137502	0		MGC10974
200023_s_at - HG-U133B	-0.86661263717398	0		EIF3S5
200093_s_at - HG-U133A	-0.86073091922176	0		HINT1
218645_at	-0.842132977275412	0		ZNF277
213846_at	-0.824280554924366	0		COX7C
236728_at	-0.819459743485574	0		
236892_s_at	-0.810032594833065	0		HOXB6
241395_at	-0.806502754696553	0		
211950_at	0.803157394705844	0*	1367.5	RBAF600
203345_s_at	0.79268995247901	0		M96
231277_x_at	-0.79165327189793	0		
212251_at	0.787798207070077	0		

complex vs. t(8;21)		samples: 36 / 13		
accuracy	1	p	decision limit	gene symbol
confidence	0.956366908409342			
gene	signal-to-noise	p	decision limit	gene symbol
201851_at	1.64654123030477	0		SH3GL1
228827_at	-1.63837794328364	0*	277.15	
214651_s_at	1.52618371146822	0		HOXA9
235521_at	1.52417126144756	0		HOXA3
204249_s_at	1.52365997713542	0*	1581.95	LMO2
203904_x_at	1.49494399498725	0		KAI1
206940_s_at	-1.48076766016125	0		POU4F1
211341_at	-1.47540487159533	0		POU4F1
209259_s_at	1.45032016623088	0		CSPG6
212058_at	1.43907164424644	0		KIAA0332
218577_at	1.42304726090167	0		FLJ20331
217963_s_at	1.41730181206619	0		HCS
206622_at	-1.41476408655437	0		TRH
200071_at - HG-U133A	1.4105258517176	0		SPF30
218933_at	1.38255573216414	0		MGC5347
205528_s_at	-1.38150242627303	0		CBFA2T1
218331_s_at	1.3810903886183	0		FLJ20360
202406_s_at	1.3795610685034	0		TIAL1
220796_x_at	1.36377544613334	0		FLJ14251
218582_at	1.35888148459997	0		FLJ20445

complex vs. t(15;17)	samples: 36 / 20			
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
205382_s_at	-2.47024872277389	0		DF
212953_x_at	-2.44599456599903	0*	4652.35	CALR
64942_at	-2.28304127550384	0		
214450_at	-2.2627370518124	0		CTSW
38487_at	-2.15395063071356	0		FLJ12442
224794_s_at	-2.14479331910386	0		LOC51148
220798_x_at	-2.06303065394458	0		FLJ11535
216032_s_at	-2.05259440043708	0		SDBCAG84
203948_s_at	-2.04245448483567	0		MPO
209732_at	1.90630142681759	0		CLECSF2
230526_at	1.90204644112897	0		FLJ20015
238022_at	-1.89121106100583	0		
200654_at	-1.73209407132843	0		P4HB
204150_at	-1.72000809746397	0		STAB1
213447_at	1.71480861978241	0		IPW
206847_s_at	1.68023930751716	0		HOXA7
203074_at	-1.65576107663154	0		ANXA8
219837_s_at	-1.65191807395586	0		C17
200931_s_at	1.6356222023809	0		VCL
201923_at	1.60784567114272	0		PRDX4

complex vs. inv(16)	samples: 36 / 12			
accuracy	1	p	decision limit	gene symbol
confidence	0.957308305034528			
gene	signal-to-noise			
203092_at	1.77664454556306	0		TIMM44
209190_s_at	-1.75723541848141	0*	1593.8	DIAPH1
201497_x_at	-1.74852845185764	0*	134.75	MYH11
205076_s_at	-1.73951655525411	0		CRA
241525_at	-1.71682483225979	0		
213779_at	1.71354352282537	0		
210982_s_at	-1.70318998731519	0		HLA-DRA
200985_s_at	1.64643993864436	0		CD59
212463_at	1.6457941052799	0		
200675_at	1.61546783522649	0*	707.85	CD81
218942_at	1.59347299102441	0		FLJ22055
200984_s_at	1.56833724351535	0		CD59
208894_at	-1.54975491884609	0		HLA-DRA
202265_at	1.53139324627965	0		BMI1
224724_at	-1.5143785002027	0		KAA1247
210715_s_at	1.49004107536748	0		SPINT2
213452_at	1.48522101377482	0		ZNF184
205382_s_at	-1.45942422076027	0		DF
201360_at	-1.45905524413008	0		CST3

complex vs. MLL	samples: 36 / 15			
accuracy	1			
confidence	0.928537448772464			
gene	signal-to-noise	p	decision limit	gene symbol
228083_at	-1.83691594955677	0		
201105_at	-1.56013660814198	0		LGALS1
201377_at	1.5390279619994	0		KIAA0144
201358_s_at	1.46121373620596	0		COPB
203387_s_at	1.43200690176451	0		KIAA0603
201585_s_at	1.42612880048733	0		SFPQ
222982_x_at	1.4232823410753	0		SLC38A2
202746_at	1.40541613814493	0*	277.15	
204951_at	1.38290450200254	0*	224.05	ARHH
203725_at	1.35090921185734	0		GADD45A
203544_s_at	1.33195316834084	0		STAM
225804_at	-1.31098146845679	0		
203386_at	1.30903268579411	0		KIAA0603
201359_at	1.3066438308133	0		COPB
201830_s_at	1.29170882160348	0		NET1
218041_x_at	1.27263528593652	0		PRO1068
223318_s_at	-1.27042416454958	0		MGC10974
212222_at	1.26786775770503	0		KIAA0077
201829_at	1.26235979300155	0		NET1
200608_s_at	1.25213416895148	0		RAD21

normal vs. all other	samples: 62 / 111			
accuracy	0.895953757225434			
confidence	0.738387670770008			
failed:	5,17,21,25,32,39,45,50,51,52,54,58,64,70,76,77,86,113			
gene	signal-to-noise	p	decision limit	gene symbol
200023_s_at - HG-U133B	0.848290349062723	0		EIF3S5
236892_s_at	0.786541449606513	0*	60.95	HOXB6
201922_at	0.746117686034684	0		YR-29
239791_at	0.744707047378434	0		HOXB6
209055_s_at	-0.714503324187594	0		CDC5L
228904_at	0.707817878234848	0*	407.75	
224935_at	0.678011793604072	0		EIF2S3
236728_at	0.65220413902298	0		
238026_at	0.649420462340497	0		RPL35A
200679_x_at	-0.648886126347934	0*	782.25	HMG1
205366_s_at	0.642743252402536	0		HOXB6
225326_at	0.638282205886151	0*	835.95	KIAA1311
205601_s_at	0.638114898511556	0		HOXB5
205600_x_at	0.637054089932379	0		HOXB5
230743_at	0.631769166997722	0		
218645_at	0.629514230580722	0		ZNF277
226236_at	0.621355082335747	0		
200023_s_at - HG-U133A	0.620074058363248	0		EIF3S5
222976_s_at	-0.616559773343974	0		NTRK1

normal vs. t(8;21)	samples: 62 / 13			
accuracy	1	p	decision limit	gene symbol
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
228827_at	-2.03460798747208	0*	162.15	
214651_s_at	1.91662233809597	0		HOXA9
205528_s_at	-1.64467496425566	0		CBFA2T1
235753_at	1.61885010435257	0		
213150_at	1.50131650688172	0		HOXA10
205529_s_at	-1.4994140185132	0		CBFA2T1
211341_at	-1.4972813333234	0		POU4F1
209905_at	1.49669514190498	0		HOXA9
217816_s_at	1.49149650897312	0		pcnp
206940_s_at	-1.48516417693355	0		POU4F1
219598_s_at	1.43454923845259	0		
205453_at	1.38558116676561	0		HOXB2
223498_at	1.34625406703267	0		
213844_at	1.29651280723136	0		HOXA5
213147_at	1.27938232308768	0		HOXA10
222448_s_at	1.27922181680816	0		UMP-CMPK
214000_s_at	-1.2765364955951	0		RGS10
235521_at	1.27567444648757	0		HOXA3
235818_at	-1.27371437711255	0		
217963_s_at	1.27141827915888	0		HCS

normal vs. t(15;17)	samples: 62 / 20			
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
212953_x_at	-2.64495441949702	0*	4541.1	CALR
203948_s_at	-2.28625389247329	0		MPO
214450_at	-2.28053432941651	0		CTSW
38487_at	-2.27507979049885	0		FLJ12442
224794_s_at	-2.14479331910386	0		LOC51148
233072_at	-2.02319157581908	0		KIAA1857
236787_at	-1.97410536661333	0		ITM3
221004_s_at	-1.94014484972668	0		CLECSF2
209732_at	1.93197336691263	0		HOXA9
214651_s_at	1.91723603396294	0		SDBCAG84
216032_s_at	-1.83899991398145	0		CCND2
200952_s_at	-1.79422847402715	0		CANX
208852_s_at	-1.77756000185084	0		P4HB
200654_at	-1.77272215049273	0		STAB1
204150_at	-1.76741205974851	0		
235753_at	1.73443643867114	0		
64942_at	-1.71976456537364	0		
203949_at	-1.70342423200997	0		MPO
205614_x_at	-1.65262473388504	0		MST1

normal vs. inv(16)	samples: 62 / 12			
accuracy	1			
confidence	0.955620690178973			
gene	signal-to-noise	p	decision limit	gene symbol
214651_s_at	1.8118390923002	0		HOXA9
209365_s_at	-1.79092214915991	0*	390.9	ECM1
200951_s_at	-1.75939101209319	0		CCND2
201497_x_at	-1.74852845185764	0		MYH11
231310_at	-1.60730854736648	0*	167.8	
235753_at	1.60402701006007	0		
223385_at	-1.57142154491015	0		CYP2S1
231259_s_at	-1.49428776750791	0		CCND2
213353_at	1.47632425092475	0		ABCA5
202370_s_at	1.47587674217457	0*	942.4	CBFB
209905_at	1.44874209939309	0		HOXA9
204661_at	-1.44586168569344	0		CDW52
200675_at	1.39363453223823	0		CD81
207194_s_at	-1.38591797740996	0		ICAM4
213150_at	1.36428212315189	0		HOXA10
235818_at	-1.35992709972839	0		
228834_at	-1.35025928739893	0		TOB1
201324_at	-1.34841230643998	0		EMP1
218942_at	1.34162679981249	0		FLJ22055

normal vs. MLL	samples: 62 / 15			
accuracy	0.948051948051948			
confidence	0.898189333713789			
failed:	50,54,68,69			
gene	signal-to-noise	p	decision limit	gene symbol
205453_at	1.38558116676561	0*	203.25	HOXB2
225406_at	1.3008944013052	0*	191.3	TSG
222465_at	1.26538127373241	0*	1271.25	C15orf15
225326_at	1.13719416264236	0		KIAA1311
200829_x_at	1.1359357025281	0		ZNF207
227786_at	1.1032082540668	0		TRAP25
200056_s_at - HG-U133B	1.0989163336081	0		C1D
238856_s_at	1.093395457322	0		
200673_at	1.0918171848605	0		LAPTM4A
226250_at	1.0869927098714	0		
233559_s_at	-1.08564709559314	0		FENS-1
227680_at	1.0800659307262	0		
228904_at	1.06689615547167	0		
225700_at	1.0577778855845	0		
202377_at	1.05091847162674	0		HSOBRGRP
229232_at	1.04560760831211	0		
231870_s_at	1.04167487270266	0		LOC51068
222982_x_at	1.04035495200911	0		SLC38A2
209160_at	1.03517022790078	0		AKR1C3
223982_s_at	1.03308565481985	0		IPLA2

t(8;21) vs. all other	samples: 13 / 160			
accuracy	0.994219653179191			
confidence	1			
failed:	30			
gene	signal-to-noise	p	decision limit	gene symbol
228827_at	1.83673626836317	0		
211341_at	1.52047414341304	0		POU4F1
205528_s_at	1.51763257492904	0		CBFA2T1
206940_s_at	1.51745205298829	0		POU4F1
205529_s_at	1.43922881664177	0*	157.65	CBFA2T1
206622_at	1.22745062154907	0		TRH
219598_s_at	-1.21843492013845	0		
214651_s_at	-1.19784094554498	0		HOXA9
221581_s_at	-1.18072565374051	0		WBSCR5
227279_at	-1.10206247133481	0		MGC15737
204811_s_at	1.07742972237323	0		CACNA2D2
213150_at	-1.06934246090682	0		HOXA10
223498_at	-1.06722279372155	0		
215087_at	-1.06292558713408	0		
209522_s_at	-1.05686457779708	0		CRAT
204495_s_at	-1.05020858389696	0		DKFZP434H132
34689_at	-1.04236110585044	0		TREX1
201425_at	-1.04073518265119	0		ALDH2
225010_at	-1.0307918013289	0		

<i>t</i> (8;21) vs. <i>t</i> (15;17)		samples: 13 / 20		
accuracy	1	p	decision limit	gene symbol
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
214450_at	-3.53862069365814	0*	1809.95	CTSW
38487_at	-3.30334484935728	0		FLJ12442
209732_at	3.18277220746091	0		CLECSF2
204150_at	-2.73329912927614	0		STAB1
201596_x_at	-2.73162867034962	0		KRT18
213944_x_at	-2.5862372690463	0		
230526_at	2.42276930706474	0		FLJ20015
212509_s_at	-2.33481477262277	0		
211990_at	2.3270695509372	0		HLA-DPA1
204319_s_at	2.25060861801642	0		RGS10
205614_x_at	-2.24846130719191	0		MST1
216320_x_at	-2.16690689445934	0		
224794_s_at	-2.14479331910386	0		LOC51148
224839_s_at	-2.07810412712239	0		GPT2
227326_at	-2.04924504239987	0		
238365_s_at	-2.03674279873081	0		
228827_at	2.03460798747208	0		
228570_at	-2.03169244854036	0		
205349_at	-2.02142471684527	0		GNA15
AFFX-HUMRGE/M10098_3_at - HG-	0.424247547600803	0.01		
U133B				

t(8;21) vs. inv(16)	samples: 13 / 12			
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
233138_at	-3.4735123827114	0*	54.25	
202283_at	-2.6160707896185	0		SERPINF1
201596_x_at	-2.55517188589615	0		KRT18
233555_s_at	-2.48943541958708	0		
226818_at	-2.3621676751726	0		
212828_at	-2.33130605042964	0		SYNJ2
227276_at	-2.31171718422321	0		TEM7R
224724_at	-2.30850265580909	0		KIAA1247
224764_at	-2.25934489179779	0		ARHGAP10
224049_at	-2.25244855640038	0		KCNK17
205453_at	-2.23059959679219	0		HOXB2
226841_at	-2.21329419316194	0		
209975_at	-2.21237181448127	0		CYP2E
205076_s_at	-2.21083117233863	0		CRA
202340_x_at	-2.18671963481275	0		NR4A1
210314_x_at	-2.17138407196792	0		TNFSF13
34689_at	-2.16463995293403	0		TREX1
235359_at	-2.12423469465025	0		
212188_at	-2.11590883979512	0		LOC115207

(8;21) vs. MLL		samples: 13 / 15		
accuracy	1	p	decision limit	gene symbol
confidence	1			
gene		signal-to-noise	p	decision limit
214651_s_at		-2.42114497347366	0	HOXA9
201105_at		-2.17374439391796	0*	LGALS1
228827_at		2.03460798747208	0	
206009_at		2.02655766969028	0	ITGA9
228083_at		-1.99768244710951	0	
213150_at		-1.98436589229381	0	HOXA10
50221_at		-1.94810783752319	0	
221581_s_at		-1.89677192380517	0	WBSCR5
235753_at		-1.88396584115232	0	
206622_at		1.79659162526109	0	TRH
209905_at		-1.76718971964498	0	HOXA9
204069_at		-1.75588643276789	0	MEIS1
209160_at		1.75500319419551	0	AKR1C3
235818_at		1.70111545046162	0	
223498_at		-1.67798456165549	0	
211404_s_at		-1.67488607654784	0	APLP2
209500_x_at		-1.66210516483391	0	TNFSF13
203949_at		1.65967693892027	0	MPO
214875_x_at		-1.65852470588382	0	APLP2
206576_s_at		1.65525942936471	0	CEACAM1

t(15;17) vs. all other	samples: 20 / 153			
accuracy	1	p	decision limit	gene symbol
confidence	0.974825330584744			
gene	signal-to-noise	p	decision limit	gene symbol
214450_at	2.37884420275909	0		CTSW
38487_at	2.3638580246371	0		FLJ12442
212953_x_at	2.2214455881427	0		CALR
224794_s_at	2.14479331910386	0		LOC51148
204150_at	1.86162641245742	0		STAB1
221004_s_at	1.76116204864653	0		ITM3
64942_at	1.69621465377368	0		
203948_s_at	1.69389165333818	0*	12531.95	MPO
219837_s_at	1.66274419263843	0		C17
209732_at	-1.62000854961475	0		CLECSF2
200654_at	1.60816308060741	0		P4HB
216032_s_at	1.56292593677518	0		SDBCAG84
203074_at	1.56165682129626	0		ANXA8
241383_at	1.55580639460104	0		
233072_at	1.55533732715567	0		KIAA1857
211990_at	-1.55075101261749	0		HLA-DPA1
236787_at	1.54395725173734	0		
210755_at	1.52750902206113	0		HGF
209344_at	1.52382095011605	0		TPM4
210788_s_at	1.50209974954928	0		LOC51635

t(15;17) vs. inv(16)	samples: 20 / 12			
accuracy	1	p	decision limit	gene symbol
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
204661_at	-3.70847055085953	0*	1899.15	CDW52
209732_at	-3.23538966029247	0		CLECSF2
241742_at	-3.11768531834572	0		PRAM-1
38487_at	3.08138549900179	0		FLJ12442
238022_at	3.0278549438122	0		
204563_at	-2.99471501611954	0		SELL
34210_at	-2.99398735377828	0		CDW52
203535_at	-2.97123029136408	0		S100A9
217478_s_at	-2.93655072055469	0		
214450_at	2.92945546081029	0		CTSW
211991_s_at	-2.91096104465505	0		HLA-DPA1
208306_x_at	-2.87060964824031	0		HLA-DRB4
213779_at	2.84856846381654	0		
211990_at	-2.76844422327205	0		HLA-DPA1
221004_s_at	2.72545702224706	0		ITM3
209312_x_at	-2.66880572066538	0		HLA-DRB1
219789_at	-2.64334906817191	0		NPR3
204425_at	-2.62831954360607	0		ARHGAP4
205076_s_at	-2.59502309617401	0		CRA
64942_at	2.28304127550384	0		

t(15;17) vs. MLL	samples: 20 / 15			
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
205624_at	3.0741697102978	0*	2052.6	CPA3
38487_at	2.78111206643545	0		FLJ12442
203948_s_at	2.68497999695567	0		MPO
221004_s_at	2.64526084301972	0		ITM3
200951_s_at	2.52924582612911	0		CCND2
206761_at	2.52586949939666	0		TACTILE
203949_at	2.44678680592607	0		MPO
214651_s_at	-2.42192013365627	0		HOXA9
200952_s_at	2.39696270141848	0		CCND2
64942_at	2.28304127550384	0		
200953_s_at	2.24845652213108	0		CCND2
204150_at	2.2435902165197	0		STAB1
212953_x_at	2.22414089725316	0		CALR
233072_at	2.22380780245301	0		KIAA1857
214450_at	2.16984309325722	0		CTSW
224794_s_at	2.14479331910386	0		LOC51148
205349_at	2.12589700684588	0		GNA15
212509_s_at	2.11142192746438	0		
224839_s_at	2.07810412712239	0		GPT2
210788_s_at	2.07490438621852	0		LOC51635

inv(16) vs. all other	samples: 12 / 161			
accuracy	0.988439306358382			
confidence	1			
failed:	4,5			
gene	signal-to-noise	p	decision limit	gene symbol
201497_x_at	1.74852845185764	0*	134.75	MYH11
200675_at	-1.37014908718923	0		CD81
233555_s_at	1.33083128494836	0		
224724_at	1.3278495786994	0		KIAA1247
241525_at	1.30966026882784	0		
202370_s_at	-1.24406045913745	0		CBFB
218942_at	-1.21682758933894	0		FLJ22055
201496_x_at	1.21510481759962	0		MYH11
204661_at	1.21332222789748	0		CDW52
222862_s_at	1.21194822636852	0		AK5
200665_s_at	1.20473287395901	0		SPARC
225330_at	-1.17881556984529	0		
34210_at	1.14323693974495	0		CDW52
223471_at	-1.13566677236541	0		
213779_at	-1.12982358521787	0		
214651_s_at	-1.12057321021092	0		HOXA9
201324_at	1.11862902082417	0		EMP1
213737_x_at	-1.10994603608752	0		
225055_at	-1.10931729132663	0		FLJ10120
201506_at	1.1081095188939	0		TGFBI

inv(16) vs. MLL	samples: 12 / 15			
accuracy	1	p	decision limit	gene symbol
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
200951_s_at	4.24994685464806	0*	75.6	CCND2
228058_at	3.25212044058077	0		
219271_at	2.57049778814556	0		FLJ12691
231259_s_at	2.43255056573718	0		CCND2
214651_s_at	-2.30388406553935	0		HOXA9
202551_s_at	2.25890379783091	0		CRIM1
205453_at	2.23059959679219	0		HOXB2
200953_s_at	2.19700687874039	0		CCND2
213737_x_at	-2.16186095833837	0		
235818_at	2.13054793207832	0		
225653_at	2.10834669134201	0		
232636_at	-2.07022186491858	0		
202746_at	2.06211630393441	0		
200665_s_at	2.03751489015447	0		SPARC
203949_at	2.01364277991339	0		MPO
202552_s_at	1.96670486082105	0		CRIM1
223471_at	-1.96529988161274	0		
201828_x_at	-1.9593150488894	0		CXX1
235359_at	1.95403665761428	0		
202747_s_at	1.9384101680124	0		ITM2A

MLL vs. all other	samples: 15 / 158			
accuracy	0.947976878612717			
confidence	1			
failed:	1,6,7,10,12,14,25,102,114			
gene	signal-to-noise	p	decision limit	gene symbol
228083_at	1.19088467978442	0*	2180.6	
222982_x_at	-1.10285933642875	0		SLC38A2
201105_at	1.03478994002288	0		LGALS1
209160_at	-1.02713455370792	0		AKR1C3
204951_at	-0.985909332656785	0		ARHH
218041_x_at	-0.943257946797628	0		PRO1068
225776_at	-0.938314906907134	0		BAZ2A
202746_at	-0.936926874759212	0		
205472_s_at	0.936018216120354	0		DACH
205453_at	-0.935915983498264	0		HOXB2
203380_x_at	-0.926524173527231	0		SFRS5
203372_s_at	0.926509074446515	0		STATI2
225285_at	-0.922143795249267	0		
203373_at	0.921657224293489	0		STATI2
201830_s_at	-0.917500470432308	0		NET1
236378_at	-0.911274344991347	0		
209816_s_at	0.911180477081636	0		CES1
218718_at	-0.905113907165327	0		PDGFC
225406_at	-0.898505260085313	0		TSG
49306_at	0.646783585229759	0		AD037

Table 36: Analysis of 8 AML subgroups according to the method described by Westfall & Young. The 226 significant genes are listed. The raw p value as well as the adjusted p value are shown. Furthermore it is indicated whether the genes were also identified as discriminative by the method described by Golub et al. (* most important gene in pairwise comparisons, + one of the top 20 significant genes)

5

geneID	Golub	rawp	Adjp
201497_x_at	*	0.0001	0.0001 MYH11
212953_x_at	*	0.0001	0.0001 CALR
214450_at	*	0.0001	0.0001 CTSW
224794_s_at	+	0.0001	0.0001 LOC51148
228827_at	*	0.0001	0.0001
38487_at	+	0.0001	0.0001 FLJ12442
203074_at	+	0.0001	0.0002 ANXA8
204150_at	+	0.0001	0.0002 STAB1
219837_s_at	+	0.0001	0.0002 C17
64942_at	+	0.0001	0.0002
203948_s_at	*	0.0001	0.0003 MPO
205528_s_at	+	0.0001	0.0003 CBFA2T1
205529_s_at	*	0.0001	0.0003 CBFA2T1
206940_s_at	+	0.0001	0.0003 POU4F1
209344_at	+	0.0001	0.0003 TPM4
210755_at	+	0.0001	0.0003 HGF
210997_at		0.0001	0.0003 HGF
211341_at	+	0.0001	0.0003 POU4F1
212285_s_at		0.0001	0.0003 AGRN
212481_s_at		0.0001	0.0003 TPM4
216320_x_at	+	0.0001	0.0003
223828_s_at		0.0001	0.0003 LGALS12
227243_s_at		0.0001	0.0003
233072_at	+	0.0001	0.0003 KIAA1857
236787_at	+	0.0001	0.0003
200952_s_at	+	0.0001	0.0004 CCND2
205614_x_at	+	0.0001	0.0004 MST1
212509_s_at	+	0.0001	0.0004
216032_s_at	+	0.0001	0.0004 SDBCAG84
221004_s_at	+	0.0001	0.0004 ITM3
241383_at	+	0.0001	0.0004
200656_s_at		0.0001	0.0005 P4HB
200953_s_at	+	0.0001	0.0005 CCND2
201496_x_at	+	0.0001	0.0005 MYH11
214203_s_at		0.0001	0.0005 PRODH

214315_x_at		0.0001	0.0005 CALR
219090_at		0.0001	0.0005 SLC24A3
227046_at		0.0001	0.0005 C17orf26
227242_s_at		0.0001	0.0005
209686_at		0.0001	0.0007 S100B
228660_x_at	*	0.0001	0.0007 SEMA4F
241525_at	+	0.0001	0.0011
210788_s_at	+	0.0001	0.0017 LOC51635
227326_at	+	0.0001	0.0023
208852_s_at	+	0.0001	0.0027 CANX
229168_at		0.0001	0.0031
242520_s_at		0.0001	0.0031
200951_s_at	*	0.0001	0.0033 CCND2
203949_at	+	0.0001	0.0033 MPO
204163_at		0.0001	0.0033 EMILIN
205663_at		0.0001	0.004 PCBP3
204116_at		0.0001	0.005 IL2RG
221253_s_at		0.0001	0.005 MGC3178
238365_s_at	+	0.0001	0.0058
200654_at	+	0.0001	0.0072 P4HB
201069_at		0.0001	0.0072 MMP2
200608_s_at	*	0.0001	0.0074 RAD21
210998_s_at		0.0001	0.0077 HGF
211668_s_at		0.0001	0.0077 PLAU
212259_s_at		0.0001	0.0077 HPIP
224839_s_at	+	0.0001	0.0077 GPT2
223321_s_at		0.0001	0.0083 FGFR1
225065_x_at	+	0.0001	0.0085
206622_at	+	0.0001	0.0086 TRH
205076_s_at	+	0.0001	0.009 CRA
231050_at		0.0001	0.009 HRLP5
235753_at	+	0.0001	0.009
214000_s_at	+	0.0001	0.0093 RGS10
231259_s_at	+	0.0001	0.0095 CCND2
200047_s_at - HG-U133A		0.0001	0.0096 YY1
204811_s_at	+	0.0001	0.0101 CACNA2D2
229621_x_at		0.0001	0.0102
205382_s_at	+	0.0001	0.0103 DF
213514_s_at		0.0001	0.0105 DIAPH1
200986_at		0.0001	0.0107 SERPING1
217419_x_at		0.0001	0.0107
229420_at		0.0001	0.0117 RPL23A

211934_x_at		0.0001	0.0122 G2AN
214651_s_at	+	0.0001	0.0123 HOXA9
208581_x_at		0.0001	0.0127 MT1X
202718_at		0.0001	0.0128 IGFBP2
200825_s_at		0.0001	0.0135 ORP150
212185_x_at		0.0001	0.0135 MT2A
219868_s_at		0.0001	0.0135 ANKHZN
203939_at		0.0001	0.0136 NT5E
200649_at		0.0001	0.0144 NUCB1
206850_at		0.0001	0.0144 RRP22
AFFX-r2-Hs28SrRNA-3_at - HG-U133B		0.0001	0.0144
218051_s_at		0.0001	0.0146 FLJ12442
208629_s_at	+	0.0001	0.0147 HADHA
209523_at	+	0.0001	0.0147
AFFX-r2-Hs28SrRNA-3_at - HG-U133A		0.0001	0.0148
57588_at		0.0001	0.0156 SLC24A3
221902_at		0.0001	0.0163
225547_at	+	0.0001	0.0163
200047_s_at - HG-U133B		0.0001	0.0172 YY1
200023_s_at - HG-U133B	+	0.0001	0.0175 EIF3S5
201008_s_at		0.0001	0.0175 TXNIP
205624_at	*	0.0001	0.0178 CPA3
AFFX-HSAC07/X00351_5_at - HG-U133A		0.0001	0.0178 ACTB
200935_at		0.0001	0.0179 CALR
228083_at	*	0.0001	0.0179
222229_x_at	+	0.0001	0.0183
224724_at	+	0.0001	0.0186 KIAA1247
211748_x_at		0.0001	0.0194 PTGDS
209190_s_at	*	0.0001	0.0206 DIAPH1
214316_x_at		0.0001	0.021 CALR
205110_s_at		0.0001	0.0212 FGF13
233555_s_at	+	0.0001	0.0215
202655_at		0.0001	0.0216 ARMET
AFFX-HUMRGE/M10098_3_at - HG- +		0.0001	0.0217
U133B			
200008_s_at - HG-U133A		0.0001	0.022 GDI2
209961_s_at		0.0001	0.022 HGF
222916_s_at		0.0001	0.0228
211456_x_at		0.0001	0.0229
219138_at		0.0001	0.023 RPL14
242845_at		0.0001	0.023
202028_s_at		0.0001	0.0232 RPL38

222862_s_at	+	0.0001	0.0232 AK5
AFFX-HSAC07/X00351_5_at - HG-U133B		0.0001	0.0232 ACTB
238022_at	+	0.0001	0.0233
222977_at		0.0001	0.0234 SURF4
211474_s_at		0.0001	0.0236
204306_s_at		0.0001	0.0237 CD151
212013_at		0.0001	0.0237 D2S448
201922_at	*	0.0001	0.0238 YR-29
203857_s_at		0.0001	0.0238 PDIR
AFFX-M27830_5_at - HG-U133B		0.0001	0.0238
242738_s_at		0.0001	0.024
AFFX-r2-Hs18SrRNA-3_s_at - HG-U133B		0.0001	0.0241
215450_at		0.0001	0.0245 SNRPE
222955_s_at		0.0001	0.0245 HT011
AFFX-M27830_5_at - HG-U133A		0.0001	0.0259
202148_s_at		0.0001	0.026 PYCR1
216609_at		0.0001	0.026
214500_at		0.0001	0.0264 H2AFY
241975_at		0.0001	0.0268
226014_at		0.0001	0.0273 EIF3S5
224407_s_at		0.0001	0.0274 MST4
AFFX-HSAC07/X00351_M_at - HG-U133B		0.0001	0.0275 ACTB
210973_s_at		0.0001	0.0276 FGFR1
213963_s_at		0.0001	0.0279 SAP30
209616_s_at	+	0.0001	0.0288 CES1
201004_at		0.0001	0.0289 SSR4
214228_x_at		0.0001	0.0289
214501_s_at		0.0001	0.0289 H2AFY
208229_at		0.0001	0.029 FGFR2
208819_at		0.0001	0.029 MEL
201564_s_at		0.0001	0.0296 SNL
201437_s_at		0.0001	0.0297 EIF4E
213048_s_at		0.0001	0.0297 SET
221943_x_at		0.0001	0.0297 RPL38
202747_s_at	+	0.0001	0.0299 ITM2A
208611_s_at		0.0001	0.0299 SPTAN1
212012_at		0.0001	0.0304 D2S448
205380_at		0.0001	0.0311 PDZK1
209975_at	+	0.0001	0.0316 CYP2E
208858_s_at		0.0001	0.0317 KIAA0747
206461_x_at		0.0001	0.0322 MT1H
210794_s_at		0.0001	0.0325

212187_x_at		0.0001	0.0326 PTGDS
AFFX-HSAC07/X00351_M_at - HG-U133A		0.0001	0.0338 ACTB
200008_s_at - HG-U133B		0.0001	0.0346 GDI2
222477_s_at		0.0001	0.0346 TM7SF3
223054_at		0.0001	0.0347 DNAJB11
231118_at		0.0001	0.0351
238367_s_at		0.0001	0.0357
201352_at		0.0001	0.0358 YME1L1
AFFX-M27830_M_at - HG-U133A		0.0001	0.0358
210933_s_at		0.0001	0.0363 MGC4655
200598_s_at		0.0001	0.0368 TRA1
213942_at		0.0001	0.037 EGFL3
222692_s_at		0.0001	0.037 FLJ23399
AFFX-r2-Hs18SrRNA-M_x_at - HG-U133A		0.0001	0.037
200646_s_at		0.0001	0.0372 NUCB1
201005_at		0.0001	0.0372 CD9
222979_s_at		0.0001	0.0373
226210_s_at		0.0001	0.0388
AFFX-r2-Hs18SrRNA-M_x_at - HG-U133B		0.0001	0.0391
214700_x_at	+	0.0001	0.0393
207076_s_at		0.0001	0.0402 ASS
216450_x_at		0.0001	0.0402
202746_at	*	0.0001	0.0404
200770_s_at		0.0001	0.0409 LAMC1
217816_s_at	+	0.0001	0.0409 pcnp
226531_at		0.0001	0.0409 FLJ14466
200093_s_at - HG-U133B	+	0.0001	0.0413 HINT1
AFFX-HUMRGE/M10098_3_at - HG-U133A		0.0001	0.0413
219793_at	+	0.0001	0.0418 SNX16
212032_s_at		0.0001	0.0423 PTOV1
228193_s_at		0.0001	0.0423 RGC32
202413_s_at	+	0.0001	0.0424 USP1
216449_x_at		0.0001	0.0427
205131_x_at		0.0001	0.0432 SCGF
217225_x_at		0.0001	0.0438 PM5
202406_s_at	+	0.0001	0.0439 TIAL1
203729_at		0.0001	0.0439 EMP3
200630_x_at		0.0001	0.0447 SET
227299_at		0.0001	0.0448 CCNI
AFFX-r2-Hs18SrRNA-3_s_at - HG-U133A		0.0001	0.0448
209905_at	+	0.0001	0.0449 HOXA9
208033_s_at		0.0001	0.0452 ATBF1

214395_x_at		0.0001	0.0452 FLJ20897
217383_at		0.0001	0.0452
201377_at	+	0.0001	0.0454 KIAA0144
206871_at		0.0001	0.0454 ELA2
203859_s_at		0.0001	0.0461 PALM
200968_s_at		0.0001	0.0462 PPIB
219634_at		0.0001	0.0463 C4ST
220798_x_at	+	0.0001	0.0463 FLJ11535
201825_s_at		0.0001	0.0466 LOC51097
224553_s_at		0.0001	0.0468 TNFRSF18
227353_at		0.0001	0.0468
225406_at	*	0.0001	0.0473 TSG
227145_at		0.0001	0.0478 LOXL4
201164_s_at	+	0.0001	0.0484 PUM1
210140_at		0.0001	0.0484 CST7
202600_s_at		0.0001	0.0487 NRIP1
210616_s_at		0.0001	0.0487 KIAA0905
212107_s_at		0.0001	0.0487 DDX9
200071_at - HG-U133A	+	0.0001	0.0491 SPF30
204082_at		0.0001	0.0491 PBX3
200707_at		0.0001	0.0492 PRKCSH
200967_at		0.0001	0.0493 PPIB
206634_at		0.0001	0.0493 SIX3
AFFX-HUMRGE/M10098_M_at - HG-U133B		0.0001	0.05

Table 37a: In total 32 cases of CLL were analyzed. 31 of 32 cases (96.9%) were assigned to the correct CLL subtype in all pairwise comparisons. The sensitivity indicated for each subgroup indicates the percentage of cases of the specific subgroup identified correctly in all pairwise comparisons. The specificity indicates for each subgroup the percentage of correct assignments to this subgroup.

5

	+12	11q-	13q-	17p-	normal	total	sensitivity %	specificity %
+12	5					5	100.00	100.00
11q-		4				4	100.00	100.00
13q-			9		1	10	90.00	100.00
17p-				4		4	100.00	100.00
Normal					9	9	100.00	90.00
Total	5	4	9	4	10	32		

Table 37b: In total 128 individual assignments of CLL were analyzed. 127 of 128 assignments (99.2%) were correct. The sensitivity indicated for each subgroup indicates the percentage of correct assignments for cases of the specific subgroup in pairwise comparisons. The specificity indicates for each subgroup the percentage of correct assignments to this subgroup.

5

	tri 12	11q	13q	17p	normal	total	sensitivity %	specificity %
tri 12	20					20	100.00	100.00
11q		16				16	100.00	100.00
13q			39		1	40	97.50	100.00
17p				16		16	100.00	97.30
Normal					36	36	100.00	100.00
Total	20	16	39	16	37	128		

Table 38: Analysis of 5 CLL subtypes according to the method described by Golub et.al.

trisomy 12	5
11q-	4
13q-	10
17p-	4
normal	9

trisomy 12 vs. all other	samples: 5 / 27	accuracy	1	confidence	0.935014380126868	gene	signal-to-noise	p	decision limit	gene symbol
205855_at	-1.76663664947048	0.01	ZNF197							
203787_at	1.48888776879594	0*	186.05	SSBP2						
240785_at	-1.47915794453041	0*	1							
241930_x_at	1.43687618531343	0								
227527_at	1.43424381736709	0								
233106_at	1.39680763010583	0								
219234_x_at	-1.36406381959263	0*	1	FLJ23142						
204992_s_at	-1.35580671258705	0	PFN2							
229722_at	-1.35323423840642	0	HSPC072							
225772_s_at	1.34357943208416	0	MGC14288							
240801_at	1.33658031665266	0	C21orf37							
236535_at	-1.28816401084294	0	FLJ22116							
213850_s_at	1.28242512478545	0	SFRS2IP							
239651_at	1.27623762574996	0								
218692_at	-1.26869683284091	0	FLJ20366							
210117_at	1.26847772500135	0	SPAG1							
229833_at	-1.2612893100757	0								
243859_at	-1.24636980625822	0.01								
242695_at	1.24259108808825	0								

trisomy 12 vs.11q-	samples: 5 / 4			
accuracy	1	p	decision limit	gene symbol
confidence	1			
gene	signal-to-noise			
233106_at	11.446952458547	0*	17.2	
240801_at	9.47372393833846	0		C21orf37
209876_at	5.71702357037612	0		GIT2
240785_at	-5.41366689652617	0.01		
238651_at	4.44936662944647	0		
224559_at	4.28565210000215	0		
204992_s_at	-4.18799798922824	0.01		PFN2
218089_at	-3.71376785745491	0		C20orf4
233520_s_at	3.68368733311458	0.01		
244248_at	-3.51882915292872	0.01		
202973_x_at	3.46577082978451	0		KIAA0914
238304_at	3.40683085127986	0.02		
209018_s_at	3.33636546986144	0.01		PINK1
235414_at	3.31145415432861	0		
228737_at	-3.19150189531835	0		C20orf100
205841_at	3.0783309837118	0.01		JAK2
210251_s_at	3.06884121765458	0		KIAA0871
227237_x_at	-3.04881893527751	0		KIAA1273
204101_at	2.96540851000724	0		MTM1
214152_at	2.94086839898829	0		PIGB

trisomy 12 vs.13q-	samples: 5 / 10			
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
241930_x_at	3.41574881140311	0*	30.05	
201125_s_at	2.1330030439147	0.01		ITGB5
214030_at	1.99357501958234	0		FLJ14393
220764_at	1.83054202690279	0		PPP4R2
229711_s_at	1.77592202191897	0		MGC5370
204422_s_at	1.73100503057285	0		FGF2
206519_x_at	1.72950110576936	0		SIGLEC6
229722_at	-1.72165455873558	0		HSPC072
224254_x_at	1.69291666318009	0.01		
244550_at	1.69227307532627	0		
240785_at	-1.67627283307722	0		
219234_x_at	-1.67623751680922	0		FLJ23142
239651_at	1.67596732335477	0		
225803_at	1.66876599612634	0		FBXO32
202371_at	-1.66225791751365	0		FLJ21174
238686_at	1.65936349841951	0		FBXO3
213249_at	-1.65347132783467	0.01		FBXL7
232841_at	-1.61894883955233	0		
37424_at	-1.60782342430755	0		HCR
238651_at	1.5823504522053	0		

trisomy 12 vs.17p-	samples: 5 / 4			
accuracy	1	p	decision limit	gene symbol
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
240801_at	9.47372393833846	0.01*	12.2	C21orf37
205855_at	-6.0211187391758	0		ZNF197
35666_at	-5.5825628661131	0		SEMA3F
210807_s_at	4.67905037269957	0		SLC16A7
238756_at	4.46774787106986	0		
213081_at	4.28614856394104	0.01		ZNF297
209992_at	3.83963180828656	0.02		PFKFB2
213922_at	3.58392947846265	0.01		KIAA0847
221642_at	3.54894468199149	0		TREX1
234862_at	3.18446048786689	0.01		
204101_at	2.96540851000724	0		MTM1
240842_at	-2.91868570817753	0		
225270_at	2.79620139853395	0		
240785_at	-2.79597266226518	0.01		
202156_s_at	2.55016914645743	0.02		CUGBP2
242738_s_at	2.48714106974951	0		
222229_x_at	2.4826745391349	0		
221761_at	2.43735081046452	0.01		ADSS
239651_at	2.38139601357287	0.01		
44065_at	1.72880244676984	0.03		FLJ14827

trisomy 12 vs. normal	samples: 5 / 9			
accuracy	1	p	decision limit	gene symbol
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
204227_s_at	-2.97871472113278	0*	52.6	TK2
239956_at	-2.19763940812654	0		
229833_at	-2.15561256145124	0		
235259_at	-2.13615684750119	0		
219234_x_at	-2.00077179509905	0		FLJ23142
205225_at	-1.99449483927763	0		ESR1
207871_s_at	-1.92495926735556	0.01		ST7
214849_at	-1.85640805976258	0		
229368_s_at	1.79940595243311	0		ZNF216
241969_at	1.7405112334814	0		ITM2B
206519_x_at	1.72950110576936	0		SIGLEC6
238752_at	-1.70821051414766	0.02		
231269_at	1.70133376942788	0.01		DJ467N11.1
210117_at	1.68428381889367	0		SPAG1
244248_at	-1.64325597313785	0		
227527_at	1.63698066130033	0		
205855_at	-1.62998714380688	0		ZNF197
230775_s_at	1.62302128109514	0		KIAA0610
235428_at	-1.61224208443187	0.01		

11q- vs. all other	samples: 4 / 28			
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
218089_at	2.10620905507106	0*	646.5	C20orf4
219846_at	-1.81092435144239	0		FLJ23040
227988_s_at	-1.72174284840356	0		CHAC
214152_at	-1.67765936203123	0		PIGB
218379_at	-1.46433593517939	0		RBM7
226743_at	-1.46222822597622	0		
211297_s_at	1.44946792759264	0		CDK7
201034_at	-1.42442867101326	0		ADD3
241754_at	-1.42345184824601	0.01		
236914_at	-1.4155743735673	0.01		
202883_s_at	-1.40974035083074	0		PPP2R1B
222619_at	1.40836172115026	0		ZNF281
210251_s_at	-1.40353417348001	0		KIAA0871
243764_at	-1.39232414452409	0.01		
232080_at	-1.38768407694403	0.01		KIAA1301
225469_at	-1.33954570434399	0.01		KRAS2
228916_at	-1.33432050535623	0		
231837_at	-1.32753771112964	0		USP28
41553_at	1.12064197016153	0		C8orf1

11q- vs. 13q-	samples: 4 / 10			
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
219846_at	-3.42496729223506	0*	29.05	FLJ23040
243579_at	2.5422955569836	0		MSI2
218089_at	2.2192149690658	0		C20orf4
236557_at	2.13608221931199	0		
236914_at	-2.11513443853125	0		
211097_s_at	-2.10829683608662	0.01		PBX2
222619_at	1.99497428726409	0		ZNF281
210563_x_at	1.98835546697322	0		CFLAR
203910_at	-1.93770224600631	0		PARG1
214152_at	-1.85345818448696	0.02		PIGB
211665_s_at	1.85212714314444	0		
224727_at	1.79450625074427	0		
212973_at	1.77498087389291	0		RPIA
216363_at	-1.75505428599984	0		
232080_at	-1.71428429043072	0.02		KIAA1301
209939_x_at	1.70364770022483	0		CFLAR
216640_s_at	1.66791014400825	0		
211015_s_at	1.66234655451608	0		HSPA4
241754_at	-1.65521937202397	0.02		
200072_s_at - HG-U133B	1.62143771744332	0		HNRPM

11q- vs. 17p-	samples: 4 / 4			
accuracy	1	p	decision limit	gene symbol
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
203910_at	-12.0891239887758	0.02*	25.2	PARG1
219788_at	-8.01365237890759	0.01		PILR
210807_s_at	5.81727222348978	0		SLC16A7
202973_x_at	-5.54682446497201	0.01		KIAA0914
224727_at	5.47118118794136	0.04		
243538_at	-5.45690493183292	0.01		
220653_at	5.40495669550229	0.01		ZIM2
236557_at	4.79134791840039	0.03		
202535_at	4.6597238034407	0.02		FADD
219846_at	-4.50391195213954	0.03		FLJ23040
223036_at	-4.37417074055808	0.04		FRSB
41553_at	4.17139530611346	0.02		C8orf1
232080_at	-3.7905538055378	0.04		KIAA1301
227212_s_at	3.74958483811803	0		
231538_at	-3.66357978886211	0.03		FLJ23499
223981_at	-3.20166631174034	0.01		NIN
210095_s_at	-3.18292733506553	0.03		IGFBP3
44669_at	1.48597424301687	0.03		

11q- vs. normal	samples: 4 / 9			
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
227988_s_at	-3.59181544150717	0*	42.9	CHAC
202883_s_at	-3.42911376512134	0		PPP2R1B
239824_s_at	-2.86491576775498	0		MGC10744
208741_at	-2.57358498823744	0		SAP18
235446_at	-2.44561600023568	0		
243024_at	-2.32550716609078	0		
214152_at	-2.28116624754023	0		PIGB
205945_at	-2.2501933683546	0		IL6R
230405_at	-2.2154536025941	0		RAD50
240449_at	-2.16736443161623	0		ZNF341
226735_at	2.13097198546745	0		
235719_at	-2.04486139000124	0		
240269_at	-2.00407877559944	0.02		
231837_at	-1.99281259915495	0.01		USP28
211584_s_at	-1.92263813056307	0		NPAT
212397_at	-1.91363941690428	0		RDX
228083_at	-1.91262419018279	0		
217185_s_at	-1.90105615613598	0		
201034_at	-1.87885968131857	0		ADD3
244636_at	1.41086397558577	0.01		

13q- vs. all other	samples: 10 / 22			
accuracy	0.90625			
confidence	0.758934573190992			
failed:	1,4,10			
gene	signal-to-noise	p	decision limit	gene symbol
240239_at	1.12265317688576	0		FLJ14779
225803_at	-1.11955038091099	0		FBXO32
214030_at	-1.07932639824253	0		FLJ14393
208612_at	-1.04692103821733	0		GRP58
205059_s_at	-1.02298997137232	0		IDUA
224324_at	-1.0017529706033	0.01		B29
220050_at	-0.942587733303296	0		C9orf9
212133_at	-0.939561276009625	0		MGC5466
209561_at	-0.895424188378393	0.01*	1	THBS3
212346_s_at	-0.86343267965412	0.01*	1	
210563_x_at	-0.857353032891431	0		CFLAR
219846_at	0.851391806455573	0		FLJ23040
200917_s_at	-0.847094054810162	0		SRPR
214693_x_at	-0.842327739447741	0*	513.4	DJ328E19.C1.1
224254_x_at	-0.840493461837671	0*	1	
216363_at	0.840371719572254	0		
206178_at	-0.839970145359486	0.01*	1	PLA2G5
201829_at	-0.83771452268015	0		NET1
242065_x_at	0.752061453727533	0		KIAA0982

13q- vs. 17p-	samples: 10 / 4			
accuracy	1	p	decision limit	gene symbol
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
205074_at	3.93082740953048	0*	47.2	SLC22A5
205059_s_at	-2.86213992210757	0		IDUA
206530_at	-2.83791228863181	0		RAB30
239302_s_at	2.16473291745382	0		
211097_s_at	2.10829683608662	0		PBX2
213922_at	2.01548216857792	0		KIAA0847
206748_s_at	-1.88775766295876	0		SPAG9
230960_at	1.78981943765595	0		
219099_at	-1.78601869648563	0		C12orf5
209399_at	1.77172423634645	0		HLCS
234682_at	-1.75764919544644	0.02		
201247_at	-1.75383479254057	0		SREBF2
227047_x_at	1.70965672311403	0		KIAA1538
227336_at	-1.67331959955983	0		DTX1
44563_at	1.6395923566301	0		FLJ10385
202137_s_at	1.63835350305949	0		BS69
204703_at	1.63405057461184	0		TG737
232841_at	1.61894883955233	0		

13q- vs. normal	samples: 10 / 9			
accuracy	0.947368421052632			
confidence	0.767885192437171			
failed:	1			
gene	signal-to-noise	p	decision limit	gene symbol
212133_at	-1.49179585241618	0		MGC5466
231945_at	1.34403975576724	0		KIAA1275
236707_at	-1.3127085187848	0		DAPP1
240113_at	1.29988454092314	0.01		
233137_at	-1.24704962815733	0*	72.3	
239279_at	1.17173879184892	0*	10.95	
217920_at	-1.16948313904991	0*	100.65	
220050_at	-1.1554548232117	0.01		C9orf9
214693_x_at	-1.12710287831488	0*	785.75	DJ328E19.C1.1
240239_at	1.12265317688576	0		FLJ14779
206633_at	1.11411516845923	0		CHRNA1
233845_at	1.10899780853203	0		
214030_at	-1.10624113689033	0		FLJ14393
214452_at	-1.10585601374159	0.01		BCAT1
244636_at	1.09426538931965	0		
229711_s_at	-1.08284772025586	0*	175.2	MGC5370
208612_at	-1.04802029197291	0		GRP58
201829_at	-1.04541705234559	0		NET1
225025_at	-1.04209808409802	0		IGSF8
56919_at	0.843685137333952	0		KIAA1449

17p- vs. all other	samples: 4 / 28			
accuracy	1			
confidence	0.964568811002079			
gene	signal-to-noise	p	decision limit	gene symbol
213922_at	-2.38687598396346	0		KIAA0847
239302_s_at	-1.90616910234578	0		
210807_s_at	-1.80157318540302	0*	1	SLC16A7
227047_x_at	-1.74312208164522	0*	1	KIAA1538
243493_at	-1.58349220512196	0.01*	1	
212601_at	-1.53446329571692	0		KIAA0399
231069_at	-1.52786491236881	0		
228183_s_at	-1.52482033281554	0		MGC4189
218938_at	-1.52269705250236	0		MGC11279
209754_s_at	-1.51357080613702	0		
229487_at	1.48496465895187	0.01		
202101_s_at	-1.48060713997599	0		RALB
204075_s_at	-1.44015391162326	0		KIAA0562
225064_at	-1.43255380391079	0		
211800_s_at	-1.42133619880381	0		USP4
44563_at	-1.41946867497272	0		FLJ10385
209003_at	-1.41936503927243	0.01		SLC25A11
233261_at	1.41906569641121	0		

17p- vs. normal	samples: 4 / 9			
accuracy	1	p	decision limit	gene symbol
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
239263_at	-5.06986350689012	0*	28.95	
224389_s_at	4.85220428207756	0.01		LOC84570
218938_at	-4.37035592768397	0		MGC11279
209558_s_at	3.96926728013304	0.01		HIP12
209003_at	-3.83037277930439	0		SLC25A11
213922_at	-3.70320846722859	0		KIAA0847
227277_at	-3.14601684537179	0		
201247_at	3.13384207920433	0.01		SREBF2
239824_s_at	-2.86491576775498	0		MGC10744
243493_at	-2.55548617887833	0		
202101_s_at	-2.51633093119791	0		RALB
238208_at	2.48580500500254	0		
232641_at	-2.43239639363709	0		
38340_at	2.39155889740356	0		HIP12
225565_at	-2.36688673011482	0		
235692_at	-2.35357613574803	0		
212587_s_at	-2.31297420341289	0		PTPRC
209178_at	2.30977713582653	0		DDX38
226101_at	-2.30435376005559	0		

normal vs. all other	samples: 9 / 23			
accuracy	1			
confidence	0.752908435315332			
gene	signal-to-noise	p	decision limit	gene symbol
217920_at	1.12626688471637	0*	120.8	
233845_at	-1.11422356526216	0		
239279_at	-1.07195619687299	0*	1	
231945_at	-1.04730583025734	0*	47.05	KIAA1275
240113_at	-1.03819026438649	0*	1	
219641_at	1.01342862157126	0*	68.05	FLJ10103
219457_s_at	1.01203293419066	0*	653.6	RIN3
211349_at	-0.983993758419454	0		SLC15A1
228408_s_at	0.980977651352115	0*	301.7	FLJ10498
214949_at	0.970683369936125	0		
235052_at	0.970295482117812	0*	18.2	
212417_at	0.947300555400096	0		SCAMP1
244636_at	-0.940508403486097	0.01		
226060_at	0.905224209711651	0		RFT1
239263_at	0.904436494271519	0.01		
200890_s_at	0.896568314554417	0		SSR1
208042_at	0.88315849081967	0		HSUB4971
206550_s_at	-0.869633758548337	0		NUP155
201813_s_at	0.854527572567661	0		KIAA0210
221543_s_at	0.842343687568175	0		C8orf2

Table 39: Analysis of 5 CLL subgroups according to the method described by Westfall & Young. The raw p value as well as the adjusted p value are shown. Furthermore it is indicated whether the genes were also identified as discriminative by the method described by Golub et al. (* most important gene in pairwise comparisons, + one of the top 20 significant genes)

5

geneID	Golub	rawp	adjp
229487_at	+	0.0016	0.4057
233261_at	+	0.0016	0.6404
235421_at		0.0003	0.7273
244876_at		0.0016	0.831
212133_at	+	0.0001	0.8508 MGC5466
232204_at		0.0008	0.889 EBF
244147_at		0.0014	0.9084
240740_at		0.0016	0.926
227527_at	+	0.0001	0.943
206519_x_at	+	0.0007	0.9529 SIGLEC6
213922_at	+	0.0001	0.9568 KIAA0847
207801_s_at		0.0011	0.9745 RNF10
212812_at		0.0003	0.9763
242329_at		0.0016	0.9777
221004_s_at		0.0012	0.9807 ITM3
209321_s_at		0.0005	0.9837 ADCY3
44563_at	+	0.0003	0.9839 FLJ10385
212813_at		0.0013	0.984 FLJ14529
217156_at		0.0012	0.9862
219099_at	+	0.0004	0.9864 C12orf5
238365_s_at		0.0004	0.988
219846_at	*	0.0003	0.9957 FLJ23040
227936_at		0.0001	0.9975
228497_at		0.0002	0.9992 DKFZp761G0313
244523_at		0.0007	0.9992 MMD
222108_at		0.0008	0.9994
212601_at	+	0.0003	0.9996 KIAA0399
222313_at		0.0015	0.9996
204208_at		0.0016	0.9997 RNGTT
210916_s_at		0.0009	0.9997
224872_at		0.0006	0.9997 KIAA1463
241930_x_at	*	0.0006	0.9997
202530_at		0.0007	0.9998 MAPK14
203026_at		0.0004	0.9998 KIAA0354
203394_s_at		0.001	0.9998 HRY

215227_x_at	0.0002	0.9998 ACP1
229138_at	0.0012	0.9998

Table 40a: In total 280 cases of leukemia and normal bone marrow (BM) were analyzed. 263 of 280 cases (93.9%) were assigned to the correct leukemia subtype in all pairwise comparisons. The sensitivity indicated for each subgroup indicates the percentage of cases of the specific subgroup identified correctly in all pairwise comparisons. The specificity indicates for each subgroup the percentage of correct assignments to this subgroup.

	ALL	AML	CLL	CML	normal BM	total	sensitivity %	specificity %
ALL	35	9	1	1		47	76.60	94.74
AML	2	172			1	175	98.29	93.48
CLL		1	34			35	97.14	97.14
CML		1		13		14	92.86	92.86
normal BM		1			8	9	88.89	88.89
total	38	184	35	14	9	280		

Table 40b: In total 1120 individual assignments of leukemia were analyzed. 1103 of 1120 assignments (98.5%) were correct. The sensitivity indicated for each subgroup indicates the percentage of correct assignments for cases of the specific subgroup in pairwise comparisons. The specificity indicates for each subgroup the percentage of correct assignments to this subgroup.

5

	ALL	AML	CLL	CML	normal BM	total	sensitivity %	specificity %
ALL	177	9	1	1		188	94.15	98.88
AML	2	698			1	700	99.71	98.31
CLL		1	139			140	99.29	99.29
CML		1		55		56	98.21	98.21
normal BM		1			35	36	97.22	97.22
total	179	710	140	56	36	1120		

Table 41: Analysis of 4 leukemia subtypes and normal bone marrow according to the method described by Golub et al.

ALL	47
AML	175
CLL	35
CML	14
normal BM	9

ALL vs. all other

samples: 47 / 233

accuracy

0.960714285714286

confidence

0.912089069819735

failed:

11,12,13,14,16,20,24,41,42,45

,46

gene	signal-to-noise	p	decision limit	gene symbol
214761_at	0.970557084257439	0		OAZ
219013_at	-0.898496343314981	0*	66.1	FLJ21634
243362_s_at	0.885999523838621	0*	72.85	LEF1
229487_at	0.879786130972461	0		
224918_x_at	-0.87724222950274	0		MGST1
231736_x_at	-0.869791217148163	0		MGST1
203373_at	0.858710621146821	0		STATI2
201540_at	0.85206943650763	0		FHL1
218589_at	0.849690653983403	0		P2Y5
210487_at	0.84637653892686	0		DNTT
219753_at	0.825247459991453	0		STAG3
223703_at	-0.822007469078868	0		CDA017
203372_s_at	0.821441808884396	0		STATI2
243363_at	0.820493794299965	0		LEF1
208248_x_at	-0.812940151824066	0		APLP2
208702_x_at	-0.8015522739222	0		APLP2
200661_at	-0.791253715797081	0		PPGB
34726_at	0.790007042454156	0		CACNB3
203795_s_at	0.78850089331931	0		BCL7A
230292_at	0.788256600173715	0		

ALL vs. AML	samples: 47 / 175			
accuracy	0.95045045045045			
confidence	0.894203385037297			
failed:	11,12,14,15,16,24,27,36,42,67			
	,115			
gene	signal-to-noise	p	decision limit	gene symbol
221558_s_at	1.12614883575596	0		LEF1
224918_x_at	-1.11745973177444	0		MGST1
41220_at	1.1150066427645	0		MSF
231736_x_at	-1.10060017375911	0		MGST1
205382_s_at	-1.01589067961124	0		DF
200661_at	-1.01253920985203	0		PPGB
208702_x_at	-1.00158300302362	0		APLP2
223703_at	-0.995387894243593	0		CD4017
211404_s_at	-0.985001465936684	0		APLP2
208248_x_at	-0.981211344877388	0		APLP2
210948_s_at	0.973218284228957	0		LEF1
243363_at	0.96583392519617	0		LEF1
214875_x_at	-0.960268914986593	0		APLP2
214761_at	0.959842337636482	0		OAZ
219013_at	-0.956595406819358	0		FLJ21634
243362_s_at	0.953556737247221	0		LEF1
204215_at	0.94873841769727	0*	886.4	MGC4175
217989_at	-0.944775256168326	0		LOC51170
203041_s_at	-0.944024039515523	0		LAMP2
AFFX-r2-Bs-dap-3_at - HG-	0.252552477574741	0		
U133A				

ALL vs. CLL	samples: 47 / 35			
accuracy	0.98780487804878			
confidence	1			
failed:	42			
gene	signal-to-noise	p	decision limit	
225927_at	-2.54386605255744	0*	1826.45	MAP3K1
224838_at	-2.29762422456477	0		
239287_at	-2.24993335468714	0		
202625_at	-2.06005808097774	0		LYN
208091_s_at	-2.03821117161393	0		DKFZP564K0822
204511_at	-2.00374139556454	0		KIAA0793
AFFX-	1.9580832868002	0		GAPD
HUMGAPDH/M33197_3_at				
- HG-U133B				
201417_at	1.9394827392449	0		
212914_at	-1.89064460393095	0		PKP4
207616_s_at	-1.88874561163207	0		TANK
223391_at	-1.87749885738082	0		LOC81537
201416_at	1.87582200205394	0		SOX4
44790_s_at	-1.85742303821942	0		FLJ21562
201462_at	-1.84559373056342	0		KIAA0193
205997_at	-1.82244878004852	0		ADAM28
219471_at	-1.82048094941098	0		FLJ21562
228390_at	-1.81369080029951	0		
206337_at	-1.81234629147377	0		CCR7
218191_s_at	-1.80317310126938	0		FLJ11240
AFFX-	1.47237903994758	0		GAPD
HUMGAPDH/M33197_M_at				
- HG-U133A				

ALL vs. CML	samples: 47 / 14			
accuracy	0.983606557377049			
confidence	1			
failed:	14			
gene	signal-to-noise	p	decision limit	gene symbol
206440_at	-2.27699665329749	0		VELI1
210254_at	-2.24512948903079	0		
205557_at	-2.24379338781824	0*	8347.8	BPI
200654_at	-2.2057677822486	0		P4HB
206676_at	-2.19594220925272	0		CEACAM8
206111_at	-2.12209587819278	0		RNASE2
212268_at	-2.06787563904532	0		SERPINB1
214317_x_at	2.05505121682362	0		RPS9
211275_s_at	-2.0481841650404	0		GYG
212531_at	-1.99958187859813	0		LCN2
206207_at	-1.98193517857499	0		CLC
203757_s_at	-1.92761412477345	0		CEACAM6
204174_at	-1.91747003112972	0		ALOX5AP
207802_at	-1.90928433527318	0		SGP28
211657_at	-1.8921241480708	0		
213572_s_at	-1.87212093424446	0		SERPINB1
203949_at	-1.85990729100683	0		MPO
204351_at	-1.8590267215838	0		S100P
229790_at	1.85536512952314	0		TERF2
231854_at	1.67066719911877	0		

ALL vs. normal BM	samples: 47 / 9			
accuracy	1	p	decision limit	gene symbol
confidence	0.957516862739848			
gene	signal-to-noise	p	decision limit	gene symbol
203645_s_at	-2.39693596113584	0		CD163
224976_at	-2.31479350464798	0		NFIA
224975_at	-2.18458278616315	0		NFIA
218424_s_at	-2.15949227895441	0		FLJ10829
223044_at	-2.14051279056572	0		SLC11A3
230988_at	-2.14049582400222	0		
225792_at	-2.11616520995308	0		
223280_x_at	-2.05336993376349	0*	2365.65	MS4A6A
224970_at	-2.02013541876615	0		NFIA
215049_x_at	-1.97618634292152	0		CD163
224356_x_at	-1.93812195252731	0*	2203.55	MS4A6A
218916_at	1.86645836675574	0*	26.2	FLJ23436
201506_at	-1.80048485113822	0		TGFB1
202443_x_at	-1.76350311549162	0		NOTCH2
226751_at	-1.75212231661127	0		DKFZP566K1924
218516_s_at	1.74956324093924	0		FLJ20421
201416_at	1.74432934603701	0		SOX4
226448_at	-1.73849176051715	0		
221731_x_at	-1.73207109032378	0		CSPG2
40189_at	1.37012925113272	0		SET

AML vs. all other	samples: 175 / 105			
accuracy	0.882142857142857			
confidence	0.867062232379983			
failed:	17,20,35,51,64,68,86,143,145,189,191,199,217,253,258,259,260, 261,262,263,264,265,266,267,268,269,270,271,272,273,274,275, 280			
gene	signal-to-noise	p	decision limit	gene symbol
205382_s_at	0.993761979191943	0		DF
221558_s_at	-0.953118583183064	0		LEF1
233177_s_at	0.898951559660059	0		KIAA1184
221969_at	-0.897763040671617	0*	607.75	PAX5
206398_s_at	-0.887949095602823	0*	365.2	CD19
41220_at	-0.874923766956177	0		MSF
200661_at	0.864835685361425	0		PPGB
203005_at	0.859889652633032	0		LTBR
211404_s_at	0.848185516601275	0		APLP2
208702_x_at	0.844435105361934	0		APLP2
210948_s_at	-0.841151060868526	0		LEF1
221739_at	0.821598909550794	0		IL27
206255_at	-0.821040810957811	0		BLK
205049_s_at	-0.820101703791881	0		CD79A
231736_x_at	0.818968232559464	0		MGST1
214875_x_at	0.818667567167621	0		APLP2
241353_s_at	0.816044719173918	0		
215785_s_at	-0.815070063021364	0		CYFIP2
242774_at	-0.813216814821168	0		SYNE-2
201200_at	0.812769337801728	0		CREG

AML vs. CLL	samples: 175 / 35			
accuracy	0.995238095238095			
confidence	1			
failed:	206			
gene	signal-to-noise	p	decision limit	gene symbol
224838_at	-3.02914553670118	0		
243780_at	-2.47595031535238	0		
223514_at	-2.32616269321224	0*	401.75	CARD11
212827_at	-2.28998110195367	0		IGHM
239287_at	-2.23009354706297	0		
44790_s_at	-2.21489306728323	0		FLJ21562
228390_at	-2.19221126790713	0		
229072_at	-2.17738285030653	0		
224837_at	-2.17198876436932	0		FOXP1
223391_at	-2.16212129696244	0		LOC81537
219471_at	-2.15559694298803	0		FLJ21562
208456_s_at	-2.12547066951316	0		RRAS2
201998_at	-2.10911401275474	0		SIAT1
223287_s_at	-2.10564435434002	0		FOXP1
212590_at	-2.10270770151805	0		
229844_at	-2.06808415651229	0		
236280_at	-2.03990689910927	0		
230768_at	-2.02994432200127	0		
208091_s_at	-2.02423665232113	0		DKFZP564K0822
208864_s_at	2.01877334646697	0		TXN

AML vs. CML	samples: 175 / 14			
accuracy	0.994708994708995			
confidence	0.981183073260496			
failed:	180			
gene	signal-to-noise	p	decision limit	gene symbol
212531_at	-2.81906069321688	0		LCN2
205557_at	-2.2207882876404	0		BPI
207802_at	-2.21833080555492	0*	3039.3	SGP28
209772_s_at	-2.16935748435446	0*	3429.4	CD24
206676_at	-2.13938671438891	0*	7865.1	CEACAM8
210244_at	-2.09652835954526	0		CAMP
216379_x_at	-2.08891207162947	0		
209771_x_at	-2.07371303677609	0		CD24
203936_s_at	-2.04218257187719	0*	7297.15	MMP9
202018_s_at	-1.88089473759452	0		LTF
201029_s_at	1.75719687256454	0*	1592.95	MIC2
223894_s_at	-1.74095406790845	0*	455.2	FTS
207269_at	-1.71722340830381	0*	15756.25	DEFA4
203757_s_at	-1.70294141320522	0		CEACAM6
205863_at	-1.70288697664328	0		S100A12
211657_at	-1.69693858255424	0		
205513_at	-1.64900632810016	0		TCN1
223839_s_at	-1.60135318115808	0		
210254_at	-1.56841234039023	0		
39835_at	1.23907392901905	0		SBF1

AML vs. normal BM	samples: 175 / 9			
accuracy	0.989130434782609			
confidence	1			
failed:	48,179			
gene	signal-to-noise	p	decision limit	gene symbol
212531_at	-2.40063827757397	0		LCN2
210244_at	-2.19732582937896	0		CAMP
202018_s_at	-2.14183206922033	0*	12387	LTF
231241_at	-2.03350599733901	0		
218516_s_at	1.74555082511394	0		FLJ20421
225792_at	-1.63422305998419	0		
228377_at	-1.59923589910665	0		KIAA1384
244652_at	-1.53426287521002	0		
225700_at	-1.53281555961668	0		
201396_s_at	1.46522297092893	0		SGT
207802_at	-1.44831955629631	0		SGP28
208141_s_at	1.43174521272245	0		MGC4293
207269_at	-1.42268720126305	0		DEFA4
200631_s_at	1.40042176845386	0		SET
208651_x_at	-1.39706589332311	0		CD24
227151_at	1.39359540599557	0		
210004_at	-1.38874742675296	0		OLR1
203367_at	1.38466765321816	0		DUSP14
218916_at	1.37378311700267	0		FLJ23436
40189_at	1.35679082157773	0		SET

CLL vs. all other	samples: 35 / 245			
accuracy	0.996428571428571			
confidence	1			
failed:	31			
gene	signal-to-noise	p	decision limit	gene symbol
224838_at	2.79416338027605	0		
239287_at	2.23575554655226	0*	630.55	
223514_at	2.14355675231863	0		CARD11
44790_s_at	2.09543551175381	0		FLJ21562
228390_at	2.08427210739342	0		
223391_at	2.06238950802763	0		LOC81537
208091_s_at	2.03394814388952	0		DKFZP564K0822
219471_at	2.03307120566838	0		FLJ21562
229072_at	2.02056757302765	0		
243780_at	2.01909938888062	0		
223287_s_at	2.00808281461583	0		FOXP1
212590_at	1.988255009037	0		
229844_at	1.97715993452055	0		
208456_s_at	1.97615733325	0		RRAS2
201998_at	1.97574573382318	0		SIAT1
225927_at	1.95021458529306	0		MAP3K1
202589_at	-1.92898152025988	0		TYMS
230768_at	1.92227084324811	0		
224837_at	1.91127793077848	0		FOXP1
214615_at	1.91102072539205	0		P2Y10

CLL vs. CML	samples: 35 / 14			
	accuracy	p	decision limit	gene symbol
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
210254_at	-4.916136683483	0*	3718.45	
205557_at	-4.69748391957959	0		BPI
206111_at	-4.58827527010058	0		RNASE2
206871_at	-4.44599783341785	0		ELA2
202503_s_at	-4.43537957592345	0		KIAA0101
209619_at	4.43385248113705	0		CD74
203949_at	-4.37548189755698	0		MPO
202589_at	-4.23719643920935	0		TYMS
212268_at	-4.17631489395545	0		SERPINB1
212531_at	-4.14992393038831	0		LCN2
206676_at	-4.00803780946535	0		CEACAM8
210334_x_at	-3.95114669210453	0		BIRC5
204670_x_at	3.87175276162045	0		HLA-DRB5
224838_at	3.70493413772712	0		
208306_x_at	3.70225355884714	0		HLA-DRB4
212750_at	3.65712314278563	0		PPP1R16B
200654_at	-3.65009107919176	0		P4HB
213572_s_at	-3.6081864481715	0		SERPINB1
207269_at	-3.56289987570257	0		DEFA4
41577_at	3.23509608373299	0		PPP1R16B

CLL vs. normal BM	samples: 35 / 9			
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
210613_s_at	-4.82300971873091	0*	459.4	SYNGR1
204776_at	-4.80025506569938	0		THBS4
218662_s_at	-4.51907004754891	0		HCAP-G
205051_s_at	-4.20900192886026	0		KIT
202503_s_at	-4.20172034150208	0		KIAA0101
202580_x_at	-4.18939678293477	0		FOXM1
202018_s_at	-4.17647701264208	0		LTF
206871_at	-4.05443661323157	0		ELA2
230988_at	-4.04866661866689	0		
224975_at	-3.82592750915745	0		NFIA
227230_s_at	-3.69195069014623	0		KIAA1211
209714_s_at	-3.58566958034221	0		CDKN3
212531_at	-3.57925128815766	0		LCN2
214575_s_at	-3.54194227378832	0		AZU1
223785_at	-3.42904648124574	0		FLJ10719
224976_at	-3.40063969780409	0		NFIA
218424_s_at	-3.38874340856322	0		FLJ10829
202705_at	-3.38096906634746	0		CCNB2
202589_at	-3.36383889155021	0		TYMS

CML vs. all other	samples: 14 / 266			
accuracy	0.982142857142857			
confidence	0.984872053615011			
failed:	1,5,7,11,28			
gene	signal-to-noise	p	decision limit	gene symbol
212531_at	2.22285326348413	0		LCN2
205557_at	2.21595356438375	0*	11581.65	BPI
206676_at	2.03792028235761	0		CEACAM8
209772_s_at	1.92045186041392	0*	3429.4	CD24
207802_at	1.85737448791579	0		SGP28
216379_x_at	1.78690596201348	0		
209771_x_at	1.78099473628645	0		CD24
203936_s_at	1.76415242821485	0		MMP9
211657_at	1.70950599523981	0		
203757_s_at	1.69567517095366	0		CEACAM6
210254_at	1.67886160490067	0		
202018_s_at	1.66318733776484	0		LTF
211275_s_at	1.64178539863162	0		GYG
205513_at	1.62356154923572	0		TCN1
205863_at	1.61881375489405	0		S100A12
223839_s_at	1.58264885795695	0		
206440_at	1.58048354996482	0		VELI1
210244_at	1.57522288410986	0		CAMP
207269_at	1.5628690030838	0		DEFA4
204174_at	1.55441937407586	0		ALOX5AP

OML vs. normal BM	samples: 14 / 9			
accuracy	1	p	decision limit	gene symbol
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
227198_at	-3.96995770729437	0*	39.95	
204562_at	-3.83910818190111	0		IRF4
227749_at	-3.11980636745679	0		
228377_at	-2.65145492785893	0		KIAA1384
226713_at	-2.28229285614419	0		
209619_at	-2.27384420268273	0		CD74
227375_at	-2.22184735546056	0		DKFZP566D1346
204057_at	-2.13119125485665	0		ICSBP1
201506_at	-2.05058862618543	0		TGFBI
221558_s_at	-2.0055054625083	0		LEF1
227867_at	-2.00414646646454	0		
225331_at	-1.95134035825926	0		
223280_x_at	-1.95125537387335	0		MS4A6A
243780_at	-1.94601159348593	0		
228055_at	-1.94418493221925	0		
204670_x_at	-1.94197079510435	0		HLA-DRB5
208683_at	-1.93662356244796	0		CAPN2
210356_x_at	-1.92014292171279	0		MS4A2
209670_at	-1.89146017871026	0		TRA
AFFX-	1.0887744230798	0		GAPD
HUMGAPDH/M33197_3_at				
- HG-U133B				

normal BM vs. all other	samples: 9 / 271		
accuracy	0.975		
confidence	0.993135080527801		
failed:	1,3,4,5,6,8,9		
gene	signal-to-noise	p	decision limit
231241_at	1.74993445464942	0*	145.7
202018_s_at	1.72201479004034	0	LTF
212531_et	1.63441866839502	0	LCN2
210244_at	1.48912390888008	0	CAMP
244652_at	1.41243941049484	0	
224976_at	1.41100451645958	0	NFIA
218916_at	-1.39948677493198	0	FLJ23436
218516_s_at	-1.39516117721544	0	FLJ20421
208141_s_at	-1.38238694283986	0	MGC4293
201396_s_at	-1.3585420884411	0	SGT
230988_at	1.30213323583922	0	
200631_s_at	-1.2906273376207	0	SET
224975_at	1.28440445542309	0	NFIA
227497_at	1.2690169947779	0*	317.95
203535_at	1.26454687252909	0	S100A9
203367_at	-1.25252661696593	0	DUSP14
40189_at	-1.24465725545763	0	SET
223785_at	1.23866083411764	0	FLJ10719
225700_at	1.22842543098158	0	
207269_at	1.22161055733689	0	DEFA4

Table 42: Analysis of 4 leukemia subgroups and normal bone marrow (BM) according to the method described by Westfall & Young. The 499 significant genes are listed. The raw p value as well as the adjusted p value are shown. Furthermore it is indicated whether the genes were also identified as discriminative by the method described by Golub et al. (* most important gene in pairwise comparisons, + one of the top 20 5 significant genes)

geneID	Golub	rawp	adjp
200998_s_at		0.0001	0.0001 CKAP4
201012_at		0.0001	0.0001 ANXA1
201079_at		0.0001	0.0001 SYNGR2
201189_s_at		0.0001	0.0001 ITPR3
201200_at	+	0.0001	0.0001 CREG
201362_at		0.0001	0.0001 NS1-BP
201812_s_at		0.0001	0.0001 LOC54543
201853_s_at		0.0001	0.0001 CDC25B
201858_s_at		0.0001	0.0001 PRG1
201889_at		0.0001	0.0001 GS3786
201962_s_at		0.0001	0.0001 SBB103
201998_at	+	0.0001	0.0001 SIAT1
202018_s_at	*	0.0001	0.0001 LTF
202080_s_at		0.0001	0.0001 KIAA1042
202254_at		0.0001	0.0001 KIAA0440
202421_at		0.0001	0.0001 IGSF3
202441_at		0.0001	0.0001 KEO4
202524_s_at		0.0001	0.0001 KIAA0275
202606_s_at		0.0001	0.0001 TLK1
202709_at		0.0001	0.0001 FMOD
202723_s_at		0.0001	0.0001 FOXO1A
202761_s_at		0.0001	0.0001 SYNE-2
202822_at		0.0001	0.0001 LPP
202880_s_at		0.0001	0.0001 PSCD1
203020_at		0.0001	0.0001 KIAA0471
203037_s_at		0.0001	0.0001 KIAA0429
203057_s_at		0.0001	0.0001 PRDM2
203143_s_at		0.0001	0.0001 KIAA0040
203217_s_at		0.0001	0.0001 SIAT9
203233_at		0.0001	0.0001 IL4R
203241_at		0.0001	0.0001 UVRAG
203288_at		0.0001	0.0001 KIAA0355
203385_at		0.0001	0.0001 DGKA
203607_at		0.0001	0.0001 SAC2

203685_at		0.0001	0.0001 BCL2
203753_at		0.0001	0.0001 TCF4
203757_s_at	+	0.0001	0.0001 CEACAM6
203881_s_at		0.0001	0.0001 DMD
203936_s_at	*	0.0001	0.0001 MMP9
204000_at		0.0001	0.0001 GNB5
204118_at		0.0001	0.0001 CD48
204192_at		0.0001	0.0001 CD37
204199_at		0.0001	0.0001 RALGPS1A
204205_at		0.0001	0.0001 MDS019
204215_at	*	0.0001	0.0001 MGC4175
204269_at		0.0001	0.0001 PIM2
204328_at		0.0001	0.0001 LAK-4P
204352_at		0.0001	0.0001 TRAF5
204401_at		0.0001	0.0001 KCNN4
204511_at	+	0.0001	0.0001 KIAA0793
204512_at		0.0001	0.0001 HIVEP1
204604_at		0.0001	0.0001 PFTK1
204674_at		0.0001	0.0001 LRMP
204731_at		0.0001	0.0001 TGFBR3
204793_at		0.0001	0.0001 KIAA0443
204882_at		0.0001	0.0001 KIAA0053
204922_at		0.0001	0.0001 FLJ22531
204951_at		0.0001	0.0001 ARHH
205019_s_at		0.0001	0.0001 VIPR1
205040_at		0.0001	0.0001 ORM1
205041_s_at		0.0001	0.0001 ORM1
205049_s_at	+	0.0001	0.0001 CD79A
205105_at		0.0001	0.0001 MAN2A1
205192_at		0.0001	0.0001 MAP3K14
205223_at		0.0001	0.0001 KIAA0645
205267_at		0.0001	0.0001 POU2AF1
205306_x_at		0.0001	0.0001 KMO
205308_at		0.0001	0.0001 LOC51101
205383_s_at		0.0001	0.0001 ZNF288
205414_s_at		0.0001	0.0001 KIAA0672
205513_at	+	0.0001	0.0001 TCN1
205547_s_at	*	0.0001	0.0001 TAGLN
205557_at	*	0.0001	0.0001 BPI
205599_at		0.0001	0.0001 TRAF1
205613_at		0.0001	0.0001 LOC51760
205627_at		0.0001	0.0001 CDA

205671_s_at		0.0001	0.0001 HLA-DOB
205691_at		0.0001	0.0001 SYNGR3
205790_at		0.0001	0.0001 SCAP1
205801_s_at		0.0001	0.0001 GRP3
205805_s_at		0.0001	0.0001 ROR1
205863_at	+	0.0001	0.0001 S100A12
205901_at		0.0001	0.0001 PNOC
205933_at		0.0001	0.0001 SETBP1
205997_at	+	0.0001	0.0001 ADAM28
206111_at	+	0.0001	0.0001 RNASE2
206126_at		0.0001	0.0001 BLR1
206150_at		0.0001	0.0001 TNFRSF7
206177_s_at		0.0001	0.0001 ARG1
206245_s_at		0.0001	0.0001 NS1-BP
206255_at	+	0.0001	0.0001 BLK
206337_at	+	0.0001	0.0001 CCR7
206398_s_at	*	0.0001	0.0001 CD19
206513_at		0.0001	0.0001 AIM2
206515_at		0.0001	0.0001 CYP4F3
206676_at	*	0.0001	0.0001 CEACAM8
206759_at		0.0001	0.0001 FCER2
206760_s_at		0.0001	0.0001 FCER2
207000_s_at		0.0001	0.0001 PPP3CC
207168_s_at		0.0001	0.0001 H2AFY
207269_at	*	0.0001	0.0001 DEFA4
207384_at		0.0001	0.0001 PGLYRP
207641_at		0.0001	0.0001 TACI
207700_s_at		0.0001	0.0001 NCOA3
207734_at		0.0001	0.0001 FLJ20340
207777_s_at		0.0001	0.0001 SP140
207802_at	*	0.0001	0.0001 SGP28
207819_s_at		0.0001	0.0001 ABCB4
207957_s_at		0.0001	0.0001 PRKCB1
208091_s_at	+	0.0001	0.0001 DKFZP564K0822
208168_s_at		0.0001	0.0001 CHIT1
208190_s_at		0.0001	0.0001 LISCH7
208195_at		0.0001	0.0001 TTN
208268_at		0.0001	0.0001 ADAM28
208456_s_at	+	0.0001	0.0001 RRAS2
208470_s_at		0.0001	0.0001 HPR
208623_s_at		0.0001	0.0001 VIL2
208657_s_at		0.0001	0.0001 MSF

208864_s_at	+	0.0001	0.0001 TXN
208913_at		0.0001	0.0001 GGA2
208914_at		0.0001	0.0001 GGA2
209060_x_at		0.0001	0.0001 NCOA3
209061_at		0.0001	0.0001 NCOA3
209062_x_at		0.0001	0.0001 NCOA3
209075_s_at		0.0001	0.0001 NIFU
209236_at		0.0001	0.0001
209306_s_at		0.0001	0.0001 SWAP70
209307_at		0.0001	0.0001 SWAP70
209374_s_at		0.0001	0.0001 IGHM
209412_at		0.0001	0.0001 TMEM1
209682_at		0.0001	0.0001 CBLB
209685_s_at		0.0001	0.0001 PRKCB1
209761_s_at		0.0001	0.0001 SP110
209765_at		0.0001	0.0001 ADAM19
209772_s_at	*	0.0001	0.0001 CD24
209780_at		0.0001	0.0001 DKFZP564F013
209827_s_at		0.0001	0.0001 IL16
209994_s_at		0.0001	0.0001 ABCB1
210004_at	+	0.0001	0.0001 OLR1
210244_at	+	0.0001	0.0001 CAMP
210262_at		0.0001	0.0001 TPX1
210268_at		0.0001	0.0001 NFX1
210279_at		0.0001	0.0001 GPR18
210356_x_at	+	0.0001	0.0001 MS4A2
210658_s_at		0.0001	0.0001 GGA2
210763_x_at		0.0001	0.0001 LY117
210789_x_at		0.0001	0.0001 CEACAM3
210948_s_at	+	0.0001	0.0001 LEF1
211105_s_at		0.0001	0.0001 NFATC1
211138_s_at		0.0001	0.0001 KMO
211352_s_at		0.0001	0.0001 NCOA3
211502_s_at		0.0001	0.0001 PFTK1
211657_at	+	0.0001	0.0001
211771_s_at		0.0001	0.0001 POU2F2
211883_x_at		0.0001	0.0001 CEACAM1
211889_x_at		0.0001	0.0001 CEACAM1
211984_at		0.0001	0.0001
212074_at		0.0001	0.0001 KIAA0810
212229_s_at		0.0001	0.0001
212231_at		0.0001	0.0001 FBXO21

212268_at	+	0.0001	0.0001 SERPINB1
212311_at		0.0001	0.0001 KIAA0746
212313_at		0.0001	0.0001
212314_at		0.0001	0.0001 KIAA0746
212345_s_at		0.0001	0.0001 DKFZP586F2423
212382_at		0.0001	0.0001
212385_at		0.0001	0.0001
212386_at		0.0001	0.0001
212387_at		0.0001	0.0001
212400_at		0.0001	0.0001
212531_at	+	0.0001	0.0001 LCN2
212569_at		0.0001	0.0001 KIAA0650
212577_at		0.0001	0.0001 KIAA0650
212579_at		0.0001	0.0001 KIAA0650
212589_at		0.0001	0.0001 RRAS2
212590_at	+	0.0001	0.0001
212614_at		0.0001	0.0001
212660_at		0.0001	0.0001 KIAA0239
212733_at		0.0001	0.0001 KIAA0226
212735_at		0.0001	0.0001 KIAA0226
212827_at	+	0.0001	0.0001 IGHM
212838_at		0.0001	0.0001 KIAA1010
212886_at		0.0001	0.0001 DKFZP434C171
212914_at	+	0.0001	0.0001 PKP4
212956_at		0.0001	0.0001 KIAA0882
212960_at		0.0001	0.0001 KIAA0882
212970_at		0.0001	0.0001
212985_at		0.0001	0.0001
213049_at		0.0001	0.0001 DKFZp566D133
213142_x_at		0.0001	0.0001 LOC54103
213295_at		0.0001	0.0001
213309_at		0.0001	0.0001 PLCL2
213353_at		0.0001	0.0001 ABCA5
213370_s_at		0.0001	0.0001 DKFZP434L243
213453_x_at		0.0001	0.0001 GAPD
213511_s_at		0.0001	0.0001
213572_s_at	+	0.0001	0.0001 SERPINB1
213600_at		0.0001	0.0001 KIAA0545
213622_at		0.0001	0.0001 COL9A2
213674_x_at		0.0001	0.0001 IGHG3
213689_x_at		0.0001	0.0001 RPL5
213772_s_at		0.0001	0.0001 GGA2

213891_s_at		0.0001	0.0001
213927_at		0.0001	0.0001
214238_at		0.0001	0.0001
214615_at	+	0.0001	0.0001 P2Y10
214686_at		0.0001	0.0001 ZNF266
214786_at		0.0001	0.0001 MAP3K1
214924_s_at		0.0001	0.0001
215100_at		0.0001	0.0001
215346_at		0.0001	0.0001 TNFRSF5
215785_s_at	+	0.0001	0.0001 CYFIP2
216044_x_at		0.0001	0.0001
216095_x_at		0.0001	0.0001 MTMR1
216218_s_at		0.0001	0.0001 PLCL2
216356_x_at		0.0001	0.0001 BAIAP3
217398_x_at		0.0001	0.0001
217418_x_at		0.0001	0.0001 MS4A2
217478_s_at		0.0001	0.0001
217504_at		0.0001	0.0001 ABCA6
217838_s_at		0.0001	0.0001 RNB6
217950_at		0.0001	0.0001 NOSIP
218090_s_at		0.0001	0.0001
218100_s_at		0.0001	0.0001 ESRRBL1
218329_at		0.0001	0.0001 PRDM4
218354_at		0.0001	0.0001 LOC51693
218531_at		0.0001	0.0001 FLJ21749
218614_at		0.0001	0.0001 FLJ10652
218974_at		0.0001	0.0001 FLJ10159
219029_at		0.0001	0.0001 FLJ21657
219073_s_at		0.0001	0.0001 OSBPL10
219221_at		0.0001	0.0001 FLJ22332
219471_at	+	0.0001	0.0001 FLJ21562
219574_at		0.0001	0.0001 FLJ20668
219690_at		0.0001	0.0001 FLJ22573
219734_at		0.0001	0.0001 FLJ20174
219820_at		0.0001	0.0001 NTT5
220001_at		0.0001	0.0001 PAD15
220007_at		0.0001	0.0001 FLJ13984
220059_at		0.0001	0.0001 BRDG1
220118_at		0.0001	0.0001 TZFP
220338_at		0.0001	0.0001 FLJ10244
220987_s_at		0.0001	0.0001 DKFZP434J037
220999_s_at		0.0001	0.0001 PRO1331

221011_s_at		0.0001	0.0001 DKFZP566J091,
221030_s_at		0.0001	0.0001 DKFZP564B1162
221234_s_at		0.0001	0.0001 BACH2
221239_s_at		0.0001	0.0001 SPAP1
221268_s_at		0.0001	0.0001 LOC81537
221331_x_at		0.0001	0.0001 CTLA4
221558_s_at	+	0.0001	0.0001 LEF1
221586_s_at		0.0001	0.0001 E2F5
221601_s_at		0.0001	0.0001 TOSO
221602_s_at		0.0001	0.0001 TOSO
221778_at		0.0001	0.0001 KIAA1718
221865_at		0.0001	0.0001
221969_at	*	0.0001	0.0001 PAX5
222073_at		0.0001	0.0001 COL4A3
222146_s_at		0.0001	0.0001
222150_s_at		0.0001	0.0001
222520_s_at		0.0001	0.0001 ESRRBL1
222996_s_at		0.0001	0.0001 HSPC195
223287_s_at	+	0.0001	0.0001 FOXP1
223391_at	+	0.0001	0.0001 LOC81537
223422_s_at		0.0001	0.0001 DKFZP564B1162
223514_at	*	0.0001	0.0001 CARD11
223522_at		0.0001	0.0001 GL012
223595_at		0.0001	0.0001 AD031
223894_s_at	*	0.0001	0.0001 FTS
224404_s_at		0.0001	0.0001 IRTA2
224405_at		0.0001	0.0001 IRTA2
224406_s_at		0.0001	0.0001 IRTA2
224482_s_at		0.0001	0.0001 MGC11316
224516_s_at		0.0001	0.0001 HSPC195
224609_at		0.0001	0.0001 CTL2
224735_at		0.0001	0.0001
224811_at		0.0001	0.0001
224833_at		0.0001	0.0001 ETS1
224837_at	+	0.0001	0.0001 FOXP1
224838_at	+	0.0001	0.0001
224994_at		0.0001	0.0001 CAMK2D
225136_at		0.0001	0.0001
225144_at		0.0001	0.0001
225230_at		0.0001	0.0001 CEPT1
225246_at		0.0001	0.0001 STIM2
225250_at		0.0001	0.0001 STIM2

225327_at	0.0001	0.0001 FLJ10980
225512_at	0.0001	0.0001
225624_at	0.0001	0.0001
225629_s_at	0.0001	0.0001 KIAA1538
225635_s_at	0.0001	0.0001
225640_at	0.0001	0.0001
225917_at	0.0001	0.0001 DKFZp762B226
225927_at	0.0001	0.0001 MAP3K1
226005_at	0.0001	0.0001
226008_at	0.0001	0.0001 HCA4
226013_at	0.0001	0.0001
226063_at	0.0001	0.0001
226122_at	0.0001	0.0001
226147_s_at	0.0001	0.0001
226156_at	0.0001	0.0001 AKT2
226247_at	0.0001	0.0001
226250_at	0.0001	0.0001
226252_at	0.0001	0.0001
226258_at	0.0001	0.0001
226301_at	0.0001	0.0001 dJ55C23.6
226326_at	0.0001	0.0001
226384_at	0.0001	0.0001 HTPAP
226408_at	0.0001	0.0001 TEAD2
226454_at	0.0001	0.0001 LOC92979
226508_at	0.0001	0.0001
226538_at	0.0001	0.0001 MAN2A1
226550_at	0.0001	0.0001
226560_at	0.0001	0.0001
226625_at	0.0001	0.0001 TGFBR3
226635_at	0.0001	0.0001
226641_at	0.0001	0.0001
226713_at	0.0001	0.0001
226878_at	0.0001	0.0001
226905_at	0.0001	0.0001
226989_at	0.0001	0.0001
227030_at	0.0001	0.0001
227047_x_at	0.0001	0.0001 KIAA1538
227121_at	0.0001	0.0001
227146_at	0.0001	0.0001
227152_at	0.0001	0.0001
227167_s_at	0.0001	0.0001
227173_s_at	0.0001	0.0001 BACH2

227189_at		0.0001	0.0001 KIAA1599
227198_at		0.0001	0.0001
227224_at		0.0001	0.0001
227261_at		0.0001	0.0001 KLF12
227393_at		0.0001	0.0001
227396_at		0.0001	0.0001
227408_s_at		0.0001	0.0001 MSTP043
227414_at		0.0001	0.0001 DKFZp547E052
227478_at		0.0001	0.0001
227533_at		0.0001	0.0001
227568_at		0.0001	0.0001
227606_s_at		0.0001	0.0001 KIAA1373
227607_at		0.0001	0.0001 KIAA1373
227670_at		0.0001	0.0001
227749_at	+	0.0001	0.0001
227767_at		0.0001	0.0001 CSNK1G3
227817_at		0.0001	0.0001
227900_at		0.0001	0.0001
228003_at		0.0001	0.0001
228007_at		0.0001	0.0001
228029_at		0.0001	0.0001 KIAA1982
228298_at		0.0001	0.0001 LOC91523
228343_at		0.0001	0.0001 POU2F2
228345_at		0.0001	0.0001
228377_at	+	0.0001	0.0001 KIAA1384
228390_at	+	0.0001	0.0001
228471_at		0.0001	0.0001
228476_at		0.0001	0.0001 KIAA1407
228518_at		0.0001	0.0001 IGHG3
228551_at		0.0001	0.0001
228555_at		0.0001	0.0001
228592_at		0.0001	0.0001
228599_at		0.0001	0.0001
228693_at		0.0001	0.0001
228984_at		0.0001	0.0001 KIAA1394
229001_at		0.0001	0.0001
229070_at		0.0001	0.0001 MGC12335
229072_at	+	0.0001	0.0001
229194_at		0.0001	0.0001
229310_at		0.0001	0.0001 KIAA1921
229383_at		0.0001	0.0001
229513_at		0.0001	0.0001

229659_s_at		0.0001	0.0001
229681_at		0.0001	0.0001
229750_at		0.0001	0.0001
229779_at		0.0001	0.0001
229844_at	+	0.0001	0.0001
229872_s_at		0.0001	0.0001 KIAA0493
229923_at		0.0001	0.0001
229934_at		0.0001	0.0001
230110_at		0.0001	0.0001
230245_s_at		0.0001	0.0001
230363_s_at		0.0001	0.0001 SAC2
230489_at		0.0001	0.0001 CD5
230499_at		0.0001	0.0001
230551_at		0.0001	0.0001
230648_at		0.0001	0.0001
230689_at		0.0001	0.0001
230753_at		0.0001	0.0001
230768_at	+	0.0001	0.0001
230793_at		0.0001	0.0001 FLJ20048
230802_at		0.0001	0.0001 DKFZP564B1162
230803_s_at		0.0001	0.0001 DKFZP564B1162
230834_at		0.0001	0.0001
230877_at		0.0001	0.0001 IGHG3
230917_at		0.0001	0.0001
230939_at		0.0001	0.0001
230983_at		0.0001	0.0001
230986_at		0.0001	0.0001
230997_at		0.0001	0.0001
231093_at		0.0001	0.0001 FCRH3
231332_at		0.0001	0.0001
231406_at		0.0001	0.0001
231418_at		0.0001	0.0001 MS4A2
231647_s_at		0.0001	0.0001 IRTA2
231656_x_at		0.0001	0.0001 OSBPL10
231775_at		0.0001	0.0001 TNFRSF10A
231793_s_at		0.0001	0.0001 CAMK2D
231794_at		0.0001	0.0001 CTLA4
231873_at		0.0001	0.0001
232027_at		0.0001	0.0001
232060_at		0.0001	0.0001
232112_at		0.0001	0.0001
232125_at		0.0001	0.0001

232210_at	0.0001	0.0001
232614_at	0.0001	0.0001
232739_at	0.0001	0.0001
232950_s_at	0.0001	0.0001 NIR3
233483_at	0.0001	0.0001
233955_x_at	0.0001	0.0001 HSPC195
234140_s_at	0.0001	0.0001 STIM2
234362_s_at	0.0001	0.0001 CTLA4
234725_s_at	0.0001	0.0001 SEMA4B
235023_at	0.0001	0.0001
235051_at	0.0001	0.0001
235061_at	0.0001	0.0001
235331_x_at	0.0001	0.0001
235353_at	0.0001	0.0001 KIAA0746
235372_at	0.0001	0.0001 FREB
235385_at	0.0001	0.0001 FLJ20668
235400_at	0.0001	0.0001 FREB
235401_s_at	0.0001	0.0001 FREB
235422_at	0.0001	0.0001 FALZ
235444_at	0.0001	0.0001
235459_at	0.0001	0.0001
235674_at	0.0001	0.0001
235982_at	0.0001	0.0001 FCRH1
236190_at	0.0001	0.0001
236226_at	0.0001	0.0001
236248_x_at	0.0001	0.0001
236265_at	0.0001	0.0001
236280_at	0.0001	0.0001
236293_at	0.0001	0.0001
236301_at	0.0001	0.0001
236341_at	0.0001	0.0001 CTLA4
236458_at	0.0001	0.0001
236796_at	0.0001	0.0001
236854_at	0.0001	0.0001
236979_at	0.0001	0.0001
237411_at	0.0001	0.0001 LOC153516
238055_at	0.0001	0.0001
238057_at	0.0001	0.0001
238376_at	0.0001	0.0001
238516_at	0.0001	0.0001 BMPR2
238593_at	0.0001	0.0001
238604_at	0.0001	0.0001

238790_at		0.0001	0.0001
239054_at		0.0001	0.0001
239122_at		0.0001	0.0001 IL24
239152_at		0.0001	0.0001
239229_at		0.0001	0.0001
239231_at		0.0001	0.0001
239278_at		0.0001	0.0001
239287_at		0.0001	0.0001
239292_at		0.0001	0.0001
239442_at		0.0001	0.0001
239679_at		0.0001	0.0001
240061_at		0.0001	0.0001
240572_s_at		0.0001	0.0001
241483_at		0.0001	0.0001
242104_at		0.0001	0.0001
242388_x_at		0.0001	0.0001
242404_at		0.0001	0.0001
242458_at		0.0001	0.0001
242463_x_at		0.0001	0.0001
242541_at		0.0001	0.0001 ABCA9
242633_x_at		0.0001	0.0001
242774_at	+	0.0001	0.0001 SYNE-2
242866_x_at		0.0001	0.0001
242932_at		0.0001	0.0001
243030_at		0.0001	0.0001
243154_at		0.0001	0.0001
243780_at	+	0.0001	0.0001
243798_at		0.0001	0.0001
243932_at		0.0001	0.0001
243968_x_at		0.0001	0.0001
244261_at		0.0001	0.0001
32541_at		0.0001	0.0001 PPP3CC
35974_at		0.0001	0.0001 LRMP
37152_at		0.0001	0.0001 PPARD
37831_at		0.0001	0.0001 KIAA0545
38149_at		0.0001	0.0001 KIAA0053
41220_at	+	0.0001	0.0001 MSF
41660_at		0.0001	0.0001 CELSR1
44790_s_at	+	0.0001	0.0001 FLJ21562
49485_at		0.0001	0.0001 PRDM4
54970_at		0.0001	0.0001 DKFZP761I2123
74694_s_at		0.0001	0.0001 FLJ23282

AFFX-HUMGAPDH/M33197_3_at - HG-U133A 0.0001 **0.0001** GAPD
AFFX-HUMGAPDH/M33197_3_at + 0.0001 **0.0001** GAPD
- HG-U133B
AFFX-HUMGAPDH/M33197_M_at + 0.0001 **0.0001** GAPD
- HG-U133A

Table 43a: Functional annotation of all genes identified with relevance to leukemia subtyping

ID	Gene Symbol	Unigene_Cluster	SWISS-PROT	Locus	
				Link	Map Location
1007_s_at_HG-U133A	DDR1	Hs.75562	Q08345	780	6p21.3
1729_at_HG-U133A	TRADD	Hs.89862	Q15628	8717	16q22
200008_s_at_HG-U133A	GDI2	Hs.56845	P50395	2665	10p15
200008_s_at_HG-U133B	GDI2	Hs.56845	P50395	2665	10p15
200023_s_at_HG-U133A	EIF3S5	Hs.7811	O00303	8665	2p16.1
200040_at_HG-U133A	KHDRBS1	Hs.119537	Q99760	10657	1p32
200047_s_at_HG-U133A	YY1	Hs.97496	P25490	7528	14q
200047_s_at_HG-U133B	YY1	Hs.97496	P25490	7528	14q
200056_s_at_HG-U133A	C1D	Hs.15164	Q13901	10438	2p13-p12
200068_s_at_HG-U133B	CANX	Hs.155560	P27824	821	5q35
200071_at_HG-U133A	SPF30	Hs.79968	O75940	10285	10q23
200072_s_at_HG-U133A	HNRPMP	Hs.79024	P52272	4670	19p13.3-p13.2
200093_s_at_HG-U133A	HINT1	Hs.256697	P49773	3094	5q31.2
200094_s_at_HG-U133A	EEF2	Hs.75309	P13639	1938	19pter-q12
200598_s_at_HG-U133A	TRA1	Hs.82689	P14625	7184	12q24.2-q24.3
200608_s_at_HG-U133A	RAD21	Hs.81848	O60216	5885	8q24
200620_at_HG-U133A	C1orf8	Hs.11441	Q9BXS4	9528	1p36-p31
200625_s_at_HG-U133A	CAP	Hs.104125	Q01518	10487	1p34.3
200630_x_at_HG-U133A	SET	Hs.145279	Q15541	6418	9q34
200631_s_at_HG-U133A	SET	Hs.145279	Q01105	6418	9q34
200646_s_at_HG-U133A	NUCB1	Hs.172609	Q96BA4	4924	19q13.2-q13.4
200649_at_HG-U133A	NUCB1	Hs.172609	Q96BA4	4924	19q13.2-q13.4
200650_s_at_HG-U133A	LDHA	Hs.2795	P00338	3939	11p15.4
200654_at_HG-U133A	P4HB	Hs.75655	P07237	5034	17q25
200655_s_at_HG-U133A	CALM1	Hs.177656	AAH08597	801	14q24-q31
200656_s_at_HG-U133A	P4HB	Hs.75655	AAH10859	5034	17q25
200659_s_at_HG-U133A	PHB	Hs.75323	P35232	5245	17q21
200661_at_HG-U133A	PPGB	Hs.118126	P10619	5476	20q13.1
200665_s_at_HG-U133A	SPARC	Hs.111779	AAH08011	6678	5q31.3-q32
200673_at_HG-U133A	LAPTM4A	Hs.111894	Q15012	9741	2p24.3
200675_at_HG-U133A	CD81	Hs.54457	P18582	975	11p15.5
200679_x_at_HG-U133A	HMG1	Hs.337757	P09429	3146	13q12
200707_at_HG-U133A	PRKCSH	Hs.1432	Q96D06	5589	19p13.1-p13.2
200742_s_at_HG-U133A	CLN2	Hs.20478	O14773	1200	11p15
200743_s_at_HG-U133A	CLN2	Hs.20478	O14773	1200	11p15
200765_x_at_HG-U133A	CTNNA1	Hs.178452	AAH00385	1495	5q31
200770_s_at_HG-U133A	LAMC1	Hs.214982	P11047	3915	1q31
200825_s_at_HG-U133A	ORP150	Hs.277704	Q9Y4L1	10525	11q23.1-q23.3

200829_x_at_HG-U133A	ZNF207	Hs.62112	O43670	7756	17q11.2
200832_s_at_HG-U133A	SCD	Hs.119597	O00767	6319	10q23-q24
200867_at_HG-U133A					
200872_at_HG-U133A	S100A10	Hs.119301	P08206	6281	1q21
200890_s_at_HG-U133A	SSR1	Hs.250773	P43307	6745	6p23
200906_s_at_HG-U133A					
200907_s_at_HG-U133A	KIAA0992	Hs.194431	Q8WX93	23022	4q32.3
200917_s_at_HG-U133A	SRPR	Hs.75730	P08240	6734	11q23-q24
200931_s_at_HG-U133A	VCL	Hs.75350	P18206	7414	10q22.1-q23
200935_at_HG-U133A	CALR	Hs.16488	P27797	811	19p13.3-p13.2
200951_s_at_HG-U133A	CCND2	Hs.75586	P30279	894	12p13
200952_s_at_HG-U133A	CCND2	Hs.75586	P30279	894	12p13
200953_s_at_HG-U133A	CCND2	Hs.75586	P30279	894	12p13
200967_at_HG-U133A	PPIB	Hs.699	Q9BVK5	5479	15q21-q22
200968_s_at_HG-U133A	PPIB	Hs.699	P23284	5479	15q21-q22
200984_s_at_HG-U133A	CD59	Hs.278573	P13987	966	11p13
200985_s_at_HG-U133A	CD59	Hs.278573	AAH01506	966	11p13
200986_at_HG-U133A	SERPING1	Hs.151242	P05155	710	11q12-q13.1
200996_at_HG-U133A	ACTR3	Hs.5321	AAD51904	10096	2q13
200998_s_at_HG-U133A	CKAP4	Hs.74368	Q07065	10970	12q23.3
201004_at_HG-U133A	SSR4	Hs.102135	Q96BQ0	6748	Xq28
201005_at_HG-U133A	CD9	Hs.1244	P21926	928	12p13.3
201008_s_at_HG-U133A	TXNIP	Hs.179526	Q16226	10628	1q12
201012_at_HG-U133A	ANXA1	Hs.78225	P04083	301	9q12-q21.2
201015_s_at_HG-U133A	JUP	Hs.2340	Q15151	3728	17q21
201029_s_at_HG-U133A	MIC2	Hs.177543	AAH02584	4267	Xp22.32
201034_at_HG-U133A	ADD3	Hs.324470	Q9UEY8	120	10q24.2-q24.3
201061_s_at_HG-U133A	EPB72	Hs.160483	P27105	2040	9q34.1
201069_at_HG-U133A	MMP2	Hs.111301	P08253	4313	16q13-q21
201079_at_HG-U133A	SYNGR2	Hs.5097	O43760	9144	17qter
201105_at_HG-U133A	LGALS1	Hs.227751	P09382	3956	22q13.1
201125_s_at_HG-U133A	ITGB5	Hs.149846	AAH06541	3693	3q21.3
201137_s_at_HG-U133A	HLA-DPB1	Hs.814	Q30174	3115	6p21.3
201152_s_at_HG-U133A	MBNL	Hs.28578	Q96P92	4154	3q25
201153_s_at_HG-U133A	MBNL	Hs.28578	Q96RE3	4154	3q25
201162_at_HG-U133A	IGFBP7	Hs.119206	Q16270	3490	4q12
201163_s_at_HG-U133A	IGFBP7	Hs.119206	Q07822	3490	4q12
201164_s_at_HG-U133A	PUM1	Hs.153834	Q14671	9698	1p35.2
201189_s_at_HG-U133A	ITPR3	Hs.77515	Q14573	3710	6p21
201200_at_HG-U133A	CREG	Hs.5710	O75629	8804	1q24
201247_at_HG-U133A	SREBF2	Hs.108689	Q12772	6721	22q13
201263_at_HG-U133A	TARS	Hs.84131	P26639	6897	5p13-cen

201278_at_HG-U133A	DAB2	Hs.81988	P98082	1601	5p13
201281_at_HG-U133A	ADRM1	Hs.90107	Q16186	11047	20q13.33
201324_at_HG-U133A	EMP1	Hs.79368	P54849	2012	12p12.3
201334_s_at_HG-U133A	ARHGEF12	Hs.6582	O15086	23365	11q23.3
201338_x_at_HG-U133A	GTF3A	Hs.75113	Q9H2K0	2971	13q12.3-q13.1
201352_at_HG-U133A	YME1L1	Hs.206521	Q9UMR9	10730	10p14
201358_s_at_HG-U133A	COPB	Hs.3059	AAL39009	1315	11p15.2
201359_at_HG-U133A	COPB	Hs.3059	P53618	1315	11p15.2
201360_at_HG-U133A	CST3	Hs.135084	P01034	1471	20p11.21
201362_at_HG-U133A	NS1-BP	Hs.197298	Q9Y480	10625	1q25.1-q31.1
201377_at_HG-U133A	KIAA0144	Hs.8127	Q9BTU3	9898	1q21.2
201396_s_at_HG-U133A	SGT	Hs.203910	O43765	6449	19p13
201416_at_HG-U133A	SOX4	Hs.83484	Q99687	6659	6p22.3
201417_at_HG-U133A					
201425_at_HG-U133A	ALDH2	Hs.195432	P05091	217	12q24.2
201433_s_at_HG-U133A	PTDSS1	Hs.77329	Q9BUQ5	9791	8q22
201437_s_at_HG-U133A	EIF4E	Hs.79306	P06730	1977	4q21-q25
201462_at_HG-U133A	KIAA0193	Hs.75137	BAA12106	9805	7p14.3-p14.1
201463_s_at_HG-U133A	TALDO1	Hs.77290	P37837	6888	11p15.5-p15.4
201482_at_HG-U133A	QSCN6	Hs.77266	O00391	5768	1q24
201485_s_at_HG-U133A	RCN2	Hs.79088	AAH04892	5955	15q23
201486_at_HG-U133A	RCN2	Hs.79088	AAH04892	5955	15q23
201496_x_at_HG-U133A	MYH11	Hs.78344	O14729	4629	16p13.13-p13.12
201497_x_at_HG-U133A	MYH11	Hs.78344	O14729	4629	16p13.13-p13.12
201506_at_HG-U133A	TGFBI	Hs.118787	Q96IU7	7045	5q31
201530_x_at_HG-U133A	EIF4A1	Hs.129673	Q9BRB1	1973	17p13
201537_s_at_HG-U133A	DUSP3	Hs.181046	Q96HQ4	1845	17q21
201540_at_HG-U133A	FHL1	Hs.239069	Q13642	2273	Xq26
201548_s_at_HG-U133A	PLU-1	Hs.143323	O95811	10765	1q32.1
201564_s_at_HG-U133A	SNL	Hs.118400	Q96IH1	6624	7p22
201585_s_at_HG-U133A	SFPQ	Hs.180610	P23246	6421	1p34.2
201592_at_HG-U133A	EIF3S3	Hs.58189	O15372	8667	8q24.11
201595_s_at_HG-U133A	HT010	Hs.6375	Q9NZ37	55854	2q32.2
201596_x_at_HG-U133A	KRT18	Hs.65114	Q96GD2	3875	12q13
201602_s_at_HG-U133A	PPP1R12A	Hs.16533	Q96L23	4659	12q15-q21
201640_x_at_HG-U133A	CLPTM1	Hs.106671	Q9BSS5	1209	19q13.2-q13.3
201644_at_HG-U133A	TSTA3	Hs.264428	Q13630	7264	8q24.3
201652_at_HG-U133A	COPS5	Hs.198767	Q9BQ17	10987	8q12.3
201753_s_at_HG-U133A	ADD3	Hs.324470	Q9UEY8	120	10q24.2-q24.3
201761_at_HG-U133A	MTHFD2	Hs.154672	P13995	10797	2p12
201810_s_at_HG-U133A	SH3BP5	Hs.109150	O60239	9467	3p24.3
201811_x_at_HG-U133A	SH3BP5	Hs.109150	Q9BRM4	9467	3p24.3

201812_s_at_HG-U133A	LOC54543	Hs.112318	Q9P0U1	54543	7p21.3
201813_s_at_HG-U133A	KIAA0210	Hs.115740	Q92609	9779	3p24.3
201825_s_at_HG-U133A	LOC51097	Hs.238126	AAH26185	51097	1q44
201828_x_at_HG-U133A	CXX1	Hs.250708	O15255	8933	Xq26
201829_at_HG-U133A	NET1	Hs.25155	Q9UEN6	10276	10p15
201830_s_at_HG-U133A	NET1	Hs.25155	Q96D82	10276	10p15
201851_at_HG-U133A	SH3GL1	Hs.97616	Q9BWP4	6455	19p13.3
201853_s_at_HG-U133A	CDC25B	Hs.153752	P30305	994	20p13
201858_s_at_HG-U133A	PRG1	Hs.1908	P10124	5552	10q22.1
201874_at_HG-U133A	FLJ21047	Hs.14891	Q8WUP4	79620	1q23.2
201889_at_HG-U133A	GS3786	Hs.29882	Q92520	10447	7q22.1-q31.1
201922_at_HG-U133A	YR-29	Hs.8170	O95478	10412	5q13.3-q14.1
201923_at_HG-U133A	PRDX4	Hs.83383	AAH03609	10549	Xp22.13
201962_s_at_HG-U133A	SBB103	Hs.153639	O75598	10193	12q12
201968_s_at_HG-U133A	PGM1	Hs.1869	AAH19920	5236	1p31
201974_s_at_HG-U133A	LOC51622	Hs.289112	O95766	51622	7p22.1
201985_at_HG-U133A	KIAA0196	Hs.8294	AAH26951	9897	8p22
201988_s_at_HG-U133A	CREBL2	Hs.13313	O60519	1389	12p13
201998_at_HG-U133A	SIAT1	Hs.2554	P15907	6480	3q27-q28
202016_at_HG-U133A	MEST	Hs.79284	O15007	4232	7q32
202018_s_at_HG-U133A	LTF	Hs.105938	Q96KZ4	4057	3q21-q23
202028_s_at_HG-U133A	RPL38	Hs.2017	AAH00603	6169	17q23-q25
202052_s_at_HG-U133A	RAI14	Hs.15165	Q9Y3T5	26064	5p13.3-p13.2
202074_s_at_HG-U133A	OPTN	Hs.278898	AAL76327	10133	10p12.33
202080_s_at_HG-U133A	KIAA1042	Hs.6705	Q9UPV9	22906	3p25.3-p24.1
202085_at_HG-U133A	TJP2	Hs.75608	Q9UDY2	9414	9q13-q21
202095_s_at_HG-U133A	BIRC5	Hs.1578	Q969L1	332	17q25
202101_s_at_HG-U133A	RALB	Hs.348024	P11234	5899	2cen-q13
202113_s_at_HG-U133A	SNX2	Hs.11183	O60749	6643	5q23
202123_s_at_HG-U133A	ABL1	Hs.146355	P00519	25	9q34.1
202137_s_at_HG-U133A	BS69	Hs.301449	Q15326	10771	10p14
202148_s_at_HG-U133A	PYCR1	Hs.79217	P32322	5831	17q25.3
202150_s_at_HG-U133A	HEF1	Hs.80261	Q14511	10543	6p25-p24
202156_s_at_HG-U133A	CUGBP2	Hs.211610	Q92950	10659	10p13
202206_at_HG-U133A	ARL7	Hs.111554	AAM12606	10123	2q37.2
202249_s_at_HG-U133A	H326	Hs.110707	Q12839	50717	1q22-q23
202254_at_HG-U133A	KIAA0440	Hs.172180	BAA23712	26037	14q24.1
202262_x_at_HG-U133A	DDAH2	Hs.247362	O95865	23564	6p21.3
202265_at_HG-U133A	BMI1	Hs.431	P35226	648	10p13
202283_at_HG-U133A	SERPINF1	Hs.173594	P36955	5176	17p13.1
202288_at_HG-U133A	FRAP1	Hs.338207	P42345	2475	1p36.2
202328_s_at_HG-U133A	PKD1	Hs.75813	Q15140	5310	16p13.3

202332_at_HG-U133A	CSNK1E	Hs.79658	AAH06490	1454	22q13.1
202340_x_at_HG-U133A	NR4A1	Hs.1119	P22736	3164	12q13
202370_s_at_HG-U133A	CBFB	Hs.179881	Q13951	865	16q22.1
202371_at_HG-U133A	FLJ21174	Hs.194329	Q8WY12	79921	Xq22.1
202377_at_HG-U133A	HSOBRGRP	Hs.23581	O15243	54741	
202382_s_at_HG-U133A	GNPI	Hs.278500	P46926	10007	5q21
202391_at_HG-U133A	BASP1	Hs.79516	Q9BWA5	10409	5p15.1-p14
202406_s_at_HG-U133A	TIAL1	Hs.182741	Q01085	7073	10q
202413_s_at_HG-U133A	USP1	Hs.35086	O94782	7398	1p32.1-p31.3
202421_at_HG-U133A	IGSF3	Hs.81234	O75054	3321	1p13
202441_at_HG-U133A	KEO4	Hs.285818	O75477	10613	10q21-q22
202443_x_at_HG-U133A	NOTCH2	Hs.8121	Q04721	4853	1p13-p11
202477_s_at_HG-U133A	GCP2	Hs.13386	Q9BSJ2	10844	10q26.3
202479_s_at_HG-U133A	GS3955	Hs.155418	Q92519	28951	2p25.1
202481_at_HG-U133A	SDR1	Hs.17144	Q9BUC8	9249	1p36.1
202503_s_at_HG-U133A	KIAA0101	Hs.81892	Q15004	9768	15q22.1
202519_at_HG-U133A	MONDOA	Hs.52081	Q8WYA5	22877	12q21.31
202524_s_at_HG-U133A	KIAA0275	Hs.74583	Q92563	9806	10pter-q25.3
202530_at_HG-U133A	MAPK14	Hs.79107	AAF36770	1432	6p21.3-p21.2
202535_at_HG-U133A	FADD	Hs.86131	Q13158	8772	11q13.3
202545_at_HG-U133A	PRKCD	Hs.155342	Q05655	5580	3p21.31
202551_s_at_HG-U133A	CRIM1	Hs.19280	Q9NZV1	51232	2p21
202552_s_at_HG-U133A	CRIM1	Hs.19280	Q9NZV1	51232	2p21
202572_s_at_HG-U133A	KIAA0964	Hs.177425	Q9Y2H0	22839	20q11.22
202580_x_at_HG-U133A	FOXM1	Hs.239	Q9BRL2	2305	12p13
202589_at_HG-U133A	TYMS	Hs.82962	P04818	7298	18p11.32
202600_s_at_HG-U133A	NRIP1	Hs.155017	P48552	8204	21q11.2
202606_s_at_HG-U133A	TLK1	Hs.18895	Q9UKI8	9874	2q31.1
202619_s_at_HG-U133A	PLOD2	Hs.41270	O00469	5352	3q23-q24
202625_at_HG-U133A	LYN	Hs.80887	P07948	4067	8q13
202626_s_at_HG-U133A	LYN	Hs.80887	P07948	4067	8q13
202655_at_HG-U133A	ARMET	Hs.75412	Q96IS4	7873	3p21.1
202705_at_HG-U133A	CCNB2	Hs.194698	O95067	9133	15q21.2
202709_at_HG-U133A	FMOD	Hs.230	Q12833	2331	1q32
202718_at_HG-U133A	IGFBP2	Hs.162	P18065	3485	2q33-q34
202723_s_at_HG-U133A	FOXO1A	Hs.170133	Q12778	2308	13q14.1
202729_s_at_HG-U133A	LTBP1	Hs.241257	Q14766	4052	2p22-p21
202746_at_HG-U133A					
202747_s_at_HG-U133A	ITM2A	Hs.17109		9452	Xq13.3-Xq21.2
202761_s_at_HG-U133A	SYNE-2	Hs.57749	Q8WXH0	23224	14q23.1-q23.2
202819_s_at_HG-U133A	TCEB3	Hs.155202	Q14241	6924	1p36.1
202822_at_HG-U133A	LPP	Hs.180398	Q93052	4026	3q27-q28

202823_at_HG-U133A	TCEB1	Hs.184693	Q15369	6921	8q13.2
202853_s_at_HG-U133A	RYK	Hs.79350	P34925	6259	3q22
202862_at_HG-U133A	FAH	Hs.73875	P16930	2184	15q23-q25
202863_at_HG-U133A	SP100	Hs.77617	Q96T95	6672	2q36.1
202880_s_at_HG-U133A	PSCD1	Hs.1050	Q15438	9267	17q25
202883_s_at_HG-U133A	PPP2R1B	Hs.108705	AAH27596	5519	11q23
202926_at_HG-U133A	NAG	Hs.15430	O95790	51594	2p24
202944_at_HG-U133A	NAGA	Hs.75372	P17050	4668	22q13-qter
202945_at_HG-U133A	FPGS	Hs.754	Q05932	2356	9cen-q34
202956_at_HG-U133A	BIG1	Hs.94631	Q9Y6D6	10565	8q13
202973_x_at_HG-U133A	KIAA0914	Hs.177664	O94988	10144	4q21.3
203005_at_HG-U133A	LTBR	Hs.1116	P36941	4055	12p13
203007_x_at_HG-U133A					
203020_at_HG-U133A	KIAA0471	Hs.242271	Q9UEL5	9910	1q24-q25
203021_at_HG-U133A	SLPI	Hs.251754	AAH20708	6590	20q12
203026_at_HG-U133A	KIAA0354	Hs.3682	O15062	9925	9p11.1
203037_s_at_HG-U133A	KIAA0429	Hs.77694	AAH23998	9788	8p22
203041_s_at_HG-U133A	LAMP2	Hs.8262	P13473	3920	Xq24
203053_at_HG-U133A	BCAS2	Hs.22960	AAH22880	10286	1p21-p13.3
203057_s_at_HG-U133A	PRDM2	Hs.26719	Q13029	7799	1p36
203074_at_HG-U133A	ANXA8	Hs.87268	Q96H89	244	10q11.2
203092_at_HG-U133A	TIMM44	Hs.123178	O43615	10469	19p13.3-p13.2
203104_at_HG-U133A	CSF1R	Hs.174142	P07333	1436	5q33-q35
203110_at_HG-U133A	PTK2B	Hs.20313	Q14289	2185	8p21.1
203133_at_HG-U133A	SEC61B	Hs.77028	P38391	10952	9q22.32-q31.3
203143_s_at_HG-U133A	KIAA0040	Hs.158282	CAB42560	9674	1q24-25
203177_x_at_HG-U133A	TFAM	Hs.75133	Q00059	7019	10q21
203188_at_HG-U133A	B3GNT6	Hs.8526	O43505	11041	11q12.1
203217_s_at_HG-U133A	SIAT9	Hs.225939	O94902	8869	2p11.2
203233_at_HG-U133A	IL4R	Hs.75545	P24394	3566	16p11.2-12.1
203241_at_HG-U133A	UVRAG	Hs.13137	Q9P2Y5	7405	11q13.5
203288_at_HG-U133A	KIAA0355	Hs.186840	O15063	9710	19q13.12
203345_s_at_HG-U133A	M96	Hs.31016	Q96G26	22823	1p22.1
203355_s_at_HG-U133A	KIAA0942	Hs.6763	Q9Y2F1	23362	8pter-p23.3
203367_at_HG-U133A	DUSP14	Hs.91448	O95147	11072	17q12
203370_s_at_HG-U133A	ENIGMA	Hs.102948	Q9BXB8	9260	5q35.3
203372_s_at_HG-U133A	STATI2	Hs.110776	O14508	8835	12q
203373_at_HG-U133A	STATI2	Hs.110776	O14508	8835	12q
203380_x_at_HG-U133A	SFRS5	Hs.166975	Q13243	6430	14q24
203385_at_HG-U133A	DGKA	Hs.172690	O75484	1606	12q13.3
203386_at_HG-U133A	KIAA0603	Hs.173802	O60343	9882	13q21.33
203387_s_at_HG-U133A	KIAA0603	Hs.173802	O60343	9882	13q21.33

203394_s_at_HG-U133A	HRY	Hs.250666	Q9BS99	3280	3q28-q29
203535_at_HG-U133A	S100A9	Hs.112405	P06702	6280	1q21
203544_s_at_HG-U133A	STAM	Hs.153487	Q92783	8027	10p14-p13
203556_at_HG-U133A	KIAA0854	Hs.30209	Q9Y6X8	22882	8q24.13
203593_at_HG-U133A	CD2AP	Hs.343211	Q9UG97	23607	6p12
203602_s_at_HG-U133A	ZNF151	Hs.33532	Q13105	7709	1p36.2-p36.1
203607_at_HG-U133A	SAC2	Hs.52463	Q9NT51	22876	10q26.13
203645_s_at_HG-U133A	CD163	Hs.74076	Q07901	9332	12p13.3
203679_at_HG-U133A	IL1RL1LG	Hs.54411	Q13445	11018	19p13.2
203685_at_HG-U133A	BCL2	Hs.79241	AAH27258	596	18q21.3
203725_at_HG-U133A	GADD45A	Hs.80409	P24522	1647	1p31.2-p31.1
203729_at_HG-U133A	EMP3	Hs.9999	P54852	2014	19q13.3
203731_s_at_HG-U133A	ZFP95	Hs.110839	Q9Y2L8	23660	7q22
203753_at_HG-U133A	TCF4	Hs.326198	P15884	6925	18q21.1
203757_s_at_HG-U133A	CEACAM6	Hs.73848	Q13774	4680	19q13.2
203787_at_HG-U133A	SSBP2	Hs.169833	Q9BWW6	23635	5q14.1
203795_s_at_HG-U133A	BCL7A	Hs.211563	Q13843	605	12q24.13
203796_s_at_HG-U133A	BCL7A	Hs.211563	Q13843	605	12q24.13
203808_at_HG-U133A	AKT2	Hs.326445	P31751	208	19q13.1-q13.2
203818_s_at_HG-U133A	SF3A3	Hs.77897	Q12874	10946	1p35.2
203857_s_at_HG-U133A	PDIR	Hs.372612	Q14554	10954	3q21.2
203859_s_at_HG-U133A	PALM	Hs.78482	O75781	5064	19p13.3
203881_s_at_HG-U133A	DMD	Hs.169470	P11532	1756	Xp21.2
203897_at_HG-U133A	LOC57149	Hs.28607	AAH17039	57149	16p11.2
203904_x_at_HG-U133A	KAI1	Hs.323949	P27701	3732	11p11.2
203910_at_HG-U133A	PARG1	Hs.70983	AAH22483	9411	1p22.1
203932_at_HG-U133A	HLA-DMB	Hs.1162	P28068	3109	6p21.3
203936_s_at_HG-U133A	MMP9	Hs.151738	P14780	4318	20q11.2-q13.1
203939_at_HG-U133A	NT5E	Hs.153952	P21589	4907	6q14-q21
203948_s_at_HG-U133A	MPO	Hs.1817	P05164	4353	17q23.1
203949_at_HG-U133A	MPO	Hs.1817	P05164	4353	17q23.1
203973_s_at_HG-U133A	CEBDP	Hs.76722	P49716	1052	8p11.2-p11.1
204000_at_HG-U133A	GNB5	Hs.155090	AAM15921	10681	15q15.3
204030_s_at_HG-U133A	SCHIP1	Hs.61490	Q9P0W5	29970	3q25.32
204044_at_HG-U133A	QPRT	Hs.8935	Q9BSG6	23475	16q13
204057_at_HG-U133A	ICSBP1	Hs.14453	Q02556	3394	16q24.1
204069_at_HG-U133A	MEIS1	Hs.170177	O00470	4211	2p14-p13
204075_s_at_HG-U133A	KIAA0562	Hs.200595	O60308	9731	1p36.32
204082_at_HG-U133A	PBX3	Hs.294101	Q96AL5	5090	9q33-q34
204101_at_HG-U133A	MTM1	Hs.75302	Q13496	4534	Xq28
204112_s_at_HG-U133A	HNMT	Hs.81182	P50135	3176	2q21.1
204116_at_HG-U133A	IL2RG	Hs.84	P31785	3561	Xq13.1

204118_at_HG-U133A	CD48	Hs.901	P09326	962	1q21.3-q22
204150_at_HG-U133A	STAB1	Hs.301989	Q9NY15	23166	3p21.31
204163_at_HG-U133A	EMILIN	Hs.63348	Q9Y6C2	11117	2p23.3-p23.2
204174_at_HG-U133A	ALOX5AP	Hs.100194	AAH18538	241	13q12
204192_at_HG-U133A	CD37	Hs.153053	Q96LM7	951	19p13-q13.4
204199_at_HG-U133A	RALGPS1A	Hs.374518	O15059	9649	9q34.13
204205_at_HG-U133A	MDS019	Hs.250619	Q9HC16	60489	22q
204208_at_HG-U133A	RNGTT	Hs.27345	Q8WUM8	8732	6q16
204214_s_at_HG-U133A	RAB32	Hs.32217	AAM21106	10981	6q24.3
204215_at_HG-U133A	MGC4175	Hs.322404	Q9BU79	79161	7q21.1-q21.2
204225_at_HG-U133A	HDAC4	Hs.91400	P56524	9759	2q37.2
204227_s_at_HG-U133A	TK2	Hs.274701	O00142	7084	16q22
204249_s_at_HG-U133A	LMO2	Hs.184585	P25791	4005	11p13
204269_at_HG-U133A	PIM2	Hs.80205	Q9P1W9	11040	Xp11.23
204285_s_at_HG-U133A	PMAIP1	Hs.96	Q13794	5366	18q21.31
204306_s_at_HG-U133A	CD151	Hs.75564	P48509	977	11p15.5
204319_s_at_HG-U133A	RGS10	Hs.82280	Q96GN0	6001	10q25
204328_at_HG-U133A	LAK-4P	Hs.16165	Q9HAG5	11322	17q25
204348_s_at_HG-U133A	AK3	Hs.274691	P27144	205	9p24-p13
204351_at_HG-U133A	S100P	Hs.2962	P25815	6286	4p16
204352_at_HG-U133A	TRAF5	Hs.29736	O00463	7188	1q32
204401_at_HG-U133A	KCNN4	Hs.10082	AAH15337	3783	19q13.2
204422_s_at_HG-U133A	FGF2	Hs.284244	P09038	2247	4q26-q27
204425_at_HG-U133A	ARHGAP4	Hs.3109	P98171	393	Xq28
204446_s_at_HG-U133A	ALOX5	Hs.89499	P09917	240	10q11.2
204484_at_HG-U133A	PIK3C2B	Hs.132463	O00750	5287	1q32
204495_s_at_HG-U133A	DKFZP434H132	Hs.17936	Q9H3J1	25958	15q22.33
204501_at_HG-U133A	NOV	Hs.235935	AAL92490	4856	8q24.1
204511_at_HG-U133A	KIAA0793	Hs.301283	Q9UFE7	9855	2q37.3
204512_at_HG-U133A	HIVEP1	Hs.306	Q14122	3096	6p24-p22.3
204562_at_HG-U133A	IRF4	Hs.82132	Q15306	3662	6p25-p23
204563_at_HG-U133A	SELL	Hs.82848	P14151	6402	1q23-q25
204604_at_HG-U133A	PFTK1	Hs.57856	Q9H3D7	5218	7q21-q22
204638_at_HG-U133A	ACP5	Hs.1211	AAH25414	54	19p13.3-p13.2
204647_at_HG-U133A	HOMER-3	Hs.166146	O95350	9454	19p13.11
204661_at_HG-U133A	CDW52	Hs.276770	P31358	1043	1p36
204663_at_HG-U133A	ME3	Hs.2838	Q16798	10873	11cen-q22.3
204670_x_at_HG-U133A	HLA-DRB5	Hs.352392	Q29972	3127	6p21.3
204672_s_at_HG-U133A	ANKRD6	Hs.30991	Q9BVM3	22881	6q14.2-q16.1
204674_at_HG-U133A	LRMP	Hs.40202	Q12912	4033	12p12.3
204703_at_HG-U133A	TG737	Hs.2291	Q13099	8100	13q12.1
204731_at_HG-U133A	TGFBR3	Hs.342874	Q9UGI2	7049	1p33-p32

204776_at_HG-U133A	THBS4	Hs.75774	P35443	7060	5q13
204793_at_HG-U133A	KIAA0443	Hs.113082	Q96LA1	9737	Xq22.1
204798_at_HG-U133A	MYB	Hs.1334	Q14024	4602	6q22-q23
204811_s_at_HG-U133A	CACNA2D2	Hs.127436	Q9UEW0	9254	3p21.3
204858_s_at_HG-U133A	ECGF1	Hs.73946	P19971	1890	22q13.33
204882_at_HG-U133A	KIAA0053	Hs.1528	P42331	9938	2p13.1
204891_s_at_HG-U133A	LCK	Hs.1765	P06239	3932	1p34.3
204922_at_HG-U133A	FLJ22531	Hs.55613	AAH28240	79703	11q12.1
204951_at_HG-U133A	ARHH	Hs.109918	Q15669	399	4p13
204992_s_at_HG-U133A	PFN2	Hs.91747	P35080	5217	3q25.1-q25.2
205019_s_at_HG-U133A	VIPR1	Hs.348500	P32241	7433	3p22
205040_at_HG-U133A	ORM1	Hs.572	P02763	5004	9q31-q32
205041_s_at_HG-U133A	ORM1	Hs.572	AAH26238	5004	9q31-q32
205049_s_at_HG-U133A	CD79A	Hs.79630	P11912	973	19q13.2
205051_s_at_HG-U133A	KIT	Hs.81665	P10721	3815	4q11-q12
205055_at_HG-U133A	ITGAE	Hs.851	P38570	3682	17p13
205059_s_at_HG-U133A	IDUA	Hs.89560	P35475	3425	4p16.3
205074_at_HG-U133A	SLC22A5	Hs.15813	O76082	6584	5q31
205076_s_at_HG-U133A	CRA	Hs.166066	Q99753	10903	1q12-q21
205101_at_HG-U133A	MHC2TA	Hs.3076	Q29675	4261	16p13
205105_at_HG-U133A	MAN2A1	Hs.63368	Q16706	4124	5q21-q22
205110_s_at_HG-U133A	FGF13	Hs.6540	Q92913	2258	Xq26.3
205131_x_at_HG-U133A	SCGF	Hs.105927	Q9Y240	6320	19q13.3
205145_s_at_HG-U133A	MYL5	Hs.170482	Q02045	4636	4p16.3
205192_at_HG-U133A	MAP3K14	Hs.47007	Q99558	9020	17q21
205223_at_HG-U133A	KIAA0645	Hs.155987	O75140	9681	22q12.3
205225_at_HG-U133A	ESR1	Hs.1657	Q9H2M0	2099	6q25.1
205267_at_HG-U133A	POU2AF1	Hs.2407	Q16633	5450	11q23.1
205306_x_at_HG-U133A	KMO	Hs.107318	O15229	8564	1q42-q44
205308_at_HG-U133A	LOC51101	Hs.118821	Q9Y372	51101	8q21.11
205312_at_HG-U133A	SPI1	Hs.157441	P17947	6688	11p11.2
205316_at_HG-U133A	SLC15A2	Hs.182575	Q16348	6565	3q21.1
205349_at_HG-U133A	GNA15	Hs.73797	P30679	2769	19p13.3
205355_at_HG-U133A	ACADSB	Hs.81934	P45954	36	10q25-q26
205366_s_at_HG-U133A	HOXB6	Hs.98428	P17509	3216	17q21-q22
205380_at_HG-U133A	PDZK1	Hs.15456	O60450	5174	1q21
205382_s_at_HG-U133A	DF	Hs.155597	P00746	1675	19p13.3
205383_s_at_HG-U133A	ZNF288	Hs.159456	Q9HC78	26137	3q13.2
205414_s_at_HG-U133A	KIAA0672	Hs.6336	O75160	9912	17p11.2
205420_at_HG-U133A	PEX7	Hs.79993	O00628	5191	6q21-q22.2
205436_s_at_HG-U133A	H2AFX	Hs.147097	P16104	3014	11q23.2-q23.3
205453_at_HG-U133A	HOXB2	Hs.2733	P14652	3212	17q21-q22

205471_s_at_HG-U133A	DACH	Hs.63931	Q9UMH4	1602	13q22
205472_s_at_HG-U133A	DACH	Hs.63931	Q9UI36	1602	13q22
205504_at_HG-U133A	BTK	Hs.159494	Q9NPI3	695	Xq21.33-q22
205513_at_HG-U133A	TCN1	Hs.2012	P20061	6947	11q11-q12
205528_s_at_HG-U133A	CBFA2T1	Hs.31551	Q06455	862	8q22
205529_s_at_HG-U133A	CBFA2T1	Hs.31551	Q06455	862	8q22
205541_s_at_HG-U133A	GSPT2	Hs.59523	Q9H909	23708	
205547_s_at_HG-U133A	TAGLN	Hs.75777	AAH04927	6876	11q23.2
205557_at_HG-U133A	BPI	Hs.89535	P17213	671	20q11.23-q12
205599_at_HG-U133A	TRAF1	Hs.2134	Q13077	7185	9q33-q34
205600_x_at_HG-U133A	HOXB5	Hs.22554	P09067	3215	17q21-q22
205601_s_at_HG-U133A	HOXB5	Hs.22554	Q96H37	3215	17q21-q22
205607_s_at_HG-U133A	LOC57147	Hs.24243	Q96C56	57147	1q22
205613_at_HG-U133A	LOC51760	Hs.26971	Q9NZ18	51760	16p13.13
205614_x_at_HG-U133A	MST1	Hs.349110	P26927	4485	3p21
205624_at_HG-U133A	CPA3	Hs.646	P15088	1359	3q21-q25
205627_at_HG-U133A	CDA	Hs.72924	P32320	978	1p36.2-p35
205640_at_HG-U133A	ALDH3B1	Hs.83155	Q9BUJ8	221	11q13
205653_at_HG-U133A	CTSG	Hs.100764	P08311	1511	14q11.2
205663_at_HG-U133A	PCBP3	Hs.121241	Q96EP6	54039	21q22.3
205668_at_HG-U133A	LY75	Hs.153563	Q75913	4065	2q24
205671_s_at_HG-U133A	HLA-DOB	Hs.1802	AAH06097	3112	6p21.3
205674_x_at_HG-U133A	FXYD2	Hs.19520	Q15332	486	11q23
205690_s_at_HG-U133A	G10	Hs.330310	P41223	8896	7q11.21
205691_at_HG-U133A	SYNGR3	Hs.6467	Q96L30	9143	16pter
205718_at_HG-U133A	ITGB7	Hs.1741	P26010	3695	12q13.13
205790_at_HG-U133A	SCAP1	Hs.19126	O15268	8631	17q21.32
205801_s_at_HG-U133A	GRP3	Hs.24024	O94931	25780	2p25.1-p24.1
205805_s_at_HG-U133A	ROR1	Hs.274243	Q01973	4919	1p32-p31
205821_at_HG-U133A	D12S2489E	Hs.74085	Q8WZ67	22914	12p13.2-p12.3
205837_s_at_HG-U133A	GYPA	Hs.108694	Q03870	2993	4q28.2-q31.1
205841_at_HG-U133A	JAK2	Hs.115541	O60674	3717	9p24
205849_s_at_HG-U133A	UQCRRB	Hs.131255	P14927	7381	8q22
205855_at_HG-U133A	ZNF197	Hs.170341	O14709	10168	3p21
205863_at_HG-U133A	S100A12	Hs.19413	P80511	6283	1q21
205899_at_HG-U133A	CCNA1	Hs.79378	P78396	8900	13q12.3-q13
205901_at_HG-U133A	PNOC	Hs.89040	Q13519	5368	8p21
205911_at_HG-U133A	PTHR1	Hs.1019	Q03431	5745	3p22-p21.1
205933_at_HG-U133A	SETBP1	Hs.151717	BAA24826	26040	18q21.1
205945_at_HG-U133A	IL6R	Hs.193400	P08887	3570	1q21
205997_at_HG-U133A	ADAM28	Hs.174030	Q9UKQ2	10863	8p12
206009_at_HG-U133A	ITGA9	Hs.222	Q13797	3680	3p21.3

206090_s_at_HG-U133A	DISC1	Hs.26985	Q9NR15	27185	1q42.1
206111_at_HG-U133A	RNASE2	Hs.728	P10153	6036	14q24-q31
206126_et_HG-U133A	BLR1	Hs.113916	P32302	643	11q23.3
206135_at_HG-U133A	KIAA0535	Hs.151449	O60284	9705	8q11.21
206150_et_HG-U133A	TNFRSF7	Hs.180841	P26842	939	12p13
206177_s_at_HG-U133A	ARG1	Hs.332405	AAL71547	383	6q23
206178_at_HG-U133A	PLA2G5	Hs.290	P39877	5322	1p36-p34
206207_at_HG-U133A	CLC	Hs.889	Q05315	1178	19q13.1
206241_at_HG-U133A	KPNA5	Hs.182971	O15131	3841	6q22.31
206245_s_at_HG-U133A	NS1-BP	Hs.197298	Q9Y6Y0	10625	1q25.1-q31.1
206255_at_HG-U133A	BLK	Hs.2243	P51451	640	8p23-p22
206295_at_HG-U133A	IL18	Hs.83077	Q14116	3606	11q22.2-q22.3
206302_s_at_HG-U133A	NUDT4	Hs.92381	Q9NZK0	11163	
206337_at_HG-U133A	CCR7	Hs.1652	P32248	1236	17q12-q21.2
206380_s_at_HG-U133A	PFC	Hs.53155	P27918	5199	Xp11.3-p11.23
206398_s_at_HG-U133A	CD19	Hs.96023	Q9BRD6	930	16p11.2
206438_x_at_HG-U133A	FLJ12975	Hs.167165	Q96GX1	79867	12q24.31
206440_at_HG-U133A	VELI1	Hs.178215	O14910	8825	12q21
206461_x_at_HG-U133A	MT1H	Hs.2667	AAH08408	4496	16q13
206488_s_at_HG-U133A	CD36	Hs.75613	P16671	948	7q11.2
206513_at_HG-U133A	AIM2	Hs.105115	O14862	9447	1q22
206515_at_HG-U133A	CYP4F3	Hs.106242	Q08477	4051	19p13.2
206519_x_at_HG-U133A	SIGLEC6	Hs.117992	O15388	946	19q13.3
206530_at_HG-U133A	RAB30	Hs.159505	AAM21104	27314	11q12-q14
206550_s_at_HG-U133A	NUP155	Hs.23255	O75694	9631	5p13
206576_s_at_HG-U133A	CEACAM1	Hs.50964	Q15600	634	19q13.2
206622_at_HG-U133A	TRH	Hs.182231		7200	3q13.3-q21
206633_at_HG-U133A	CHRNA1	Hs.2266	P02708	1134	2q24-q32
206634_at_HG-U133A	SIX3	Hs.227277	O95343	6496	2p16-p21
206676_at_HG-U133A	CEACAM8	Hs.41	AAH26263	1088	19q13.2
206748_s_at_HG-U133A	SPAG9	Hs.129872	O60271	9043	17q24.1
206759_at_HG-U133A	FCER2	Hs.1416	P06734	2208	19p13.3
206760_s_at_HG-U133A	FCER2	Hs.1416	P06734	2208	19p13.3
206761_at_HG-U133A	TACTILE	Hs.142023	Q8WUE2	10225	3q13.2
206772_at_HG-U133A	PTHR2	Hs.159499	P49190	5746	2q33
206781_at_HG-U133A	DNAJC4	Hs.172847	Q9NNZ3	3338	11q13
206804_at_HG-U133A	CD3G	Hs.2259	P09693	917	11q23
206847_s_at_HG-U133A	HOXA7	Hs.355540	P31268	3204	7p15-p14
206850_at_HG-U133A	RRP22	Hs.73088	Q92737	10633	22q12.2
206871_at_HG-U133A	ELA2	Hs.99863	AAA35792	1991	19p13.3
206940_s_at_HG-U133A	POU4F1	Hs.211588	Q01851	5457	13q21.1-q22
206956_at_HG-U133A	BGLAP	Hs.2558	P02818	632	1q25-q31

206995_x_at_HG-U133A	SREC	Hs.57735	Q14162	8578	17p13.3
207000_s_at_HG-U133A	PPP3CC	Hs.75206	Q9BSS6	5533	8p21.2
207030_s_at_HG-U133A	CSRP2	Hs.10526	Q16527	1466	12q21.1
207057_at_HG-U133A	SLC16A7	Hs.132183	O60669	9194	12q13
207076_s_at_HG-U133A	ASS	Hs.160786	P00966	445	9q34.1
207168_s_at_HG-U133A	H2AFY	Hs.75258	Q9H8P3	9555	5q31.3-q32
207194_s_at_HG-U133A	ICAM4	Hs.108287	Q14773	3386	19p13.2-cen
207224_s_at_HG-U133A	SIGLEC7	Hs.274470	Q9UJ86	27036	19q13.3
207269_at_HG-U133A	DEFA4	Hs.2582	P12838	1669	8p23
207384_at_HG-U133A	PGLYRP	Hs.137583	O75594	8993	19q13.2-q13.3
207403_at_HG-U133A	IRS4	Hs.159609	O14654	8471	Xq22.3
207520_at_HG-U133A					
207543_s_at_HG-U133A	P4HA1	Hs.76768	P13674	5033	10q21.3-q23.1
207616_s_at_HG-U133A	TANK	Hs.146847	Q92844	10010	2q24-q31
207641_at_HG-U133A	TACI	Hs.158341	O14836	23495	17p11.2
207654_x_at_HG-U133A	DR1	Hs.16697	Q01658	1810	1p22.1
207655_s_at_HG-U133A	BLNK	Hs.167746	O75499	29760	10q23.2-q23.33
207697_x_at_HG-U133A	LILRB2	Hs.22405	O75017	10288	19q13.4
207700_s_at_HG-U133A	NCOA3	Hs.225977	Q9UPG7	8202	20q12
207734_at_HG-U133A	FLJ20340	Hs.272794	Q9NXB4	54900	1q31.1
207760_s_at_HG-U133A	NCOR2	Hs.287994	Q9Y618	9612	12q24
207777_s_at_HG-U133A	SP140	Hs.309943	Q13342	11262	2q36.1
207801_s_at_HG-U133A	RNF10	Hs.5094	Q9ULW4	9921	12q24.23
207802_at_HG-U133A	SGP28	Hs.54431	P54108	10321	6p12.2
207809_s_at_HG-U133A	ATP6IP1	Hs.6551	AAH00724	537	Xq28
207819_s_at_HG-U133A	ABCB4	Hs.73812	P21439	5244	7q21.1
207871_s_at_HG-U133A	ST7	Hs.5814	Q9NRC1	7982	7q31.1-q31.3
207957_s_at_HG-U133A	PRKCB1	Hs.77202	P05771	5579	16p11.2
207971_s_at_HG-U133A	KIAA0582	Hs.79507	O60326	23177	2p14
207983_s_at_HG-U133A	STAG2	Hs.8217	Q9H1N8	10735	Xq25
207996_s_at_HG-U133A	C18orf1	Hs.153498	O15165	753	18p11.2
208033_s_at_HG-U133A	ATBF1	Hs.101842	Q15911	463	16q22.3-q23.1
208042_at_HG-U133A	HSU84971	Hs.104530	Q9BU84	29905	5q14.1
208091_s_at_HG-U133A	DKFZP564K0822	Hs.4750	Q9H0W4	81552	7p14.1
208141_s_at_HG-U133A	MGC4293	Hs.91103	Q9BU89	83475	19p13.3
208146_s_at_HG-U133A	CPVL	Hs.95594	Q96AR7	54504	7p15-p14
208168_s_at_HG-U133A	CHIT1	Hs.91093	Q9H3V8	1118	1q31-q32
208190_s_at_HG-U133A	LISCH7	Hs.361379	Q9UQL3	51599	19q13.13
208195_at_HG-U133A	TTN	Hs.172004	Q15598	7273	2q24.3
208217_at_HG-U133A	GABRR2	Hs.99927	P28476	2570	6q13-q16.3
208229_at_HG-U133A	FGFR2	Hs.278581	Q9UIH4	2263	10q26
208248_x_at_HG-U133A	APLP2	Hs.279518	Q06481	334	11q24

208268_at_HG-U133A	ADAM28	Hs.174030	Q9UKQ2	10863	8p12
208302_at_HG-U133A	HB-1	Hs.158320	O97980	57824	5q33.1
208306_x_at_HG-U133A	HLA-DRB4	Hs.318720	AAM00252	3126	6p21.3
208456_s_at_HG-U133A	RRAS2	Hs.206097	P17082	22800	11p15.2
208470_s_at_HG-U133A	HPR	Hs.328822	Q92659	3250	16q22.1
208581_x_at_HG-U133A	MT1X	Hs.278462		4501	16q13
208611_s_at_HG-U133A	SPTAN1	Hs.77196	Q13813	6709	9q33-q34
208612_at_HG-U133A	GRP58	Hs.289101	P30101	2923	15q15
208614_s_at_HG-U133A	FLNB	Hs.81008	Q9NT26	2317	3p14.3
208623_s_at_HG-U133A	VIL2	Hs.155191	Q9UJU1	7430	6q25-q26
208629_s_at_HG-U133A	HADHA	Hs.75860	P40939	3030	2p23
208645_s_at_HG-U133A					
208646_at_HG-U133A					
208650_s_at_HG-U133A	CD24	Hs.286124	AAH07674	934	6q21
208651_x_at_HG-U133A	CD24	Hs.286124	AAH07674	934	6q21
208657_s_at_HG-U133A	MSF	Hs.181002	Q96QF3	10801	17q25
208664_s_at_HG-U133A	TTC3	Hs.118174	P53804	7267	21q22.2
208674_x_at_HG-U133A	DDOST	Hs.34789	Q9BUI2	1650	1p36.1
208683_at_HG-U133A	CAPN2	Hs.76288	Q9HBB1	824	1q41-q42
208689_s_at_HG-U133A	RPN2	Hs.75722	AAH20222	6185	20q12-q13.1
208697_s_at_HG-U133A	EIF3S6	Hs.106673	AAH08419	3646	8q22-q23
208702_x_at_HG-U133A	APLP2	Hs.279518	AAD47291	334	11q24
208703_s_at_HG-U133A	APLP2	Hs.279518	Q9BT36	334	11q24
208710_s_at_HG-U133A	AP3D1	Hs.75056	O14617	8943	19p13.3
208741_at_HG-U133A	SAP18	Hs.23964	O00422	10284	13q11
208754_s_at_HG-U133A	NAP1L1	Hs.302649	P55209	4673	12q14.1
208819_at_HG-U133A	MEL	Hs.5947	AAM21091	4218	19p13.1
208852_s_at_HG-U133A	CANX	Hs.155560	P27824	821	5q35
208858_s_at_HG-U133A	KIAA0747	Hs.8309	O94848	23344	12q12
208864_s_at_HG-U133A	TXN	Hs.76136	P10599	7295	9q31
208890_s_at_HG-U133A	PLXNB2	Hs.3989	Q9BSU7	23654	22q13.33
208894_at_HG-U133A	HLA-DRA	Hs.76807	P01903	3122	6p21.3
208908_s_at_HG-U133A	CAST	Hs.359682	O95360	831	5q14-q22
208913_at_HG-U133A	GGA2	Hs.155546	Q9UJY4	23062	16p12
208914_at_HG-U133A	GGA2	Hs.155546	Q9UJY4	23062	16p12
208918_s_at_HG-U133A	FLJ13052	Hs.220324	AAM01195	65220	1p36.33-p36.21
209003_at_HG-U133A	SLC25A11	Hs.184877	Q02978	8402	17p13.3
209018_s_at_HG-U133A	PINK1	Hs.6163	Q9BXM7	65018	1p36
209019_s_at_HG-U133A	PINK1	Hs.6163	AAH28215	65018	1p36
209023_s_at_HG-U133A	STAG2	Hs.8217	Q9H1N8	10735	Xq25
209055_s_at_HG-U133A	CDC5L	Hs.155174	BAA24862	988	6p21
209060_x_at_HG-U133A	NCOA3	Hs.225977	O15406	8202	20q12

209061_at_HG-U133A	NCOA3	Hs.225977	O15406	8202	20q12
209062_x_at_HG-U133A	NCOA3	Hs.225977	O15406	8202	20q12
209075_s_at_HG-U133A	NIFU	Hs.9908	Q99617	23479	12q24.1
209085_x_at_HG-U133A	RFC1	Hs.166563	P35251	5981	4p14-p13
209101_at_HG-U133A	CTGF	Hs.75511	AAA75378	1490	6q23.1
209135_at_HG-U133A	ASPH	Hs.283664	AAH25236	444	8q12.1
209160_at_HG-U133A	AKR1C3	Hs.78183	Q9UKL9	8644	10p15-p14
209167_at_HG-U133A	GPM6B	Hs.5422	Q13491	2824	Xp22.2
209168_at_HG-U133A	GPM6B	Hs.5422	Q13491	2824	Xp22.2
209169_at_HG-U133A	GPM6B	Hs.5422	Q13491	2824	Xp22.2
209170_s_at_HG-U133A	GPM6B	Hs.5422	Q13491	2824	Xp22.2
209178_at_HG-U133A	DDX38	Hs.78054	Q92620	9785	16q21-q22.3
209186_at_HG-U133A	ATP2A2	Hs.1526	P16615	488	12q23-q24.1
209188_x_at_HG-U133A	DR1	Hs.16697	Q01658	1810	1p22.1
209190_s_at_HG-U133A	DIAPH1	Hs.26584	O60610	1729	5q31
209197_at_HG-U133A	KIAA0080	Hs.74554	Q14998	23208	
209236_at_HG-U133A					1
209253_at_HG-U133A	SCAM-1	Hs.33787	O60504	10174	8p21.2
209259_s_at_HG-U133A	CSPG6	Hs.24485	O60464	9126	10q25
209267_s_at_HG-U133A	LOC64116	Hs.284205	Q96SM9	64116	4q22-q24
209306_s_at_HG-U133A	SWAP70	Hs.153026	O75135	23075	11p15
209307_at_HG-U133A	SWAP70	Hs.153026	O75135	23075	11p15
209312_x_at_HG-U133A	HLA-DRB1	Hs.308026	Q9TQE1	3123	6p21.3
209321_s_at_HG-U133A	ADCY3	Hs.8402	O60266	109	2p24-p22
209344_at_HG-U133A	TPM4	Hs.250641	P07226	7171	19p13.1
209354_at_HG-U133A	TNFRSF14	Hs.279899	Q92956	8764	1p36.3-p36.2
209365_s_at_HG-U133A	ECM1	Hs.81071	O43266	1893	1q21
209369_at_HG-U133A	ANXA3	Hs.1378	P12429	306	4q13-q22
209374_s_at_HG-U133A	IGHM	Hs.153261	Q8WUX4	3507	14q32.33
209380_s_at_HG-U133A	ABCC5	Hs.108660	O15440	10057	3q27
209399_at_HG-U133A	HLCS	Hs.79375	P50747	3141	21q22.13
209412_at_HG-U133A	TMEM1	Hs.94479	P48553	7109	21q22.3
209428_s_at_HG-U133A	ZFPL1	Hs.155165	O14616	7542	11q13
209490_s_at_HG-U133A	PPT2	Hs.81737	Q9UMR5	9374	6p21.3
209499_x_at_HG-U133A	TNFSF13	Hs.54673	Q96HV6	8741	17p13.1
209500_x_at_HG-U133A	TNFSF13	Hs.54673	O75888	8741	17p13.1
209522_s_at_HG-U133A	CRAT	Hs.12068	Q9BW16	1384	9q34.1
209523_at_HG-U133A					
209558_s_at_HG-U133A	HIP12	Hs.96731	O75146	9026	12q24
209561_at_HG-U133A	THBS3	Hs.169875	P49746	7059	1q21
209604_s_at_HG-U133A	GATA3	Hs.169946	Q96J04	2625	10p15
209616_s_at_HG-U133A	CES1	Hs.76688	Q96EE8	1066	16q13-q22.1

209619_at_HG-U133A	CD74	Hs.84298	P04233	972	5q32
209628_at_HG-U133A	P15-2	Hs.25010	Q9NPJ8	55916	Xq22.3
209670_at_HG-U133A	TRA	Hs.74647	Q8WUD0	6955	14q11.2
209679_s_at_HG-U133A	LOC57228	Hs.206501	O95332	57228	12q11
209682_at_HG-U133A	CBLB	Hs.3144	Q13191	868	3q13.12
209685_s_at_HG-U133A	PRKCB1	Hs.77202	P05771	5579	16p11.2
209686_at_HG-U133A	S100B	Hs.83384	P04271	6285	21q22.3
209714_s_at_HG-U133A	CDKN3	Hs.84113	Q9BPW7	1033	14q22
209732_at_HG-U133A	CLECSF2	Hs.85201	Q9BS74	9976	12p13-p12
209735_at_HG-U133A	ABCG2	Hs.194720	Q96LD6	9429	4q22
209754_s_at_HG-U133A					
209761_s_at_HG-U133A	SP110	Hs.38125	Q14976	3431	2q37.1
209765_at_HG-U133A	ADAM19	Hs.278679	Q9H013	8728	5q32-q33
209771_x_at_HG-U133A	CD24	Hs.286124	P25063	934	6q21
209772_s_at_HG-U133A	CD24	Hs.286124	P25063	934	6q21
209780_at_HG-U133A	DKFZP564F013	Hs.128653	Q9H099	57157	7q11.23-q21
209806_at_HG-U133A	H2B/S	Hs.247817	O60814	85236	6p21.33
209815_at_HG-U133A	PTCH	Hs.159526	Q13635	5727	9q22.3
209822_s_at_HG-U133A	VLDLR	Hs.73729	P98155	7436	9p24
209825_s_at_HG-U133A	UMPK	Hs.75939	Q92528	7371	1q23
209827_s_at_HG-U133A	IL16	Hs.82127	Q14005	3603	15q26.3
209831_x_at_HG-U133A	DNASE2	Hs.118243	O00115	1777	19p13.2
209876_at_HG-U133A	GIT2	Hs.57734	Q96CI2	9815	12q24.1
209891_at_HG-U133A	AD024	Hs.21137	Q9HBM1	57405	2q31.1
209905_at_HG-U133A	HOXA9	Hs.127428	AAH06537	3205	7p15-p14
209939_x_at_HG-U133A	CFLAR	Hs.195175	O15519	8837	2q33-q34
209961_s_at_HG-U133A	HGF	Hs.809	Q13494	3082	7q21.1
209975_at_HG-U133A	CYP2E	Hs.75183	P05181	1571	10q24.3-qter
209992_at_HG-U133A	PFKFB2	Hs.211585	Q9H3P1	5208	1q31
209994_s_at_HG-U133A	ABCB1	Hs.21330	P08183	5243	7q21.1
210004_at_HG-U133A	OLR1	Hs.77729	AAH22295	4973	12p13.2-p12.3
210024_s_at_HG-U133A	UBE2E3	Hs.4890	Q969T4	10477	2q32.1
210036_s_at_HG-U133A	KCNH2	Hs.188021	AAL37559	3757	7q35-q36
210038_at_HG-U133A					
210045_at_HG-U133A	IDH2	Hs.5337	P48735	3418	15q26.1
210052_s_at_HG-U133A	C20orf1	Hs.9329	AAD33965	22974	20q11.2
210053_at_HG-U133A	TAF5	Hs.96103	Q15542	6877	10q24-q25.2
210095_s_at_HG-U133A	IGFBP3	Hs.77326	P17936	3486	7p13-p12
210116_at_HG-U133A	SH2D1A	Hs.151544	AAH20732	4068	Xq25-q26
210117_at_HG-U133A	SPAG1	Hs.153057	Q07617	6674	8q22
210128_s_at_HG-U133A	LTB4R	Hs.28408	Q15722	1241	14q11.2-q12
210140_at_HG-U133A	CST7	Hs.143212	O76096	8530	20p11.21

210145_at_HG-U133A	PLA2G4A	Hs.211587	P47712	5321	1q25
210151_s_at_HG-U133A	DYRK3	Hs.38018	O43781	8444	1q32
210192_at_HG-U133A	ATP8A1	Hs.144931	Q9Y2Q0	10396	4p14-p12
210244_at_HG-U133A	CAMP	Hs.51120	P49913	820	3p21.3
210251_s_at_HG-U133A	KIAA0871	Hs.7972	O94948	22902	4q13.2
210254_at_HG-U133A					
210262_at_HG-U133A	TPX1	Hs.2042	AAH22011	7180	6p21-qter
210268_at_HG-U133A	NFX1	Hs.3187	Q12986	4799	9p12
210279_at_HG-U133A	GPR18	Hs.88269	Q96HI6	2841	13q32
210298_x_at_HG-U133A	FHL1	Hs.239069	O95212	2273	Xq26
210299_s_at_HG-U133A	FHL1	Hs.239069	O95212	2273	Xq26
210314_x_at_HG-U133A	TNFSF13	Hs.54673	O75888	8741	17p13.1
210334_x_at_HG-U133A	BIRC5	Hs.1578	O15392	332	17q25
210356_x_at_HG-U133A	MS4A2	Hs.89751	P11836	931	11q12-q13.1
210358_x_at_HG-U133A	MGC2306	Hs.760	P23769	84724	3q22.1
210448_s_at_HG-U133A	P2RX5	Hs.77807	Q93086	5026	17p13
210487_at_HG-U133A	DNTT	Hs.272537	Q96E50	1791	10q23-q24
210519_s_at_HG-U133A					
210563_x_at_HG-U133A	CFLAR	Hs.195175	O15519	8837	2q33-q34
210609_s_at_HG-U133A	PIG3	Hs.50649	Q9BWB8	9540	2p23.3
210613_s_at_HG-U133A	SYNGR1	Hs.6139	O43759	9145	22q13.1
210616_s_at_HG-U133A	KIAA0905	Hs.70266	O94979	22872	4q21.22
210658_s_at_HG-U133A	GGA2	Hs.155546	Q9UJY4	23062	16p12
210664_s_at_HG-U133A	TFPI	Hs.170279	P10646	7035	2q31-q32.1
210715_s_at_HG-U133A	SPINT2	Hs.31439	O43291	10653	19q13.1
210749_x_at_HG-U133A	DDR1	Hs.75562	Q08345	780	6p21.3
210755_at_HG-U133A	HGF	Hs.809	Q02935	3082	7q21.1
210763_x_at_HG-U133A	LY117	Hs.88411	O00452	7940	6p21.3
210788_s_at_HG-U133A	LOC51635	Hs.109201	Q9UKU2	51635	14q22.3
210789_x_at_HG-U133A	CEACAM3	Hs.11	P40198	1084	19q13.2
210794_s_at_HG-U133A					
210807_s_at_HG-U133A	SLC16A7	Hs.132183	O60669	9194	12q13
210817_s_at_HG-U133A	NDP52	Hs.154230	Q9BTF7	10241	17q23.2
210896_s_at_HG-U133A	ASPH	Hs.283664	AAH25236	444	8q12.1
210916_s_at_HG-U133A		Hs.306278	O95370		
210933_s_at_HG-U133A	MGC4655	Hs.55923	Q9BSU1	84752	16q23.1
210934_at_HG-U133A	BLK	Hs.2243	P51451	640	8p23-p22
210948_s_at_HG-U133A	LEF1	Hs.44865	Q9UJU2	51176	4q23-q25
210973_s_at_HG-U133A	FGFR1	Hs.748	Q02063	2260	8p11.2-p11.1
210982_s_at_HG-U133A	HLA-DRA	Hs.76807	P01903	3122	6p21.3
210997_at_HG-U133A	HGF	Hs.809	Q02935	3082	7q21.1
210998_s_at_HG-U133A	HGF	Hs.809	P14210	3082	7q21.1

211015_s_at_HG-U133A	HSPA4	Hs.90093	Q9BUK9	3308	5q31.1-q31.2
211031_s_at_HG-U133A	CYLN2	Hs.104717	Q9BRH8	7461	7q11.23
211097_s_at_HG-U133A	PBX2	Hs.93728	Q9BTW4	5089	6p21.3
211101_x_at_HG-U133A	LILRA2	Hs.94498	O75020	11027	19q13.4
211105_s_at_HG-U133A	NFATC1	Hs.96149	O95644	4772	18q23
211126_s_at_HG-U133A	CSRP2	Hs.10526	Q16527	1466	12q21.1
211138_s_at_HG-U133A	KMO	Hs.107318	O15229	8564	1q42-q44
211275_s_at_HG-U133A	GYG	Hs.174071	P46976	2992	3q24-q25.1
211297_s_at_HG-U133A	CDK7	Hs.184298	P50613	1022	2p15-cen
211341_at_HG-U133A	POU4F1	Hs.211588	Q01851	5457	13q21.1-q22
211349_at_HG-U133A	SLC15A1	Hs.2217	O14496	6564	13q33-q34
211352_s_at_HG-U133A	NCOA3	Hs.225977	Q9UPG7	8202	20q12
211404_s_at_HG-U133A	APLP2	Hs.279518	AAD47291	334	11q24
211456_x_at_HG-U133A		Hs.367850	Q9BXG3		
211474_s_at_HG-U133A		Hs.355890	Q9BSM3		
211495_x_at_HG-U133A	TNFSF13	Hs.54673	Q75888	8741	17p13.1
211502_s_at_HG-U133A	PFTK1	Hs.57856	O94921	5218	7q21-q22
211540_s_at_HG-U133A	RB1	Hs.75770	P06400	5925	13q14.2
211574_s_at_HG-U133A	MCP	Hs.83532	Q15429	4179	1q32
211584_s_at_HG-U133A	NPAT	Hs.89385	Q13632	4863	11q22-q23
211657_at_HG-U133A					
211665_s_at_HG-U133A					
211668_s_at_HG-U133A	PLAU	Hs.77274	Q96SE8	5328	10q24
211709_s_at_HG-U133A	SCGF	Hs.105927	Q9Y470	6320	19q13.3
211743_s_at_HG-U133A	PRG2	Hs.99962	P13727	5553	11q12
211748_x_at_HG-U133A	PTGDS	Hs.8272	P41222	5730	9q34.2-q34.3
211771_s_at_HG-U133A	POU2F2	Hs.1101	Q9BRS4	5452	19q13.31
211787_s_at_HG-U133A	EIF4A1	Hs.129673	Q9BRB1	1973	17p13
211796_s_at_HG-U133A	TRB	Hs.303157	P04435	6957	7q34
211800_s_at_HG-U133A	USP4	Hs.77500	Q13107	7375	3p21.3
211819_s_at_HG-U133A	SH3D5	Hs.108924	Q9BX64	10580	10q23.3-q24.1
211824_x_at_HG-U133A	DEFCAP	Hs.104305	Q9H5Z7	22861	17p13
211852_s_at_HG-U133A	ATRN	Hs.194019	O75882	8455	20p13
211883_x_at_HG-U133A	CEACAM1	Hs.50964	Q13854	634	19q13.2
211889_x_at_HG-U133A	CEACAM1	Hs.50964	Q13854	634	19q13.2
211918_x_at_HG-U133A	PLAC3	Hs.293896	Q96PH7	60676	1q23-q25
211934_x_at_HG-U133A	G2AN	Hs.76847	Q9P0X0	23193	11q13.1
211950_at_HG-U133A	RBAF600	Hs.297641	AAL83880	23352	1p36.13
211953_s_at_HG-U133A	KPNB3	Hs.113503	AAH01497	3843	13q32.2
211984_at_HG-U133A		Hs.374441			
211990_at_HG-U133A	HLA-DPA1	Hs.914	Q95HB9	3113	6p21.3
211991_s_at_HG-U133A	HLA-DPA1	Hs.914	Q95HB9	3113	6p21.3

212012_at_HG-U133A	D2S448	Hs.118893	Q92626	7837	2pter-p25.1
212013_at_HG-U133A	D2S448	Hs.118893	Q92626	7837	2pter-p25.1
212020_s_at_HG-U133A	MKI67	Hs.80976	P46013	4288	10q25-qter
212022_s_at_HG-U133A	MKI67	Hs.80976	P46013	4288	10q25-qter
212032_s_at_HG-U133A	PTOV1	Hs.19555	Q9HBN4	53635	19q13.33
212058_at_HG-U133A	KIAA0332	Hs.7976	O15042	23350	3q24
212074_at_HG-U133A	KIAA0810	Hs.7531	Q96CZ7	23353	7p22.3
212107_s_at_HG-U133A	DDX9	Hs.74578	Q12803	1660	1q25
212133_at_HG-U133A	MGC5466	Hs.83724	Q96F03	81614	15q11.1
212146_at_HG-U133A	KIAA0842	Hs.74569	O94928	23207	1p36.13
212150_at_HG-U133A	KIAA0143	Hs.84087	Q14156	23167	8q24.12
212171_x_at_HG-U133A	VEGF	Hs.73793	Q96KJ0	7422	6p12
212185_x_at_HG-U133A	MT2A	Hs.118786	P02795	4502	16q13
212187_x_at_HG-U133A	PTGDS	Hs.8272	P41222	5730	9q34.2-q34.3
212188_at_HG-U133A	LOC115207	Hs.109438	Q96CX2	115207	13q22.1
212207_at_HG-U133A	KIAA1025	Hs.4084	Q9UFD8	23389	12q24.21
212222_at_HG-U133A	KIAA0077	Hs.112396	Q14997	23198	2p16.2
212229_s_at_HG-U133A					
212231_at_HG-U133A	FBXO21	Hs.184227	O94952	23014	12q24.21
212232_at_HG-U133A	KIAA1014	Hs.6834	Q9H985	23360	11q12.1
212236_x_at_HG-U133A					
212250_at_HG-U133A		Hs.243901	AAL92861		
212251_at_HG-U133A		Hs.243901	AAL92861		
212259_s_at_HG-U133A	HPIP	Hs.8068	Q9HA02	57326	1q21.2
212268_at_HG-U133A	SERPINB1	Hs.183583	P30740	1992	6p25
212271_at_HG-U133A	MAPK1	Hs.324473	P28482	5594	22q11.21
212281_s_at_HG-U133A	MAC30	Hs.199695	Q07823	27346	17q11.1
212285_s_at_HG-U133A	AGRN	Hs.273330	Q96IC1	180	1p36.3-p32
212287_at_HG-U133A	JJAZ1	Hs.197803	Q15022	23512	17q11.2
212293_at_HG-U133A	KIAA0630	Hs.12259	AAH28408	23323	1p11.2
212309_at_HG-U133A	CLASP2	Hs.108614	Q9H7A3	23122	3p22.2-p22.1
212311_at_HG-U133A	KIAA0746	Hs.49500	Q96G59	23231	4p15.31
212313_at_HG-U133A		Hs.5019	Q8WUX9		
212314_at_HG-U133A	KIAA0746	Hs.49500	O94847	23231	4p15.31
212345_s_at_HG-U133A	DKFZP586F2423	Hs.13659	Q9H6N8	64764	7q34
212346_s_at_HG-U133A					
212349_at_HG-U133A	POFUT1	Hs.178292	BAA11497	23509	
212357_at_HG-U133A	KIAA0280	Hs.75400	Q92567	23201	11q13.3
212365_at_HG-U133A	MYO1B	Hs.121576	O43795	4430	2q12-q34
212382_at_HG-U133A		Hs.289068			
212385_at_HG-U133A		Hs.289068			
212386_at_HG-U133A		Hs.289068			

212387_at_HG-U133A		Hs.289068			
212397_at_HG-U133A	RDX	Hs.263671	P35241	5962	11q23
212400_at_HG-U133A		Hs.349755			
212417_at_HG-U133A	SCAMP1	Hs.31218	Q96BX1	9522	5q13.3-q14.1
212449_s_at_HG-U133A	LYPLA1	Hs.12540	O75608	10434	8q11.23
212463_at_HG-U133A		Hs.99766			
212469_at_HG-U133A	IDN3	Hs.225767	Q9Y6Y4	25836	5p13.1
212479_s_at_HG-U133A	FLJ13910	Hs.75277	Q9H6W5	64795	2p11.1
212480_at_HG-U133A	KIAA0376	Hs.4791	O15081	23384	22q11.21
212481_s_at_HG-U133A	TPM4	Hs.250641	P07226	7171	19p13.1
212484_at_HG-U133A	MTVR	Hs.18686		23625	
212509_s_at_HG-U133A		Hs.356623			
212531_at_HG-U133A	LCN2	Hs.204238	P80188	3934	9q34
212535_at_HG-U133A		Hs.288993			
212538_at_HG-U133A	KIAA1058	Hs.8021	Q9BZ29	23348	13q32.3
212549_at_HG-U133A		Hs.24064			
212569_at_HG-U133A	KIAA0650	Hs.8118	Q9UG39	23347	18p11.31
212577_at_HG-U133A	KIAA0650	Hs.8118	O75141	23347	18p11.31
212579_at_HG-U133A	KIAA0650	Hs.8118	O75141	23347	18p11.31
212586_at_HG-U133A	ARTS-1	Hs.247043	AAK37778	51752	5q15
212587_s_at_HG-U133A	PTPRC	Hs.170121	P08575	5788	1q31-q32
212589_at_HG-U133A	RRAS2	Hs.206097	AAM12638	22800	11p15.2
212590_at_HG-U133A					
212592_at_HG-U133A		Hs.76325	Q8WW49		
212601_at_HG-U133A	KIAA0399	Hs.100955	BAB85062	23140	17p13.3
212614_at_HG-U133A		Hs.12702			
212629_s_at_HG-U133A	PRKCL2	Hs.69171	Q16513	5586	1p22.1
212658_at_HG-U133A	LHFPL2	Hs.79299	Q92605	10184	5q13.3
212660_at_HG-U133A	KIAA0239	Hs.9729	Q96GQ6	23338	5q31.1
212667_at_HG-U133A	SPARC	Hs.111779	AAH04974	6678	5q31.3-q32
212686_at_HG-U133A	KIAA1157	Hs.21894	Q9ULR3	57460	12q13.13
212719_at_HG-U133A	SCOP	Hs.38176	BAA25532	23239	18q21.32
212733_at_HG-U133A	KIAA0226	Hs.141296	Q92622	9711	3q29
212735_at_HG-U133A	KIAA0226	Hs.141296	Q92622	9711	3q29
212750_at_HG-U133A	PPP1R16B	Hs.45719	O94912	26051	20q11.23
212778_at_HG-U133A	KIAA0602	Hs.37656	O60342	23241	
212783_at_HG-U133A	DKFZp761B2423	Hs.91065	Q9NPX4	55524	
212812_at_HG-U133A		Hs.288232			
212813_at_HG-U133A	FLJ14529	Hs.334703	Q8WWL8	84887	11q25
212827_at_HG-U133A	IGHM	Hs.153261	Q96GA6	3507	14q32.33
212828_at_HG-U133A	SYNJ2	Hs.61289	O15056	8871	6q25.3
212838_at_HG-U133A	KIAA1010	Hs.23860	Q9Y2L3	23268	10q25.1

212886_at_HG-U133A	DKFZP434C171	Hs.209100	AAH16647	26112	5q33.1
212895_s_at_HG-U133A	ABR	Hs.118021	Q12979	29	17p13.3
212914_at_HG-U133A	PKP4	Hs.152151	Q99569	8502	2q23-q31
212953_x_at_HG-U133A	CALR	Hs.16488	P13796	811	19p13.3-p13.2
212956_at_HG-U133A	KIAA0882	Hs.90419	BAA74905	23158	4q31.1
212960_at_HG-U133A	KIAA0882	Hs.90419	BAA74905	23158	4q31.1
212967_x_at_HG-U133A	NAP1L1	Hs.302649	AAH02387	4673	12q14.1*
212970_at_HG-U133A		Hs.15740			
212973_at_HG-U133A	RPIA	Hs.79886	Q96BJ6	22934	2p11.1
212975_at_HG-U133A	KIAA0870	Hs.18166	Q9UFX2	22898	8q24.3
212985_at_HG-U133A		Hs.15740			
212989_at_HG-U133A		Hs.153716			
212998_x_at_HG-U133A	HLA-DQB1	Hs.73931	AAH12106	3119	6p21.3
213048_s_at_HG-U133A	SET	Hs.145279	Q01105	6418	9q34
213049_at_HG-U133A	DKFZp566D133	Hs.167031	Q9Y408	26134	9q31
213073_at_HG-U133A	KIAA0321	Hs.8663	Q96H43	23503	14q23.3
213081_at_HG-U133A	ZNF297	Hs.206770	Q8WV82	9278	6p21.3
213101_s_at_HG-U133A	IL27	Hs.10927	Q9BTK7	56005	19p13.3
213142_x_at_HG-U133A	LOC54103	Hs.12969	Q9UMH3	54103	7p12.3
213147_at_HG-U133A	HOXA10	Hs.110637	AAH13971	3206	7p15-p14
213150_at_HG-U133A	HOXA10	Hs.110637	AAH13971	3206	7p15-p14
213159_at_HG-U133A	KIAA0805	Hs.55947	O94897	23226	14q22.1-q23.3
213238_at_HG-U133A	ATP10D	Hs.173540	Q96SR3	57205	4p12
213249_at_HG-U133A	FBXL7	Hs.76798	O94926	23194	5p15.1
213288_at_HG-U133A		Hs.90797			
213295_at_HG-U133A		Hs.26295			
213309_at_HG-U133A	PLCL2	Hs.54886	Q9H8L0	23228	3p24.3
213313_at_HG-U133A	GAPCENA	Hs.55099	Q9UG67	23637	9q34.11
213353_at_HG-U133A	ABCA5	Hs.180513	Q9NY14	23461	17q24.3
213370_s_at_HG-U133A	DKFZP434L243	Hs.21695	Q9Y4Q9	25944	3
213447_at_HG-U133A	IPW	Hs.5022		3653	15q11-q12
213452_at_HG-U133A	ZNF184	Hs.158174	AAH22992	7738	6p21.3
213453_x_at_HG-U133A	GAPD	Hs.169476	Q16768	2597	12p13
213474_at_HG-U133A		Hs.356517			
213504_at_HG-U133A	MOV34-34KD	Hs.15591	O15387	10980	7q11.1
213511_s_at_HG-U133A		Hs.347187	Q96FD1		
213514_s_at_HG-U133A	DIAPH1	Hs.26584	O60610	1729	5q31
213539_at_HG-U133A	CD3D	Hs.95327		915	11q23
213572_s_at_HG-U133A	SERPINB1	Hs.183583	P30740	1992	6p25
213582_at_HG-U133A	ATP11A	Hs.29189	Q9H7W0	23250	13q34
213600_at_HG-U133A	KIAA0545	Hs.129943	BAA25471	23094	19q13.13
213622_at_HG-U133A	COL9A2	Hs.37165	Q14055	1298	1p33-p32

213624_at_HG-U133A	ASM3A	Hs.42945	Q92484	10924	6
213639_s_at_HG-U133A	KIAA0557	Hs.101414	O60304	26048	16p13.13
213674_x_at_HG-U133A	IGHG3	Hs.300697	AAH24289	3502	14q32.33
213689_x_at_HG-U133A	RPL5	Hs.180946	P46777	6125	1p22.1
213716_s_at_HG-U133A	SECTM1	Hs.95655	O00466	6398	17q25
213725_x_at_HG-U133A		Hs.22907			
213737_x_at_HG-U133A		Hs.205125			
213772_s_at_HG-U133A	GGA2	Hs.155546	Q9UJY4	23062	16p12
213779_at_HG-U133A					
213798_s_at_HG-U133A	CAP	Hs.104125	Q01518	10487	1p34.3
213810_s_at_HG-U133A	FLJ10342	Hs.101514	Q9BQB1	55122	6q16.1
213844_at_HG-U133A	HOXA5	Hs.37034	Q96CY6	3202	7p15-p14
213846_at_HG-U133A	COX7C	Hs.3462	P15954	1350	5q14
213850_s_at_HG-U133A	SFRS2IP	Hs.51957	Q99590	9169	12p11.21
213854_at_HG-U133A	SYNGR1	Hs.6139	O43759	9145	22q13.1
213857_s_at_HG-U133A	CD47	Hs.82685	Q96A60	961	3q13.1-q13.2
213891_s_at_HG-U133A		Hs.289068			
213894_at_HG-U133A	KIAA0960	Hs.29900	BAA76804	23249	7p22.1
213895_at_HG-U133A	EMP1	Hs.79368	P54849	2012	12p12.3
213902_at_HG-U133A	ASAHI	Hs.75811	Q13510	427	8p22-p21.3
213922_at_HG-U133A	KIAA0847	Hs.125836	O94932	26044	15q14
213927_at_HG-U133A		Hs.170267			
213942_at_HG-U133A	EGFL3	Hs.56186	O75095	1953	1p36.3
213944_x_at_HG-U133A		Hs.323067	Q96DH5		
213963_s_at_HG-U133A	SAP30	Hs.20985	O75446	8819	4q34.1
213979_s_at_HG-U133A	CTBP1	Hs.239737	Q13363	1487	4p16
214000_s_at_HG-U133A	RGS10	Hs.82280	AAM12648	6001	10q25
214017_s_at_HG-U133A	DDX34	Hs.151706	Q14147	9704	19q13.3
214030_at_HG-U133A	FLJ14393	Hs.23294	Q96C17	84864	3q22.1
214051_at_HG-U133A	TMSNB	Hs.56145	Q99406	11013	Xq21.33-q22.3
214109_at_HG-U133A	LRBA	Hs.62354	P50851	987	4q31.22-q31.23
214116_at_HG-U133A	BTD	Hs.78885	P43251	686	3p25
214144_at_HG-U133A	POLR2D	Hs.194638	Q96FU3	5433	2q21
214152_at_HG-U133A	PIGB	Hs.247118	Q8WVN7	9488	15q21-q22
214203_s_at_HG-U133A	PRODH	Hs.343874	Q9UF13	5625	22q11.21
214228_x_at_HG-U133A					
214238_at_HG-U133A		Hs.18081			
214310_s_at_HG-U133A	ZFPL1	Hs.155165	O14616	7542	11q13
214315_x_at_HG-U133A	CALR	Hs.16488	P27797	811	19p13.3-p13.2
214316_x_at_HG-U133A	CALR	Hs.16488	P13796	811	19p13.3-p13.2
214317_x_at_HG-U133A	RPS9	Hs.180920	P46781	6203	19q13.4
214321_at_HG-U133A	NOV	Hs.235935	P48745	4856	8q24.1

214394_x_at_HG-U133A	FLJ20897	Hs.334798	Q96I38	84338	8q24.3
214395_x_at_HG-U133A	FLJ20897	Hs.334798	Q9H7G6	84338	8q24.3
214430_at_HG-U133A	GLA	Hs.69089	BAA34059	2717	Xq22
214439_x_at_HG-U133A	BIN1	Hs.193163	O00499	274	2q14
214450_at_HG-U133A	CTSW	Hs.87450	P56202	1521	11q13.1
214452_at_HG-U133A	BCAT1	Hs.157205	Q96MY9	586	12pter-q12
214475_x_at_HG-U133A	CAPN3	Hs.40300	Q9BQC8	825	15q15.1-q21.1
214500_at_HG-U133A	H2AFY	Hs.75258	Q96D41	9555	5q31.3-q32
214501_s_at_HG-U133A	H2AFY	Hs.75258	O75367	9555	5q31.3-q32
214505_s_at_HG-U133A	FHL1	Hs.239069	O95212	2273	Xq26
214523_at_HG-U133A	CEBPE	Hs.158323	Q15744	1053	14q11.2
214558_at_HG-U133A	GPR12	Hs.123034		2835	13q12
214575_s_at_HG-U133A	AZU1	Hs.72885		566	19p13.3
214615_at_HG-U133A	P2Y10	Hs.296433		27334	Xq21.1
214651_s_at_HG-U133A	HOXA9	Hs.127428	P31269	3205	7p15-p14
214686_at_HG-U133A	ZNF266	Hs.118281	Q14584	10781	19p13.2
214693_x_at_HG-U133A	DJ328E19.C1.1	Hs.218329	Q9UJI9	25832	1q12-1q21.2
214700_x_at_HG-U133A					
214761_at_HG-U133A	OAZ	Hs.137168	BAA34480	23090	16q12
214786_at_HG-U133A	MAP3K1	Hs.170610	Q13233	4214	5q11.2
214789_x_at_HG-U133A	SRP46	Hs.155160	Q96TA3	10929	11q22
214849_at_HG-U133A		Hs.188757	Q9BTH8		
214875_x_at_HG-U133A	APLP2	Hs.279518	Q14662	334	11q24
214894_x_at_HG-U133A	MACF1	Hs.108258	BAA32310	23499	1p32-p31
214911_s_at_HG-U133A					
214924_s_at_HG-U133A					
214949_at_HG-U133A					
214950_at_HG-U133A					
215001_s_at_HG-U133A	GLUL	Hs.170171	AAH11700	2752	1q31
215049_x_at_HG-U133A	CD163	Hs.74076	Q07900	9332	12p13.3
215087_at_HG-U133A					
215100_at_HG-U133A					
215115_x_at_HG-U133A	NTRK3	Hs.26776	Q16288	4916	15q25
215215_s_at_HG-U133A					
215227_x_at_HG-U133A	ACP1	Hs.75393	AAH07422	52	2p25
215346_at_HG-U133A	TNFRSF5	Hs.25648	P25942	958	20q12-q13.2
215379_x_at_HG-U133A	IGLJ3	Hs.181125	Q8WUK3	28831	22q11.1-q11.2
215450_at_HG-U133A	SNRPE	Hs.334612	P08578	6635	1q32
215537_x_at_HG-U133A					
215622_x_at_HG-U133A	HSPC226	Hs.30127	Q9BXW1	51533	3p21.31
215785_s_at_HG-U133A	CYFIP2	Hs.258503	Q14650	26999	5q34
215855_s_at_HG-U133A					

215925_s_at_HG-U133A					
216015_s_at_HG-U133A					
216032_s_at_HG-U133A	SDBCAG84	Hs.169992	Q9H276	51614	20pter-q12
216044_x_at_HG-U133A					
216095_x_at_HG-U133A	MTMR1	Hs.372428	Q13613	8776	Xq28
216218_s_at_HG-U133A	PLCL2	Hs.54886	Q9H8L0	23228	3p24.3
216304_x_at_HG-U133A					
216320_x_at_HG-U133A					
216356_x_at_HG-U133A	BAIAP3	Hs.134846	BAA34454	8938	16p13.3
216363_at_HG-U133A					
216379_x_at_HG-U133A					
216399_s_at_HG-U133A					
216449_x_at_HG-U133A					
216450_x_at_HG-U133A					
216609_at_HG-U133A		Hs.336933	O60744		
216640_s_at_HG-U133A					
216652_s_at_HG-U133A					
216680_s_at_HG-U133A	EPHB4	Hs.155227	Q96L35	2050	7q22
216698_x_at_HG-U133A					
216833_x_at_HG-U133A		Hs.372513	Q12832		
216860_s_at_HG-U133A	GDF11	Hs.339699	O95390	10220	12q12
217047_s_at_HG-U133A					
217080_s_at_HG-U133A	HOMER-2B	Hs.93564	O95349	9455	15q24.3
217156_at_HG-U133A					
217179_x_at_HG-U133A					
217185_s_at_HG-U133A					
217223_s_at_HG-U133A					
217225_x_at_HG-U133A	PM5	Hs.227823	Q9H049	23420	16p13.11
217375_at_HG-U133A					
217383_at_HG-U133A					
217398_x_at_HG-U133A					
217418_x_at_HG-U133A	MS4A2	Hs.89751	AAH02807	931	11q12-q13.1
217419_x_at_HG-U133A					
217478_s_at_HG-U133A					
217504_at_HG-U133A	ABCA6	Hs.15780	Q8WWZ6	23460	17q24.3
217520_x_at_HG-U133A		Hs.356777			
217521_at_HG-U133A		Hs.276590			
217559_at_HG-U133A	RPL10L	Hs.308332	Q96L21	140801	14q13-q21
217716_s_at_HG-U133A	SEC61A1	Hs.306079	Q9BU16	29927	3q21.3
217768_at_HG-U133A	LOC51637	Hs.110803	Q9Y224	51637	14q21.3
217816_s_at_HG-U133A	pcnp	Hs.283728	Q96CU3	57092	3q13.11
217838_s_at_HG-U133A	RNB6	Hs.241471	AAH23997	51466	14q32.32

217916_s_at_HG-U133A	BM-009	Hs.92918	Q9NW21	51571	8q24.22
217920_st_HG-U133A		Hs.362793	AAH15874		
217950_at_HG-U133A	NOSIP	Hs.7236	Q9Y314	51070	19q13.33
217963_s_at_HG-U133A	HCS	Hs.169248	P00001	54205	7p21.2
217966_s_at_HG-U133A	C1orf24	Hs.48778	Q9H9Y8	116496	1q25
217979_at_HG-U133A	NET-6	Hs.284243	O95857	27075	7p21.3
217988_at_HG-U133A	HEI10	Hs.107003	Q9NPC3	57820	14q11.1
217989_at_HG-U133A	LOC51170	Hs.12150	Q9UKU4	51170	4q21.3
217994_x_at_HG-U133A					
218039_at_HG-U133A	ANKT	Hs.279905	AAH24772	51203	15q13.3
218041_x_at_HG-U133A	PRO1068	Hs.343878		55439	
218051_s_at_HG-U133A	FLJ12442	Hs.84753	Q96C80	64943	
218089_at_HG-U133A	C20orf4	Hs.11314	Q9Y312	25980	20pter-q12
218090_s_at_HG-U133A					
218094_s_at_HG-U133A	C20orf35	Hs.179666	Q9BVL1	55861	20q13.11
218100_s_at_HG-U133A	ESRRBL1	Hs.170318	Q9NWB7	55081	3q13.13
218109_s_at_HG-U133A	FLJ14153	Hs.7503	Q9H3U5	64747	3q25.31
218122_s_at_HG-U133A	SENP2	Hs.3355	BAA92569	59343	3q28
218144_s_at_HG-U133A	FLJ22056	Hs.24956	Q9H6N1	64423	14q32.33
218151_x_at_HG-U133A	FLJ11856	Hs.6459	Q9HAB3	79581	8q24.3
218168_s_at_HG-U133A	CABC1	Hs.273186	Q9HBQ1	56997	1q42.11
218172_s_at_HG-U133A	PRO2577	Hs.241576		55493	8q24.13
218191_s_at_HG-U133A	FLJ11240	Hs.339833	Q9BY56	55788	6q14.1
218223_s_at_HG-U133A	LOC51177	Hs.173380	Q9NRV3	51177	1q21.3
218224_at_HG-U133A	PNMA1	Hs.194709	O95144	9240	14q24.1
218237_s_at_HG-U133A	SLC38A1	Hs.18272	Q9H2H9	81539	12p11.21
218259_at_HG-U133A	KIAA1243	Hs.151076	BAA86557	57496	16p13.2
218319_at_HG-U133A	PELI1	Hs.7886	Q9HCX0	57162	2p13.3
218329_at_HG-U133A	PRDM4	Hs.21807	Q9UKN5	11108	12q23-q24.1
218331_s_at_HG-U133A	FLJ20360	Hs.26434	Q9HTA4	54906	10p15.1
218338_at_HG-U133A	EDR1	Hs.305985	Q9BU63	1911	12p13
218341_at_HG-U133A	FLJ11838	Hs.72531	Q9HAB8	79717	1p34.1
218351_at_HG-U133A	FLJ20502	Hs.23956	Q9NX08	54951	
218354_at_HG-U133A	LOC51693	Hs.27445	Q9UL33	51693	16q24.3
218355_at_HG-U133A	KIF4A	Hs.279766	O95239	24137	Xq13.1
218379_at_HG-U133A	RBM7	Hs.5887	Q9NUT4	10179	11q23.1-q23.2
218384_at_HG-U133A	CRHSP-24	Hs.92198	Q9BQ53	23589	16p13.3
218424_s_at_HG-U133A	FLJ10829	Hs.57655	AAM08128	55240	2q21.2
218464_s_at_HG-U133A	FLJ10700	Hs.295909	Q9H6F3	55731	17q11.2
218468_s_at_HG-U133A	CKTSF1B1	Hs.40098	O60565	26585	15q13-q15
218469_at_HG-U133A	CKTSF1B1	Hs.40098	O60565	26585	15q13-q15
218482_at_HG-U133A	DC6	Hs.283740	Q9NPA8	56943	8q23.2

218499_at_HG-U133A	MST4	Hs.23643	Q96SR7	51765	Xq26.1
218516_s_at_HG-U133A	FLJ20421	Hs.13328	Q9NX62	54928	8q11.23
218517_at_HG-U133A	FLJ22479	Hs.238246	Q96SQ1	79960	4q26-q27
218531_at_HG-U133A	FLJ21749	Hs.288761	Q9H6X4	80194	11q12.2
218543_s_at_HG-U133A	FLJ22693	Hs.12646	Q9H610	64761	7q32.2
218549_s_at_HG-U133A	LOC51115	Hs.44222	Q96DB5	51115	8
218577_at_HG-U133A	FLJ20331	Hs.50848	Q9NXC1	55631	1p31.1
218582_at_HG-U133A	FLJ20445	Hs.343748	Q9NX47	54708	10q23.33
218589_at_HG-U133A	P2Y5	Hs.189999	P43657	10161	13q14
218614_at_HG-U133A	FLJ10652	Hs.236844	Q9NVL6	55196	12p12.1
218642_s_at_HG-U133A	MGC2217	Hs.323164	Q9BUK0	79145	8q11.22
218645_at_HG-U133A	ZNF277	Hs.42636	CAD28546	11179	7q31.1
218662_s_at_HG-U133A	HCAP-G	Hs.193602	Q96SV9	64151	4p16-p15
218663_at_HG-U133A	HCAP-G	Hs.193602	Q9BUR3	64151	4p16-p15
218692_at_HG-U133A	FLJ20366	Hs.8358	Q96D80	55638	8q23.2
218718_at_HG-U133A	PDGFC	Hs.43080	Q9NRA1	56034	4q32
218764_at_HG-U133A	MGC5363	Hs.1880	Q9BVQ0	79030	14q22.1-q22.3
218836_at_HG-U133A	FLJ22638	Hs.183232	Q96F16	79897	6p21.31
218913_s_at_HG-U133A	LOC51291	Hs.49427	Q9P107	51291	19p11-p12
218916_at_HG-U133A	FLJ23436	Hs.85658	Q9H5H4	79724	16p11.1
218933_at_HG-U133A	MGC5347	Hs.5555	Q9BVQ7	79029	15q15.1
218938_at_HG-U133A	MGC11279	Hs.10915	Q9H469	79176	10q24.32
218942_at_HG-U133A	FLJ22055	Hs.144502	AAH28596	79837	12q13.11
218974_at_HG-U133A	FLJ10159	Hs.22505	Q9NWB3	55084	6q21
219013_at_HG-U133A	FLJ21634	Hs.97056	Q9H6C2	63917	7q34-q36
219027_s_at_HG-U133A	MYO9A	Hs.23395	Q9NTG2	4649	15q22-q23
219029_at_HG-U133A	FLJ21657	Hs.26498	Q96D39	64417	5p12
219033_at_HG-U133A	FLJ21308	Hs.29977	Q9H754	79668	5q11.1
219036_at_HG-U133A	BITE	Hs.42315	Q96B31	80321	3q22-q23
219073_s_at_HG-U133A	OSBPL10	Hs.321622	Q9NX98	114884	3p22.3
219076_s_at_HG-U133A	PXMP2	Hs.49912	Q96GB0	5827	
219079_at_HG-U133A	b5&b5R	Hs.5741	AAH25380	51167	6pter-q22.33
219084_at_HG-U133A	NSD1	Hs.99010	Q96L73	64324	5q35.3
219090_at_HG-U133A	SLC24A3	Hs.12321	Q9HC58	57419	20p13
219099_at_HG-U133A	C12orf5	Hs.24792	Q9NQ88	57103	12p13.3
219111_s_at_HG-U133A	MGC2835	Hs.70582	AAL85336	79039	12q24.11
219138_at_HG-U133A	RPL14	Hs.738	Q96GR0	9045	3p22-p21.2
219156_at_HG-U133A	FLJ11271	Hs.109654	Q96IA4	55333	14q22.1-q24.3
219202_at_HG-U133A	FLJ22341	Hs.25485	Q9H6E9	79651	17q25.3
219221_at_HG-U133A	FLJ22332	Hs.111092	Q9H6F0	79779	3q24
219229_at_HG-U133A	SLC21A11	Hs.14805	Q9UIG8	28232	15q26
219234_x_at_HG-U133A	FLJ23142	Hs.20999	Q9H5R5	79634	2q31.1

219271_at_HG-U133A	FLJ12691	Hs.15830	Q9BRH1	79623	2p23.2
219280_at_HG-U133A	WDR9	Hs.225674	Q96QH0	54014	21q22.2
219291_at_HG-U133A	MDS009	Hs.64641	Q9NRU6	56986	15q15.2
219312_s_at_HG-U133A	RINZF	Hs.237146	Q96MH9	65986	8q13-q21.1
219329_s_at_HG-U133A	3-Apr	Hs.9527	Q96RT2	51374	2p23.3
219337_at_HG-U133A	FLJ20584	Hs.126704	Q9NWW0	54991	1p36.33
219358_s_at_HG-U133A	CENTA2	Hs.28802	Q96SD5	55803	17q11.2
219360_s_at_HG-U133A	TRPM4	Hs.31608	AAM18083	54795	19q13.33
219362_at_HG-U133A	FLJ22643	Hs.43579	Q9H631	79688	9q21.33
219452_at_HG-U133A	LOC64174	Hs.115537	Q9H4A9	64174	16q22.2
219457_s_at_HG-U133A	RIN3	Hs.180040	Q9H6A5	79890	14q32.13
219463_at_HG-U133A	C20orf103	Hs.22920	Q9UJQ1	24141	20p12
219471_at_HG-U133A	FLJ21562	Hs.288708	Q9H714	80183	13q14.11
219477_s_at_HG-U133A	LOC55901	Hs.325667	Q9NS62	55901	13q14.13
219478_at_HG-U133A	WFDC1	Hs.36688	Q9HAU1	58189	16q24.3
219518_s_at_HG-U133A	FLJ22637	Hs.296178	Q9H634	80237	15q14
219574_at_HG-U133A	FLJ20668	Hs.12920	CAD28529	55016	4q32.2
219598_s_at_HG-U133A					
219615_s_at_HG-U133A	KCNK5	Hs.127007	Q95279	8645	6p21
219631_at_HG-U133A	FLJ12929	Hs.278956	Q8WVX8	80002	8q22.3
219634_at_HG-U133A	C4ST	Hs.287402	Q9NPF2	50515	12q
219641_at_HG-U133A	FLJ10103	Hs.42140	Q9NWD5	55070	15q25.3
219654_at_HG-U133A	PTPLA	Hs.114062	Q96FW7	9200	10p14-p13
219667_s_at_HG-U133A	BANK	Hs.193736	Q9NWP2	55024	4q22.2
219690_at_HG-U133A	FLJ22573	Hs.352548	Q9H665	79713	19q13.13
219734_at_HG-U133A	FLJ20174	Hs.114556	Q9NXL6	54847	3q13.31
219753_at_HG-U133A	STAG3	Hs.20132	Q9UJ98	10734	7q22
219763_at_HG-U133A	KIAA1608	Hs.300842	BAB13434	57706	9q34.11
219788_at_HG-U133A	PILR	Hs.122591	Q9UKJ1	29992	7q22
219789_at_HG-U133A	NPR3	Hs.123655	P17342	4883	5p14-p13
219793_at_HG-U133A	SNX16	Hs.128645	P57768	64089	8q21.13
219812_at_HG-U133A	MGC2463	Hs.323634	Q9BVK3	79037	7q11.1
219820_at_HG-U133A	NTT5	Hs.59260	Q9GZN6	28968	19q13.1-q13.4
219837_s_at_HG-U133A	C17	Hs.13872	Q9NRR1	54360	4p16-p15
219846_at_HG-U133A	FLJ23040	Hs.169813	Q9H5U2	80248	1q21.2
219868_s_at_HG-U133A	ANKHZN	Hs.352146	Q9P2R3	51479	17p13
219869_s_at_HG-U133A	LOC64116	Hs.284205	Q9BVC0	64116	4q22-q24
219891_at_HG-U133A	FLJ20208	Hs.131776	Q9NXJ5	54858	19p13.11
220000_at_HG-U133A	SIGLEC5	Hs.117005	O15389	8778	19q13.3
220001_at_HG-U133A	PADI5	Hs.117232	Q9UM07	23569	1p36.13
220007_at_HG-U133A	FLJ13984	Hs.135146	Q9H825	79828	2q31.1
220050_at_HG-U133A	C9orf9	Hs.62595	Q96E40	11092	9q34

220059_at_HG-U133A	BRDG1	Hs.121128	Q9ULZ2	26228	4q13.1
220118_at_HG-U133A	TZFP	Hs.99430	Q8WVP2	27033	19q13.1
220307_at_HG-U133A	CD244	Hs.157872	Q9Y288	51744	1q23.1
220338_at_HG-U133A	FLJ10244	Hs.274419	Q9NW78	55103	1q24.1
220564_at_HG-U133A	FLJ11218	Hs.274413	Q9BS33	55328	10q23.33
220653_at_HG-U133A	ZIM2	Hs.201776	Q9NZV7	23619	19q13.4
220744_s_at_HG-U133A	WDR10	Hs.70202	Q9NV68	55764	3q21
220755_s_at_HG-U133A					
220764_at_HG-U133A	PPP4R2	Hs.356686	Q8WXX6	56340	3q29
220768_s_at_HG-U133A	CSNK1G3	Hs.129206	Q9Y6M4	1456	5q23
220796_x_at_HG-U133A	FLJ14251	Hs.281462	Q96I93	79939	19p13.12
220798_x_at_HG-U133A	FLJ11535	Hs.225170	Q9HAJ4	79948	19p13.3
220924_s_at_HG-U133A	SLC38A2	Hs.298275	Q96QD8	54407	12q
220987_s_at_HG-U133A	DKFZP434J037	Hs.172012	Q9H093	81788	1q31.1-q31.2
220999_s_at_HG-U133A	PRO1331	Hs.301824	AAH26892	81032	5q33.2
221004_s_at_HG-U133A	ITM3	Hs.111577	CAD28460	81618	2q37
221006_s_at_HG-U133A	MY014	Hs.67619	Q96D79	81609	1q21.1
221011_s_at_HG-U133A	DKFZP566J091	Hs.57209	Q9H0Q1	81606	2p23.1
221030_s_at_HG-U133A	DKFZP564B1162	Hs.93589	Q9H0T6	83478	4q21.23-q21.3
221188_s_at_HG-U133A	CIDEB	Hs.288835	AAH25332	27141	14q11.2
221206_at_HG-U133A	FLJ21459	Hs.3769	Q9H729	79569	3q21.2
221234_s_at_HG-U133A	BACH2	Hs.88414	Q9BYV9	60468	6q15
221239_s_at_HG-U133A	SPAP1	Hs.194976	AAM12152	79368	1q21
221253_s_at_HG-U133A	MGC3178	Hs.6101	CAD29430	81567	6p25.2
221268_s_at_HG-U133A	LOC81537	Hs.24678	Q9H189	81537	14q23.1
221331_x_at_HG-U133A	CTLA4	Hs.247824	O95653	1493	2q33
221486_at_HG-U133A					
221543_s_at_HG-U133A	C8orf2	Hs.125849	O94905	11160	8p11.2
221555_x_at_HG-U133A	CDC14B	Hs.22116	O60730	8555	9q22.32
221558_s_at_HG-U133A	LEF1	Hs.44865	Q9UJU2	51176	4q23-q25
221581_s_at_HG-U133A	WBSCR5	Hs.56607	Q9BXX8	7462	7q11.23
221586_s_at_HG-U133A	E2F5	Hs.2331	Q15329	1875	8q21.13
221601_s_at_HG-U133A	TOSO	Hs.58831	O60667	9214	1q31.3
221602_s_at_HG-U133A	TOSO	Hs.58831	O60667	9214	1q31.3
221617_at_HG-U133A					
221642_at_HG-U133A	TREX1	Hs.278408	AAD48774	11277	3p21.3-p21.2
221731_x_at_HG-U133A	CSPG2	Hs.81800	P13611	1462	5q14.3
221739_at_HG-U133A	IL27	Hs.10927	Q969H8	56005	19p13.3
221755_at_HG-U133A		Hs.356684	Q9HBR0		
221761_at_HG-U133A	ADSS	Hs.90011	P30520	159	1cen-q12
221770_at_HG-U133A	RPE	Hs.125845	Q96MI0	6120	2q32-q33.3
221778_at_HG-U133A	KIAA1718	Hs.222707	Q9C0E5	80853	7q33-q35

221802_s_at_HG-U133A	KIAA1598	Hs.23740	AAH22348	57698	10q26.2
221834_et_HG-U133A		Hs.351343			
221858_at_HG-U133A	KIAA0608	Hs.100960	Q9UG83	23232	10q24.2
221865_at_HG-U133A		Hs.170226			
221902_at_HG-U133A		Hs.7967			
221943_x_at_HG-U133A	RPL38	Hs.2017	P23411	6169	17q23-q25
221969_at_HG-U133A	PAX5	Hs.22030	Q02548	5079	9p13
221980_at_HG-U133A					
221991_at_HG-U133A	NXPH3	Hs.55069	AAH22541	11248	17q22
222062_at_HG-U133A	WSX1	Hs.132781	AAH28003	9466	19p13.11
222073_at_HG-U133A	COL4A3	Hs.530	Q01955	1285	2q36-q37
222108_at_HG-U133A					
222146_s_at_HG-U133A					
222147_s_at_HG-U133A					
222150_s_at_HG-U133A					
222154_s_at_HG-U133A	DKFZP564A2416	Hs.5297	Q8WV53	26010	2q33.1
222163_s_at_HG-U133A	MGC5347	Hs.5555	Q9HA41	79029	15q15.1
222166_at_HG-U133A					
222203_s_at_HG-U133A					
222229_x_at_HG-U133A					
222237_s_at_HG-U133A					
222275_at_HG-U133A		Hs.27362			
222282_at_HG-U133A		Hs.294014			
222313_at_HG-U133A		Hs.293334			
222335_at_HG-U133A		Hs.44888			
222422_s_at_HG-U133B	MGC10924	Hs.9788	Q9BT67	80762	5q31.3
222448_s_at_HG-U133B	UMP-CMPK	Hs.11463	P30085	51727	
222465_at_HG-U133B	C15orf15	Hs.284162	AAH26267	51187	15q21
222477_s_at_HG-U133B	TM7SF3	Hs.10071	Q9NUS4	51768	12q11-q12
222492_at_HG-U133B	FLJ21324	Hs.4746	Q9BTJ7	60683	21q22.3
222520_s_at_HG-U133B	ESRRBL1	Hs.170318	BAB87803	55081	3q13.13
222619_at_HG-U133B	ZNF281	Hs.59757	Q9Y2X9	23528	1q32.1
222680_s_at_HG-U133B	RAMP	Hs.126774	Q96SN0	51514	
222692_s_at_HG-U133B	FLJ23399	Hs.299883	Q9NSQ8	64778	3q26.31
222698_s_at_HG-U133B	IMPACT	Hs.284245	Q9H2X4	55364	18q11.2-q12.1
222862_s_at_HG-U133B	AK5	Hs.18268	Q9Y6K8	26289	1p31
222915_s_at_HG-U133B	BANK	Hs.193736	Q8WYN5	55024	4q22.2
222916_s_at_HG-U133B					
222955_s_at_HG-U133B	HT011	Hs.355726	Q9NRV0	55855	Xq26.1
222976_s_at_HG-U133B	NTRK1	Hs.85844	AAH15403	4914	1q21-q22
222977_at_HG-U133B	SURF4	Hs.284296	O15260	6836	9q34.2
222979_s_at_HG-U133B					

222982_x_at_HG-U133B	SLC38A2	Hs.298275	BAA92620	54407	12q
222996_s_at_HG-U133B	HSPC195	Hs.15093	Q9NV51	51523	5q31.3
223036_at_HG-U133B	FRSB	Hs.9081	Q9BR63	10056	2q36.3
223044_at_HG-U133B	SLC11A3	Hs.5944	Q9NP59	30061	2q32
223054_at_HG-U133B	DNAJB11	Hs.278605	Q9UBS4	51726	3q28
223226_x_at_HG-U133B	MGC3181	Hs.324618	Q9BWG4	84713	19p13.11
223246_s_at_HG-U133B	STRBP	Hs.8215	Q9BXG4	55342	9q34.11
223253_et_HG-U133B	UCC1	Hs.46721	Q96J80	54749	7p14.1
223276_at_HG-U133B	NID67	Hs.29444	Q9BZL3	85027	
223280_x_at_HG-U133B	MS4A6A	Hs.17914	AAL56223	64231	11q12.1
223287_s_at_HG-U133B	FOXP1	Hs.274344	AAL56661	27086	3p14.1
223314_at_HG-U133B	MGC11352	Hs.101395	Q9BU34	81619	10q23.2
223318_s_at_HG-U133B	MGC10974	Hs.111099	Q9BT30	84266	19p13.3
223321_s_at_HG-U133B	FGFRL1	Hs.193326	Q9H4D7	53834	4p16
223382_s_at_HG-U133B	NIN283	Hs.320834	Q96K16	84937	16q22.3
223385_at_HG-U133B	CYP2S1	Hs.98370	Q96SQ9	29785	19q13.1
223391_at_HG-U133B	LOC81537	Hs.24678	Q9H189	81537	14q23.1
223401_at_HG-U133B	MDS006	Hs.47668	Q9BVD4	56985	17p12
223422_s_at_HG-U133B	DKFZP564B1162	Hs.93589	Q9H0T6	83478	4q21.23-q21.3
223449_at_HG-U133B	SEMA6A	Hs.263395	Q96JU9	57556	5q23.1
223462_at_HG-U133B	MGC4618	Hs.89072	Q9BSA9	84286	4p16.3
223467_at_HG-U133B	RASD1	Hs.25829	AAM21071	51655	17p11.2
223469_at_HG-U133B	MGC10812	Hs.4188	Q9BSM8	83542	19p13.11
223471_at_HG-U133B					
223474_at_HG-U133B	C14orf4	Hs.179260	Q96JG2	64207	14q24.3
223482_at_HG-U133B	TMPIT	Hs.314243	Q9BXJ8	83862	7p12.3
223498_at_HG-U133B		Hs.15053	Q9HCQ3		
223514_at_HG-U133B	CARD11	Hs.293867	AAL34460	84433	7p22
223522_at_HG-U133B	GL012	Hs.21379	Q9H2N8	81571	9q34.11
223595_at_HG-U133B	AD031	Hs.44004	Q9H2Q1	83935	11q22.2
223703_at_HG-U133B	CDA017	Hs.39780	Q9H2I8	83938	10q23.1
223712_at_HG-U133B	DCOHM	Hs.150186	AAM18136	84105	5q31.2
223785_at_HG-U133B	FLJ10719	Hs.334828	Q96JN1	55215	15q25-q26
223828_s_at_HG-U133B	LGALS12	Hs.284183	AAH28222	85329	11q13
223839_s_at_HG-U133B					
223894_s_at_HG-U133B	FTS	Hs.288929	Q9H8T0	64400	16q12.2
223939_at_HG-U133B	GPR91	Hs.279575	AAL95690	56670	3q24-3q25.1
223981_at_HG-U133B	NIN	Hs.44054	BAB13391	51199	14q21.3
223982_s_at_HG-U133B	IPLA2	Hs.44198	Q9NP80	50640	7q31
224044_at_HG-U133B	FLJ11040	Hs.14202	Q9H067	55288	17q11.2
224049_at_HG-U133B	KCNK17	Hs.162282	AAH25726	89822	6p21.1
224076_s_at_HG-U133B	WHSC1L1	Hs.27721	Q9BYU8	54904	8p11.2

224221_s_at_HG-U133B	VAV3	Hs.267659	Q9UKW4	10451	1p13.2
224254_x_at_HG-U133B					
224324_at_HG-U133B	B29	Hs.131072	Q9BYG7	83876	18q21
224356_x_at_HG-U133B	MS4A6A	Hs.17914	AAH22854	64231	11q12.1
224389_s_at_HG-U133B	LOC84570	Hs.148642	Q9BXR9	84570	4q24
224404_s_at_HG-U133B	IRTA2	Hs.191958	Q96RD9	83416	1q21
224405_at_HG-U133B	IRTA2	Hs.191958	Q96RD9	83416	1q21
224406_s_at_HG-U133B	IRTA2	Hs.191958	Q96RD9	83416	1q21
224407_s_at_HG-U133B	MST4	Hs.23643	Q9BXC3	51765	Xq26.1
224435_at_HG-U133B	MGC4248	Hs.334437	Q9BRX8	84293	10q23.2
224482_s_at_HG-U133B	MGC11316	Hs.7985	Q9BRI9	85018	17q11.2
224516_s_at_HG-U133B	HSPC195	Hs.15093	Q9NV51	51523	5q31.3
224520_s_at_HG-U133B	MGC13168	Hs.9451	Q9BR80	84821	12q13.2
224553_s_at_HG-U133B	TNFRSF18	Hs.212680	Q9Y5U5	8784	1p36.3
224559_at_HG-U133B					
224570_s_at_HG-U133B		Hs.350268			
224609_at_HG-U133B	CTL2	Hs.105509	Q8WY97	57153	19p13.1
224664_at_HG-U133B		Hs.178485	Q96DE5		
224681_at_HG-U133B	GNA12	Hs.182874	AAM12615	2768	7p22-p21
224710_at_HG-U133B	RAB34	Hs.301853	Q96AR4	83871	17q11.1
224724_at_HG-U133B	KIAA1247	Hs.43857	Q9UJR3	55959	20q12-13.2
224727_at_HG-U133B		Hs.250465			
224735_at_HG-U133B		Hs.22546	Q8WVVT9		
224739_at_HG-U133B	MG61	Hs.5326	Q96MW6	64840	Xp11.23
224764_at_HG-U133B	ARHGAP10	Hs.11611	BAA92662	57584	
224772_at_HG-U133B	MGC14961	Hs.6298	BAA86465	57177	1q32.3
224794_s_at_HG-U133B	LOC51148	Hs.23954	Q9HBP2	51148	9q34.2
224804_s_at_HG-U133B	FLJ00005	Hs.367690	P28906	57184	
224811_at_HG-U133B		Hs.5724			
224823_at_HG-U133B		Hs.288965			
224833_at_HG-U133B	ETS1	Hs.18063	P14921	2113	11q23.3
224837_at_HG-U133B	FOXP1	Hs.274344	BAB85050	27086	3p14.1
224838_at_HG-U133B					
224839_s_at_HG-U133B	GPT2	Hs.355862	AAK31794	84706	
224847_at_HG-U133B		Hs.180059	AAH27989		
224848_at_HG-U133B		Hs.180059	AAH27989		
224872_at_HG-U133B	KIAA1463	Hs.21104	Q9P265	57609	12q11
224918_x_at_HG-U133B	MGST1	Hs.355733	P10620	4257	12p12.3-p12.1
224928_at_HG-U133B					
224932_at_HG-U133B	PRSS2	Hs.241561	P07478	5645	7q34
224935_at_HG-U133B	EIF2S3	Hs.211539	AAH19906	1968	Xp22.2-p22.1
224967_at_HG-U133B		Hs.23703			

224970_at_HG-U133B	NFIA	Hs.173933	Q12857	4774	1p31.3-p31.2
224975_at_HG-U133B	NFIA	Hs.173933	AAH22264	4774	1p31.3-p31.2
224976_at_HG-U133B	NFIA	Hs.173933	Q12857	4774	1p31.3-p31.2
224994_at_HG-U133B	CAMK2D	Hs.111460	Q13557	817	4q25
225003_at_HG-U133B	MBC3205	Hs.43621	Q96HM3	90585	19p13.2
225010_at_HG-U133B					
225014_at_HG-U133B		Hs.235026	Q9BRT5		
225019_at_HG-U133B	CAMK2D	Hs.111460	Q13557	817	4q25
225025_at_HG-U133B	IGSF8	Hs.332012	Q9BTG9	93185	1q23.1
225051_at_HG-U133B		Hs.268024			
225055_at_HG-U133B	FLJ10120	Hs.339808	Q9NWC8	55073	17q21.32
225064_at_HG-U133B		Hs.250535			
225065_x_at_HG-U133B		Hs.295362	AAH27986		
225073_at_HG-U133B	HSPC232	Hs.281428	Q96NB9	51535	12p11.23
225080_at_HG-U133B	MYO1C	Hs.286226	O00159	4641	17p13
225085_at_HG-U133B		Hs.96513	Q96D48		
225129_at_HG-U133B	MDS026	Hs.85752	Q9P1Y7	55844	
225136_at_HG-U133B		Hs.18585			10
225144_at_HG-U133B		Hs.28959			
225175_s_at_HG-U133B	CTL2	Hs.105509	Q8WY97	57153	19p13.1
225230_at_HG-U133B	CEPT1	Hs.125031	Q9Y6K0	10390	1p12
225246_at_HG-U133B	STIM2	Hs.278894	Q9P246	57620	4p15.2
225250_at_HG-U133B	STIM2	Hs.278894	Q9P246	57620	4p15.2
225270_at_HG-U133B					
225277_at_HG-U133B		Hs.9070	Q8WV10		
225285_at_HG-U133B					
225305_at_HG-U133B		Hs.27769			
225306_s_at_HG-U133B		Hs.27769			
225314_at_HG-U133B		Hs.95835			
225326_at_HG-U133B	KIAA1311	Hs.61441	Q9P2N5	54439	
225327_at_HG-U133B	FLJ10980	Hs.29716	Q9NV24	56204	15q15.3
225330_at_HG-U133B		Hs.104679	Q96FP4		
225331_at_HG-U133B		Hs.170307			
225344_at_HG-U133B					
225386_s_at_HG-U133B	LOC92906	Hs.91684	Q8WV9	92906	2p22.3
225406_at_HG-U133B	TSG	Hs.247302	Q9GZX9	57045	18p11.3
225426_at_HG-U133B		Hs.356739			
225452_at_HG-U133B	PPARBP	Hs.15589	Q15648	5469	17q12
225469_at_HG-U133B	KRAS2	Hs.351221	P01118	3845	12p12.1
225510_at_HG-U133B	CHN1	Hs.22660	P15882	1123	2q31-q32.1
225512_at_HG-U133B		Hs.23853	Q96NB8		
225547_at_HG-U133B		Hs.372680			

225553_at_HG-U133B		Hs.56847				
225563_at_HG-U133B		Hs.30348				
225565_at_HG-U133B		Hs.22315				
225592_at_HG-U133B	NRM	Hs.57222	Q9UN92	11270	6p21.31	
225624_at_HG-U133B		Hs.194478	Q9H7K6			
225629_s_at_HG-U133B	KIAA1538	Hs.35096	BAA96062	57659	17p13.2	
225635_s_at_HG-U133B		Hs.279607				
225640_at_HG-U133B		Hs.279607				
225653_at_HG-U133B		Hs.105664	Q9H6G8			
225660_at_HG-U133B	SEMA6A	Hs.263395	Q9H2E6	57556	5q23.1	
225670_at_HG-U133B		Hs.18955				
225700_at_HG-U133B						
225713_at_HG-U133B	KIAA1898	Hs.22410	Q96PY9	114790	2q36.3	
225735_at_HG-U133B						
225772_s_at_HG-U133B	MGC14288	Hs.181073	Q96I36	84987	12p11.1	
225776_at_HG-U133B	BAZ2A	Hs.277401	Q9UIF9	11176	12q24.3-qter	
225782_at_HG-U133B		Hs.339024				
225790_at_HG-U133B		Hs.339024				
225792_at_HG-U133B		Hs.299254				
225803_at_HG-U133B	FBXO32	Hs.61661	Q969P5	114907	8q24.13	
225804_at_HG-U133B		Hs.284163	Q8WUJ1			
225889_at_HG-U133B		Hs.285833	Q96BG3			
225897_at_HG-U133B		Hs.330716				
225902_at_HG-U133B		Hs.35274				
225917_at_HG-U133B	DKFZp762B226	Hs.7041	BAA86522	55918	12q23.1	
225927_at_HG-U133B	MAP3K1	Hs.170610	Q13233	4214	5q11.2	
225959_s_at_HG-U133B	NIN283	Hs.320834	Q9H083	84937	16q22.3	
226005_at_HG-U133B		Hs.296273				
226008_at_HG-U133B	HCA4	Hs.94011	AAM08357	145961	15q12	
226013_at_HG-U133B		Hs.347459				
226014_at_HG-U133B	EIF3S5	Hs.7811	O00303	8665	2p16.1	
226043_at_HG-U133B	AGS3	Hs.239370	Q96G60	26086	9q34.3	
226060_at_HG-U133B	RFT1	Hs.334614	Q96J03	91869	3p21.31	
226063_at_HG-U133B		Hs.4248	Q8WY83			
226066_at_HG-U133B						
226101_at_HG-U133B		Hs.374424				
226120_at_HG-U133B	LOC123016	Hs.55158	AAH26351	123016	14q31.3	
226122_at_HG-U133B						
226147_s_at_HG-U133B		Hs.205126				
226156_at_HG-U133B	AKT2	Hs.326445	P31751	208	19q13.1-q13.2	
226165_at_HG-U133B	E2F5	Hs.2331	Q15329	1875	8q21.13	
226188_at_HG-U133B						

226190_at_HG-U133B		Hs.57776			
226210_s_at_HG-U133B		Hs.374572			
226236_at_HG-U133B		Hs.349092			
226244_at_HG-U133B		Hs.293815			
226247_at_HG-U133B		Hs.287830			
226250_at_HG-U133B		Hs.374454			
226252_at_HG-U133B		Hs.374454			
226258_at_HG-U133B		Hs.337603			
226291_at_HG-U133B	ALS2	Hs.27669	BAB13389	57679	2q33.2
226299_at_HG-U133B	pknbeta	Hs.44101	Q9UM03	29941	9q34.2
226301_at_HG-U133B	dJ55C23.6	Hs.347144		116843	6q22.3-q23.3
226324_s_at_HG-U133B	SLB	Hs.127401	Q9UG01	26160	2p23.3
226326_at_HG-U133B		Hs.11356			
226342_at_HG-U133B		Hs.236443			
226384_at_HG-U133B	HTPAP	Hs.169341	Q9BY45	84513	8p11.21
226408_at_HG-U133B	TEAD2	Hs.166556	Q15562	8463	19q13.3
226435_at_HG-U133B		Hs.301152			
226438_at_HG-U133B					
226448_at_HG-U133B		Hs.38516	Q96GI7		
226450_at_HG-U133B		Hs.98401			
226454_at_HG-U133B	LOC92979	Hs.65377	Q96GG2	92979	12q13.11
226496_at_HG-U133B		Hs.27774	AAH22434		
226499_at_HG-U133B		Hs.21812			
226508_at_HG-U133B		Hs.25328			
226531_at_HG-U133B	FLJ14466	Hs.55148	Q96BP7	84876	12q24.31
226538_at_HG-U133B	MAN2A1	Hs.63368	Q16706	4124	5q21-q22
226545_at_HG-U133B					
226546_at_HG-U133B		Hs.90286			
226550_at_HG-U133B		Hs.91389			
226560_at_HG-U133B		Hs.13234			
226590_at_HG-U133B		Hs.349208			
226607_at_HG-U133B	L3MBTL	Hs.119021	Q9UFX9	26013	20p13
226625_at_HG-U133B	TGFBR3	Hs.342874	Q03167	7049	1p33-p32
226634_at_HG-U133B		Hs.98613	AAH26167		
226635_at_HG-U133B		Hs.279607			
226641_at_HG-U133B		Hs.11571			
226646_at_HG-U133B	KLF2	Hs.107740	Q9Y5W3	10365	19p13.13-p13.11
226713_at_HG-U133B		Hs.55098			
226726_at_HG-U133B	LOC129642	Hs.356547	Q96KY4	129642	2p25.2
226734_at_HG-U133B		Hs.306915			
226735_at_HG-U133B		Hs.25119	Q9NZK9		
226741_at_HG-U133B	LOC51234	Hs.250905	Q96KX9	51234	15q13.1

226743_at_HG-U133B		Hs.235709			
226751_at_HG-U133B	DKFZP566K1924	Hs.26358	Q9UFZ0	25927	2p13.3
226783_at_HG-U133B		Hs.54982			
226795_at_HG-U133B		Hs.118913			
226818_at_HG-U133B		Hs.288581			
226841_at_HG-U133B		Hs.288581			
226844_at_HG-U133B		Hs.293849			
226876_at_HG-U133B		Hs.345588	Q96CJ4		
226878_at_HG-U133B		Hs.11135			
226905_at_HG-U133B		Hs.345588	Q96CJ4		
226936_at_HG-U133B		Hs.35962			
226939_at_HG-U133B		Hs.44833			
226989_at_HG-U133B		Hs.108972			
227030_at_HG-U133B		Hs.318893			
227038_at_HG-U133B		Hs.29567			
227039_at_HG-U133B	AKAP13	Hs.372326	Q8WXQ6	11214	15q24-q25
227041_at_HG-U133B		Hs.30977			
227046_at_HG-U133B	C17orf26	Hs.3402	Q8WZ81	201266	17q21.31
227047_x_at_HG-U133B	KIAA1538	Hs.35096	Q9P1Z0	57659	17p13.2
227056_at_HG-U133B	KIAA0141	Hs.63510	Q969R4	9812	5q31.3
227065_at_HG-U133B	COL5A2	Hs.82985	CAA75002	1290	2q14-q32
227121_at_HG-U133B		Hs.374267			
227145_at_HG-U133B	LOXL4	Hs.306814	Q96JB6	84171	10q24
227146_at_HG-U133B		Hs.309165			
227151_at_HG-U133B		Hs.32365	Q8WV41		
227152_at_HG-U133B		Hs.323822	Q9HCM1		
227167_s_at_HG-U133B		Hs.61426	Q9NYI4		
227173_s_at_HG-U133B	BACH2	Hs.88414	Q9BYV9	60468	6q15
227189_at_HG-U133B	KIAA1599	Hs.285714	Q9HCH3	57699	6p21.1
227198_at_HG-U133B		Hs.125019			
227206_at_HG-U133B		Hs.108593			
227212_s_at_HG-U133B		Hs.352417	AAH22374		
227224_at_HG-U133B		Hs.174104			
227230_s_at_HG-U133B	KIAA1211	Hs.205293	Q9ULK9	57482	4q11
227237_x_at_HG-U133B	KIAA1273	Hs.23413	Q9BUK4	57516	1p36.32
227242_s_at_HG-U133B		Hs.348805			
227243_s_at_HG-U133B					
227249_at_HG-U133B	NUDE1	Hs.263925	Q9NXR1	54820	16p13.11
227261_at_HG-U133B	KLF12	Hs.23510	Q9Y4X4	11278	13q22
227276_at_HG-U133B	TEM7R	Hs.33033	Q96E59	84898	10p12.1
227277_at_HG-U133B		Hs.33074			
227279_at_HG-U133B	MGC15737	Hs.39122	Q969E4	85012	Xq22.1

227299_at_HG-U133B		Hs.79933	Q14094	10983	4q13.3
227326_at_HG-U133B		Hs.11924			
227336_at_HG-U133B	DTX1	Hs.124024	Q9BS04	1840	12q24.11
227353_at_HG-U133B		Hs.15284	AAH28076		
227367_at_HG-U133B		Hs.184067			
227375_at_HG-U133B	DKFZP566D1346	Hs.22612	AAH28840	81573	1p32.3-p31.3
227388_at_HG-U133B		Hs.26268			
227393_at_HG-U133B		Hs.288455			
227396_at_HG-U133B		Hs.374451			
227407_at_HG-U133B		Hs.356851			
227408_s_at_HG-U133B	MSTP043	Hs.306881	Q9H3E2	83891	4q35.1
227414_at_HG-U133B	DKFZp547E052	Hs.49359	BAB85031	84236	
227415_at_HG-U133B		Hs.47094			
227478_at_HG-U133B		Hs.128052			
227497_at_HG-U133B		Hs.196008			
227525_at_HG-U133B	LOC113263	Hs.18987	Q96FD0	113263	7p22.2
227527_at_HG-U133B		Hs.3640			
227533_at_HG-U133B		Hs.5415			
227556_at_HG-U133B	ATP1B1	Hs.78629	P05026	481	1q22-q25
227568_at_HG-U133B					
227584_at_HG-U133B		Hs.112461			
227587_at_HG-U133B	MGC15906	Hs.104938	Q969K0	84971	19p13.2
227606_s_at_HG-U133B	KIAA1373	Hs.16229	Q96FJ0	57559	10q23.33
227607_at_HG-U133B	KIAA1373	Hs.16229	Q96FJ0	57559	10q23.33
227627_at_HG-U133B	SGKL	Hs.279696	Q9P1Q7	23678	8q12.3-8q13.1
227646_at_HG-U133B	EBF	Hs.32425	Q9UH73	1879	5q34
227670_at_HG-U133B		Hs.50456	Q96N20		
227680_at_HG-U133B		Hs.348788			
227700_x_at_HG-U133B	FLJ10709	Hs.273357	Q96A50	55210	1p36.32
227701_at_HG-U133B					
227709_at_HG-U133B	RCN1	Hs.167791	AAH10120	5954	11p13
227729_at_HG-U133B		Hs.107265			
227744_s_at_HG-U133B	HNRPD	Hs.303627	Q14103	3184	4q21.1-q21.2
227749_at_HG-U133B		Hs.15085			
227767_at_HG-U133B	CSNK1G3	Hs.129206	Q9Y6M4	1456	5q23
227786_at_HG-U133B	TRAP25	Hs.336898	AAL89787	90390	8q24.11
227812_at_HG-U133B		Hs.48376			
227817_at_HG-U133B		Hs.352385			
227829_at_HG-U133B		Hs.86543	Q8WY62		
227867_at_HG-U133B		Hs.36723			
227900_at_HG-U133B		Hs.144139			
227936_at_HG-U133B		Hs.280858	Q8WUD2		

227988_s_at_HG-U133B	CHAC	Hs.53542	Q96RL7	23230	9q21
227998_at_HG-U133B	MGC17528	Hs.300893	Q96FQ6	140576	
227999_at_HG-U133B	LOC170394	Hs.157728	Q96F43	170394	10q26.3
228003_at_HG-U133B		Hs.95898			
228007_at_HG-U133B					
228024_at_HG-U133B	PAK1	Hs.62402	Q13153	5058	11q13-q14
228029_at_HG-U133B	KIAA1982	Hs.22969		170960	
228055_at_HG-U133B		Hs.104433			
228058_at_HG-U133B		Hs.105887	Q96DA0		
228083_at_HG-U133B		Hs.13768			
228092_at_HG-U133B		Hs.155924	Q96AG7		
228174_at_HG-U133B		Hs.356345			
228176_at_HG-U133B		Hs.55902			
228183_s_at_HG-U133B	MGC4189	Hs.334808	Q9BT00	84268	17p13.2
228193_s_at_HG-U133B	RGC32	Hs.76640	Q9UL69	28984	13q13.3
228211_at_HG-U133B		Hs.44367			
228242_at_HG-U133B		Hs.101624			
228266_s_at_HG-U133B	CGI-142	Hs.127842	Q9Y3E1	50810	15q11.2
228298_at_HG-U133B	LOC91523	Hs.258494	Q96B20	91523	12p11.21
228328_at_HG-U133B		Hs.7326			
228343_at_HG-U133B	POU2F2	Hs.1101	P09086	5452	19q13.31
228345_at_HG-U133B		Hs.34656			
228361_at_HG-U133B		Hs.231444	Q96ID7		
228377_at_HG-U133B	KIAA1384	Hs.88442	Q9P2G3	57565	18q12.1
228379_at_HG-U133B		Hs.356630			
228390_at_HG-U133B		Hs.184430			
228408_s_at_HG-U133B	FLJ10498	Hs.109045	Q9H831	55153	4q21.1
228410_at_HG-U133B	GAB3	Hs.102630	Q8WWW8	139716	Xq28
228424_at_HG-U133B	NAALADASEL	Hs.13967	Q9UQQ1	10004	11q12
228471_at_HG-U133B		Hs.145053			
228476_at_HG-U133B	KIAA1407	Hs.15370	Q9P2E0	57577	3q13.2
228485_s_at_HG-U133B	CDW92	Hs.179902	Q96KU3	23446	9q31.2
228496_s_at_HG-U133B	CRIM1	Hs.19280	Q9NZV1	51232	2p21
228497_at_HG-U133B	DKFZp761G0313	Hs.21710	AAH26358	55356	1p13.1
228518_at_HG-U133B	IGHG3	Hs.300697	P01860	3502	14q32.33
228551_at_HG-U133B					
228555_at_HG-U133B		Hs.32553			
228570_at_HG-U133B		Hs.5027			
228592_at_HG-U133B		Hs.86693			
228599_at_HG-U133B		Hs.86693			
228652_at_HG-U133B		Hs.109540			
228660_x_at_HG-U133B	SEMA4F	Hs.25887	O95754	10505	2p12

228693_at_HG-U133B		Hs.55098			
228708_at_HG-U133B		Hs.25318			
228737_at_HG-U133B	C20orf100	Hs.26608	Q96NM4	84969	20q13.11
228766_at_HG-U133B		Hs.325823			
228827_at_HG-U133B		Hs.90858			
228834_at_HG-U133B	TOB1	Hs.178137	P50616	10140	17q21
228904_at_HG-U133B		Hs.156044			
228916_at_HG-U133B		Hs.24380	Q96MI1		
228984_at_HG-U133B	KIAA1394	Hs.32156	Q9P2F3	57571	11q12.2
228988_at_HG-U133B	ZNF6	Hs.326801	Q9Y4J6	7552	Xq13-q21.1
229001_at_HG-U133B		Hs.39911	Q9H7J1		
229003_x_at_HG-U133B		Hs.351871			
229061_s_at_HG-U133B	SLC25A13	Hs.9599	Q9UJS0	10165	7q21.3
229070_at_HG-U133B	MGC12335	Hs.97411	Q96IZ2	84830	6p22.3
229072_at_HG-U133B		Hs.26339			
229138_at_HG-U133B		Hs.59698			
229168_at_HG-U133B		Hs.55407	Q9NT93		
229194_at_HG-U133B		Hs.126695			
229232_at_HG-U133B		Hs.194071			
229253_at_HG-U133B	CTMP	Hs.293691	Q96AB5	117145	1q21
229280_s_at_HG-U133B					
229302_at_HG-U133B		Hs.40808			
229310_at_HG-U133B	KIAA1921	Hs.348392	Q96PW7	114818	2p23.3
229344_x_at_HG-U133B	KIAA1238	Hs.236463	Q9ULI2	57494	12p13.32
229362_at_HG-U133B		Hs.374508			
229368_s_at_HG-U133B	ZNF216	Hs.3776	O76080	7763	9q13-q21
229383_at_HG-U133B		Hs.107369			
229420_at_HG-U133B	RPL23A	Hs.350046	AAH14459	6147	17q11
229487_at_HG-U133B		Hs.120785			
229513_at_HG-U133B					
229575_at_HG-U133B		Hs.122642			
229621_x_at_HG-U133B		Hs.348805			
229637_at_HG-U133B		Hs.25768			
229659_s_at_HG-U133B		Hs.205126			
229681_at_HG-U133B		Hs.17551			
229711_s_at_HG-U133B	MGC5370	Hs.332938	Q96J14	84825	12q13.2
229722_at_HG-U133B	HSPC072	Hs.87329		29075	20p11.23
229745_x_at_HG-U133B		Hs.134185	Q96B18		
229750_at_HG-U133B		Hs.143087			
229779_at_HG-U133B		Hs.119471			
229790_at_HG-U133B	TERF2	Hs.100030	AAH24890	7014	16q22.1
229817_at_HG-U133B	DKFZP434M098	Hs.93738	Q9UFL4	25863	

229833_at_HG-U133B		Hs.33728			
229844_at_HG-U133B		Hs.59368			
229848_at_HG-U133B	ZNF10	Hs.104115	AAH24182	7556	12q24.33
229872_s_at_HG-U133B	KIAA0493	Hs.36475		57234	1q21.3
229923_at_HG-U133B					
229934_at_HG-U133B		Hs.38218			
229937_x_at_HG-U133B		Hs.149924			
230110_at_HG-U133B		Hs.210792			
230245_s_at_HG-U133B		Hs.181297			
230292_at_HG-U133B		Hs.25447	Q96DJ9		
230363_s_at_HG-U133B	SAC2	Hs.52463	Q9Y2H2	22876	10q26.13
230405_at_HG-U133B	RAD50	Hs.41587	O43254	10111	5q31
230441_at_HG-U133B		Hs.374272			
230489_at_HG-U133B	CD5	Hs.58685	AAH27901	921	11q13
230499_at_HG-U133B		Hs.121572			
230526_at_HG-U133B	FLJ20015	Hs.80618	Q96MU9	54459	17q25
230551_at_HG-U133B		Hs.107331			
230588_s_at_HG-U133B	MCPR	Hs.40137	Q9H8D0	64682	2q12.1
230636_s_at_HG-U133B	BTEB1	Hs.150557	Q13886	687	9q13
230648_at_HG-U133B		Hs.181297			
230650_at_HG-U133B		Hs.152460			
230659_at_HG-U133B	KIAA0212	Hs.154332	Q92611	9695	3p26.1
230689_at_HG-U133B		Hs.163426			
230713_at_HG-U133B		Hs.182185			
230743_at_HG-U133B		Hs.183096	Q96FJ8		
230753_at_HG-U133B		Hs.11594			
230768_at_HG-U133B		Hs.58753			
230775_s_at_HG-U133B	KIAA0610	Hs.118087	O60349	23111	13q13.1
230793_at_HG-U133B	FLJ20048	Hs.116470	Q9NXU7	55604	6p21.32
230795_at_HG-U133B	H4F2	Hs.55468	AAH19846	3022	1q21
230802_at_HG-U133B	DKFZP564B1162	Hs.93589	Q9H0T6	83478	4q21.23-q21.3
230803_s_at_HG-U133B	DKFZP564B1162	Hs.93589	Q9H0T6	83478	4q21.23-q21.3
230834_at_HG-U133B		Hs.114516			
230877_at_HG-U133B	IGHG3	Hs.300697	AAH24289	3502	14q32.33
230917_at_HG-U133B		Hs.372303			
230939_at_HG-U133B		Hs.130352			
230960_at_HG-U133B		Hs.128292			
230983_at_HG-U133B		Hs.137319			
230986_at_HG-U133B		Hs.141120			
230988_at_HG-U133B		Hs.15155			
230997_at_HG-U133B		Hs.131816			
231002_s_at_HG-U133B	NUP88	Hs.172108	Q99567	4927	17p13

231050_at_HG-U133B	HRLP5	Hs.120869	Q96KN8	117245	11q13.2
231069_at_HG-U133B		Hs.295727			
231093_at_HG-U133B	FCRH3	Hs.123296	Q96LA4	115352	1q21-q22
231101_at_HG-U133B	PPP2R5E	Hs.173328	Q16537	5529	7p11.2-p12
231118_at_HG-U133B		Hs.133081	Q96LS3		
231181_at_HG-U133B		Hs.88651			
231215_at_HG-U133B		Hs.126962			
231241_at_HG-U133B		Hs.155635			
231259_s_at_HG-U133B	CCND2	Hs.75586	P30279	894	12p13
231269_at_HG-U133B	DJ467N11.1	Hs.143917		63921	6q16.1-q16.3
231277_x_at_HG-U133B		Hs.14822			
231310_at_HG-U133B		Hs.113170			
231332_at_HG-U133B		Hs.254986			
231406_at_HG-U133B		Hs.129568			
231418_at_HG-U133B	MS4A2	Hs.89751	AAH02807	931	11q12-q13.1
231472_at_HG-U133B		Hs.124087			
231538_at_HG-U133B	FLJ23499	Hs.17546	Q9H5F2	64776	11q13-q22
231552_at_HG-U133B		Hs.235240			
231567_s_at_HG-U133B	TSP-NY	Hs.97643	Q9BYZ5	84660	12q24.31
231647_s_at_HG-U133B	IRTA2	Hs.191958	Q96RD9	83416	1q21
231656_x_at_HG-U133B	OSBPL10	Hs.321622	Q9BTU5	114884	3p22.3
231736_x_at_HG-U133B	MGST1	Hs.355733	P10620	4257	12p12.3-p12.1
231775_at_HG-U133B	TNFRSF10A	Hs.249190	O00220	8797	8p21
231793_s_at_HG-U133B	CAMK2D	Hs.111460	Q13557	817	4q25
231794_at_HG-U133B	CTLA4	Hs.247824	Q96P43	1493	2q33
231837_at_HG-U133B	USP28	Hs.142856	Q96RU2	57646	11q23
231854_at_HG-U133B		Hs.120905			
231870_s_at_HG-U133B	LOC51068	Hs.181022	Q9Y2Z6	51068	
231873_at_HG-U133B		Hs.315284			
231887_s_at_HG-U133B	KIAA1274	Hs.300646	BAA86588	27143	10q22.3
231897_at_HG-U133B					
231926_at_HG-U133B					
231945_at_HG-U133B	KIAA1275	Hs.102796	Q96SK6	27145	6q14.2
231969_at_HG-U133B	DKFZp762K222	Hs.159200	Q9P2F5	56977	4q35.1
231981_at_HG-U133B					
231982_at_HG-U133B					
232027_at_HG-U133B					
232035_at_HG-U133B	H4FH	Hs.93758	AAH10926	8365	6p21.3
232060_at_HG-U133B					
232080_at_HG-U133B	KIAA1301	Hs.8707	Q9NPS9	57520	2q33.1
232112_at_HG-U133B		Hs.220745			
232125_at_HG-U133B		Hs.202577			

232127_at_HG-U133B					
232201_at_HG-U133B	NKD2	Hs.240951	Q969F2	85409	5p15.3
232204_at_HG-U133B	EBF	Hs.32425	Q9UH73	1879	5q34
232210_at_HG-U133B		Hs.206868			
232231_at_HG-U133B					
232234_at_HG-U133B	C20orf24	Hs.184062	Q9UI05	55969	20q11.22
232614_at_HG-U133B		Hs.171395			
232636_at_HG-U133B					
232641_at_HG-U133B					
232739_at_HG-U133B					
232841_at_HG-U133B					
232950_s_at_HG-U133B	NIR3	Hs.272759	Q9BZ72	57605	12q24.31
233072_at_HG-U133B	KIAA1857	Hs.163642	BAB47486	84628	9q34
233106_at_HG-U133B		Hs.367825			
233137_at_HG-U133B					
233138_at_HG-U133B		Hs.178533			
233177_s_at_HG-U133B	KIAA1184	Hs.100747	Q96IG7	64583	2q36.1
233195_at_HG-U133B					
233261_at_HG-U133B		Hs.293916			
233328_x_at_HG-U133B					
233483_at_HG-U133B		Hs.193857	Q9H7M0		
233500_x_at_HG-U133B	LLT1	Hs.136748	Q8WUP7	29121	12p13
233520_s_at_HG-U133B					
233555_s_at_HG-U133B					
233559_s_at_HG-U133B	FENS-1	Hs.44743	Q9H8N9	57590	2q36.3
233589_x_at_HG-U133B					
233613_x_at_HG-U133B		Hs.296737			
233813_at_HG-U133B					
233845_at_HG-U133B		Hs.283921	Q9UI64		
233955_x_at_HG-U133B	HSPC195	Hs.15093	AAH17439	51523	5q31.3
234005_x_at_HG-U133B	STK36	Hs.26996	Q9H9N9	27148	2q36.1
234032_at_HG-U133B					
234107_s_at_HG-U133B					
234132_at_HG-U133B					
234140_s_at_HG-U133B	STIM2	Hs.278894	Q9P246	57620	4p15.2
234362_s_at_HG-U133B	CTLA4	Hs.247824	O95653	1493	2q33
234584_s_at_HG-U133B	ATE1	Hs.355315	O95260	11101	10q26.3
234643_x_at_HG-U133B					
234660_s_at_HG-U133B	DIS3	Hs.323346	Q8WWI2	22894	13q21.33
234682_at_HG-U133B					
234725_s_at_HG-U133B	SEMA4B	Hs.9598	Q8WY86	10509	15q25
234726_s_at_HG-U133B					

234764_x_at_HG-U133B					
234839_at_HG-U133B					
234862_at_HG-U133B					
235023_at_HG-U133B		Hs.292896			
235051_at_HG-U133B		Hs.55098			
235052_at_HG-U133B		Hs.50405			
235061_at_HG-U133B		Hs.291000	Q96NT4		
235101_at_HG-U133B	KIAA1014	Hs.6834	Q9H985	23360	11q12.1
235124_at_HG-U133B		Hs.153400			
235259_at_HG-U133B		Hs.97415	AAH23002		
235263_at_HG-U133B	DKFZP434A0131	Hs.15423	Q9NT73	54441	7q11.23-q21.1
235278_at_HG-U133B		Hs.136585			
235287_at_HG-U133B		Hs.180059	AAH27989		
235291_s_at_HG-U133B		Hs.268180			
235331_x_at_HG-U133B		Hs.126695			
235353_at_HG-U133B	KIAA0746	Hs.49500	O94847	23231	4p15.31
235359_at_HG-U133B		Hs.162185			
235372_at_HG-U133B	FREB	Hs.266331	Q96PJ4	84824	1q23.1
235385_at_HG-U133B	FLJ20668	Hs.12920	Q9NWR0	55016	4q32.2
235400_at_HG-U133B	FREB	Hs.266331	AAM13980	84824	1q23.1
235401_s_at_HG-U133B	FREB	Hs.266331	AAM13980	84824	1q23.1
235414_at_HG-U133B		Hs.164102			
235421_at_HG-U133B		Hs.351250			
235422_at_HG-U133B	FALZ	Hs.99872	Q12830	2186	17q24
235428_at_HG-U133B		Hs.104480			
235444_at_HG-U133B		Hs.235860			
235446_at_HG-U133B		Hs.293702			
235459_at_HG-U133B		Hs.136316			
235483_at_HG-U133B		Hs.180711			
235502_at_HG-U133B		Hs.79204			
235521_at_HG-U133B	HOXA3	Hs.248074	O43365	3200	7p15-p14
235604_x_at_HG-U133B		Hs.256801			
235647_at_HG-U133B		Hs.293411			
235674_at_HG-U133B		Hs.13849			
235692_at_HG-U133B		Hs.31922			
235706_at_HG-U133B	CPM	Hs.334873	P14384	1368	12q15
235719_at_HG-U133B		Hs.99237			
235749_at_HG-U133B					
235753_at_HG-U133B		Hs.196169			
235818_at_HG-U133B		Hs.133355			
235823_at_HG-U133B		Hs.49892			
235982_at_HG-U133B	FCRH1	Hs.180644	Q96LA6	115350	1q21-q22

236019_at_HG-U133B		Hs.19440			
236190_at_HG-U133B		Hs.115772			
236226_at_HG-U133B		Hs.126808			
236248_x_at_HG-U133B		Hs.167090			
236265_at_HG-U133B		Hs.88013			
236280_at_HG-U133B		Hs.176920			
236293_at_HG-U133B		Hs.283313			
236301_at_HG-U133B		Hs.46645			
236341_at_HG-U133B	CTLA4	Hs.247824	095653	1493	2q33
236378_at_HG-U133B		Hs.231898			
236458_at_HG-U133B		Hs.163426			
236535_at_HG-U133B	FLJ22116	Hs.34497	Q9H6M0	79677	2p24.1
236557_at_HG-U133B		Hs.186838			
236606_at_HG-U133B		Hs.47150			
236648_at_HG-U133B		Hs.144057			
236656_s_at_HG-U133B		Hs.265499			
236707_at_HG-U133B	DAPP1	Hs.62643	CAD28547	27071	4q25-q27
236728_at_HG-U133B		Hs.26330			
236787_at_HG-U133B		Hs.126630			
236796_at_HG-U133B		Hs.118659			
236837_x_at_HG-U133B		Hs.129137			
236854_at_HG-U133B		Hs.48984			
236892_s_at_HG-U133B	HOXB6	Hs.98428	P17509	3216	17q21-q22
236908_at_HG-U133B		Hs.143905			
236914_at_HG-U133B		Hs.131601			
236979_at_HG-U133B		Hs.168974			
237006_at_HG-U133B		Hs.24128			
237068_at_HG-U133B		Hs.200815			
237291_at_HG-U133B		Hs.159362			
237337_at_HG-U133B		Hs.115580			
237411_at_HG-U133B	LOC153516	Hs.38173	Q96FQ0	153516	5q12.1
237431_at_HG-U133B		Hs.97562			
237864_at_HG-U133B		Hs.196988			
238012_at_HG-U133B		Hs.37916			
238022_at_HG-U133B		Hs.237396			
238026_at_HG-U133B	RPL35A	Hs.287361	P18077	6165	3q29-qter
238039_at_HG-U133B		Hs.27167			
238055_at_HG-U133B					
238057_at_HG-U133B		Hs.252124			
238066_at_HG-U133B	RBP7	Hs.292718	Q96R05	116362	1p36.22
238155_at_HG-U133B		Hs.171689			
238208_at_HG-U133B		Hs.113106			

238304_at_HG-U133B		Hs.21868			
238365_s_at_HG-U133B		Hs.158272			
238367_s_at_HG-U133B		Hs.158272			
238376_at_HG-U133B		Hs.169738			
238392_at_HG-U133B		Hs.145480			
238516_at_HG-U133B	BMPR2	Hs.53250	Q13161	659	2q33-q34
238583_at_HG-U133B		Hs.133878			
238587_at_HG-U133B	MGC15437	Hs.55067	Q96IG9	84959	11q24.1
238593_at_HG-U133B		Hs.152003			
238604_at_HG-U133B		Hs.140489			
238651_at_HG-U133B		Hs.23096			
238652_at_HG-U133B		Hs.313541			
238686_at_HG-U133B	FBXO3	Hs.16577	Q9UK99	26273	11p12
238750_at_HG-U133B		Hs.218707			
238752_at_HG-U133B		Hs.122155			
238756_at_HG-U133B		Hs.41294			
238790_at_HG-U133B		Hs.156100			
238791_at_HG-U133B		Hs.267124			
238824_at_HG-U133B		Hs.145569			
238856_s_at_HG-U133B		Hs.72045	Q96HF0		
239054_at_HG-U133B		Hs.144616			
239071_at_HG-U133B		Hs.173904			
239122_at_HG-U133B	IL24	Hs.315463	Q13007	11009	1q32
239152_at_HG-U133B		Hs.243023			
239214_at_HG-U133B		Hs.123244			
239229_at_HG-U133B		Hs.50125			
239231_at_HG-U133B		Hs.63187			
239263_at_HG-U133B		Hs.97855			
239278_at_HG-U133B		Hs.182606			
239279_at_HG-U133B		Hs.158094			
239287_at_HG-U133B		Hs.128654			
239292_at_HG-U133B		Hs.124786			
239302_s_at_HG-U133B		Hs.293056			
239393_at_HG-U133B		Hs.371883			
239442_at_HG-U133B		Hs.173776			
239478_x_at_HG-U133B		Hs.169812			
239538_at_HG-U133B		Hs.146509			
239597_at_HG-U133B		Hs.369984			
239647_at_HG-U133B		Hs.150905			
239651_at_HG-U133B		Hs.189394			
239679_at_HG-U133B		Hs.163778			
239699_s_at_HG-U133B		Hs.144252			

239791_at_HG-U133B	H0XB6	Hs.98428	P17509	3216	17q21-q22
239824_s_at_HG-U133B	MGC10744	Hs.25092	Q96T82	84314	17p13.1
239835_at_HG-U133B	KIAA1842	Hs.116665	Q96JI5	84541	3p14
239956_at_HG-U133B		Hs.254980			
240061_at_HG-U133B		Hs.186649			
240106_at_HG-U133B		Hs.44705			
240113_at_HG-U133B		Hs.193133			
240201_at_HG-U133B		Hs.130173			
240239_at_HG-U133B	FLJ14779	Hs.243662	Q969W8	84924	19q13.13
240269_at_HG-U133B		Hs.164923			
240449_at_HG-U133B	ZNF341	Hs.322414	Q9BYN7	84905	20q11.21
240572_s_at_HG-U133B		Hs.156100			
240581_at_HG-U133B		Hs.132650			
240740_at_HG-U133B		Hs.370884			
240785_at_HG-U133B		Hs.243602			
240801_at_HG-U133B	C21orf37	Hs.46707		54076	21q21.1
240842_at_HG-U133B		Hs.371904			
241353_s_at_HG-U133B		Hs.160874			
241370_at_HG-U133B		Hs.100691			
241383_at_HG-U133B		Hs.62189			
241395_at_HG-U133B		Hs.145990			
241421_at_HG-U133B		Hs.130694			
241464_s_at_HG-U133B		Hs.126691			
241483_at_HG-U133B		Hs.62772			
241525_at_HG-U133B		Hs.132051			
241734_at_HG-U133B		Hs.107622	Q96DK2		
241742_at_HG-U133B	PRAM-1	Hs.239276	Q96QH2	84106	19p13.2
241754_at_HG-U133B		Hs.59504			
241795_at_HG-U133B		Hs.369626			
241810_at_HG-U133B		Hs.202088			
241930_x_at_HG-U133B		Hs.186898			
241969_at_HG-U133B	ITM2B	Hs.239625	Q9Y287	9445	13q14.3
241975_at_HG-U133B		Hs.44098			
241985_at_HG-U133B		Hs.224569			
242065_x_at_HG-U133B	KIAA0982	Hs.27207	Q8WVG2	22884	10p15.3
242104_at_HG-U133B		Hs.191782			
242223_at_HG-U133B		Hs.151609			
242292_at_HG-U133B		Hs.31110	AAH25725		
242329_at_HG-U133B		Hs.152541			
242363_at_HG-U133B		Hs.87372			
242388_x_at_HG-U133B		Hs.123581			
242404_at_HG-U133B		Hs.40937			

242414_at_HG-U133B		Hs.148324			
242434_at_HG-U133B		Hs.191581			
242448_at_HG-U133B		Hs.131929			
242458_at_HG-U133B		Hs.102398			
242463_x_at_HG-U133B		Hs.370309			
242520_s_at_HG-U133B		Hs.193754			
242525_at_HG-U133B		Hs.163105			
242541_at_HG-U133B	ABCA9	Hs.301496	Q8WWZ5	10350	17q24
242633_x_at_HG-U133B		Hs.186589			
242695_at_HG-U133B		Hs.126767			
242729_at_HG-U133B		Hs.166999			
242738_s_at_HG-U133B		Hs.163208			
242774_at_HG-U133B	SYNE-2	Hs.57749	BAA76855	23224	14q23.1-q23.2
242845_at_HG-U133B					
242866_x_at_HG-U133B		Hs.147381			
242932_at_HG-U133B		Hs.163481			
242975_s_at_HG-U133B	GNAS	Hs.273385	O60726	2778	20q13.2-q13.3
243000_at_HG-U133B		Hs.180059	AAH27989		
243020_at_HG-U133B		Hs.220823			
243024_at_HG-U133B		Hs.293707			
243030_at_HG-U133B		Hs.269493			
243154_at_HG-U133B		Hs.86650			
243228_at_HG-U133B		Hs.32406			
243362_s_at_HG-U133B	LEF1	Hs.44865	Q9UJU2	51176	4q23-q25
243363_at_HG-U133B	LEF1	Hs.44865	Q9UJU2	51176	4q23-q25
243493_at_HG-U133B		Hs.60260			
243538_at_HG-U133B		Hs.5840			
243579_at_HG-U133B	MSI2	Hs.173179	Q96DH6	124540	17q23.3
243756_at_HG-U133B		Hs.120855			
243764_at_HG-U133B		Hs.177164			
243780_at_HG-U133B		Hs.136232			
243798_at_HG-U133B		Hs.257490			
243859_at_HG-U133B		Hs.250488			
243932_at_HG-U133B		Hs.149809			
243968_x_at_HG-U133B		Hs.174767			
244147_at_HG-U133B		Hs.118088			
244230_at_HG-U133B		Hs.293142			
244248_at_HG-U133B		Hs.133396			
244257_at_HG-U133B		Hs.370262			
244261_at_HG-U133B		Hs.105866			
244523_at_HG-U133B	MMD	Hs.79889	AAH26324	23531	17q
244550_at_HG-U133B		Hs.370395			

244636_at_HG-U133B		Hs.209222			
244652_at_HG-U133B		Hs.190129			
244740_at_HG-U133B		Hs.23133	Q96HF5		
244876_at_HG-U133B		Hs.191950			
266_s_at_HG-U133A	CD24	Hs.286124	AAH07674	934	6q21
32541_at_HG-U133A	PPP3CC	Hs.75206	P48454	5533	8p21.2
34210_at_HG-U133A	CDW52	Hs.276770	Q9BW46	1043	1p36
34689_at_HG-U133A	TREX1	Hs.278408	AAD48774	11277	3p21.3-p21.2
34726_at_HG-U133A	CACNB3	Hs.250712	P54284	784	12q13
35666_at_HG-U133A	SEMA3F	Hs.32981	Q13275	6405	3p21.3
35974_at_HG-U133A	LRMP	Hs.40202	Q12912	4033	12p12.3
36004_at_HG-U133A	IKBKG	Hs.43505	Q9Y6K9	8517	Xq28
36566_at_HG-U133A	CTNS	Hs.64837	O60931	1497	17p13
36612_at_HG-U133A	KIAA0280	Hs.75400	Q92567	23201	11q13.3
36920_at_HG-U133A	MTM1	Hs.75302	Q13496	4534	Xq28
37152_at_HG-U133A	PPARD	Hs.106415	Q03181	5467	6p21.2-p21.1
37424_at_HG-U133A	HCR	Hs.110746	AAK55759	54535	6p21.3
37831_at_HG-U133A	KIAA0545	Hs.129943	BAA25471	23094	19q13.13
38149_at_HG-U133A	KIAA0053	Hs.1528	P42331	9938	2p13.1
38269_at_HG-U133A	PKD2	Hs.91146	AAH25307	25865	19q13.2
38340_at_HG-U133A	HIP12	Hs.96731	O75146	9026	12q24
38487_at_HG-U133A	FLJ12442	Hs.84753	Q9HZ8	64943	
39650_s_at_HG-U133A	KIAA0435	Hs.31438	O43162	9845	1q42.2
39835_at_HG-U133A	SBF1	Hs.112049	Q96GR9	6305	22q13.33
40148_at_HG-U133A	APBB2	Hs.324125	Q92870	323	4p14
40189_at_HG-U133A	SET	Hs.145279	Q01105	6418	9q34
41220_at_HG-U133A	MSF	Hs.181002	Q96QF5	10801	17q25
41553_at_HG-U133A	C8orf1	Hs.40539	Q9Y236	734	8q21
41577_at_HG-U133A	PPP1R16B	Hs.45719	BAA74846	26051	20q11.23
41660_at_HG-U133A	CELSR1	Hs.252387	Q9BWQ5	9620	22q13.3
44065_at_HG-U133A	FLJ14827	Hs.250820	Q96K25	84934	12q24.11
44563_at_HG-U133A	FLJ10385	Hs.30922	Q9BUR4	55135	17p13.2
44669_at_HG-U133A		Hs.356460			
44790_s_at_HG-U133A	FLJ21562	Hs.288708	Q9H714	80183	13q14.11
45633_at_HG-U133A	FLJ13912	Hs.47125	Q9BRX5	64785	16q21
46142_at_HG-U133A	FLJ12681	Hs.58362	Q9H6G4	64788	16p13.3
49306_at_HG-U133A	AD037	Hs.296162	Q9H2L5	83937	10q11.23
49485_at_HG-U133A	PRDM4	Hs.21807	Q9UFA6	11108	12q23-q24.1
50221_at_HG-U133A		Hs.23391	P19484		
50277_at_HG-U133A	GGA1	Hs.238296	Q9UJY5	26088	22q13.31
51192_at_HG-U133A	SSH-3	Hs.29173	BAB85080	54961	11q12.2
54970_at_HG-U133A	DKFZP761I2123	Hs.77978	O94790	83637	7p15.1

55093_at_HG-U133A	KIAA1402	Hs.86392	Q9P2E5	54480	7q35
56256_at_HG-U133A	LOC51092	Hs.33724	Q9Y357	51092	11q23.3
56919_at_HG-U133A	KIAA1449	Hs.109778	AAH26353	57599	3p21.33
57588_at_HG-U133A	SLC24A3	Hs.12321	Q9HC58	57419	20p13
58780_s_at_HG-U133A	FLJ10357	Hs.22451	Q96G35	55701	14q11.1
59697_at_HG-U133A		Hs.21349			
635_s_at_HG-U133A	PPP2R5B	Hs.75199	Q15173	5526	11q12
64942_at_HG-U133A		Hs.7967			
74694_s_at_HG-U133A	FLJ23282	Hs.170253	Q9H5N1	79874	
77508_r_at_HG-U133A	FLJ23282	Hs.170253	Q9H5N1	79874	
90610_at_HG-U133A	LRRN1	Hs.125742	Q8WV85	4034	7q22
AFFX-M27830_5_at_HG-U133A					
AFFX-M27830_5_at_HG-U133B					
AFFX-M27830_M_at_HG-U133A					
AFFX-r2-Bs-dap-3_at_HG-U133A					
AFFX-r2-Ec-bioD-3_at_HG-U133A					

Table 43b: Full sequences descriptions of all genes identified with relevance to leukemia subtyping

ID	Gene Symbol	Gene Title	Sequence Description
1007_s_at_HG-U133A	DDR1	discoidin domain receptor family, member 1	U48705 /FEATURE=mRNA /DEFINITION=HSU48705 Human receptor tyrosine kinase DDR gene, complete cds
1729_at_HG-U133A	TRADD	TNFRSF1A-associated via death domain	L41690 /FEATURE=/DEFINITION=HUMTRADD Homo sapiens TNF receptor-associated protein (TRADD) mRNA, 3' end of cds
200008_s_at_HG-U133A	GDI2	GDP dissociation inhibitor 2	gb:D13988.1 /DEF=Human rab GDI mRNA, complete cds. /FEA=mRNA /PROD=human rab GDI /DB_XREF=gi:285974 /UG=Hs 56845 GDP dissociation inhibitor 2 /FL=gb:BC005145.1 gb:D13988.1 gb:NM_001494.2
200008_s_at_HG-U133B	GDI2	GDP dissociation inhibitor 2	gb:D13988.1 /DEF=Human rab GDI mRNA, complete cds. /FEA=mRNA /PROD=human rab GDI /DB_XREF=gi:285974 /UG=Hs 56845 GDP dissociation inhibitor 2 /FL=gb:BC005145.1 gb:D13988.1 gb:NM_001494.2
200023_s_at_HG-U133A	EIF3S5	eukaryotic translation initiation factor 3, subunit 5 (epsilon, 47kD)	gb:NM_003754.1 /DEF=Homo sapiens eukaryotic translation initiation factor 3, subunit 5 (epsilon, 47kD) (EIF3S5), mRNA. /FEA=mRNA /GEN=EIF3S5 /PROD=eukaryotic translation initiation factor 3, subunit 5 (epsilon, 47kD) /DB_XREF=gi:4503518 /UG=Hs.7811 eukaryotic translation initiation factor 3, subunit 5 (epsilon, 47kD) /FL=gb:BC000490.1 gb:U94855.1 gb:NM_003754.1
200040_at_HG-U133A	KHDRBS1	KH domain containing, RNA binding, signal transduction associated 1	gb:NM_006559.1 /DEF=Homo sapiens GAP-associated tyrosine phosphoprotein p62 (Sam68) (SAM68), mRNA. /FEA=mRNA /GEN=SAM68 /PROD=GAP-associated tyrosine phosphoprotein p62(Sam68) /DB_XREF=gi:573026 /UG=Hs.119537 GAP-associated tyrosine phosphoprotein p62 (Sam68) /FL=gb:BC000717.1 gb:M88108.1 gb:NM_006559.1
200047_s_at_HG-U133A	YY1	YY1 transcription factor	gb:NM_003403.2 /DEF=Homo sapiens YY1 transcription factor (YY1), mRNA. /FEA=mRNA /GEN=YY1 /PROD=YY1 transcription factor /DB_XREF=gi:6042207 /UG=Hs.97496 YY1 transcription factor /FL=gb:M77698.1 gb:M76541.1 gb:NM_003403.2

200047_s_at_HG-U133B	YY1	YY1 transcription factor	gb:NM_003403.2 /DEF=Homo sapiens YY1 transcription factor (YY1), mRNA. /FEA=mRNA /GEN=YY1 /PROD=YY1 transcription factor /DB_XREF=gi:6042207 /UG=Hs.97496 YY1 transcription factor /FL=gb:M77698.1 gb:M76541.1
200056_s_at_HG-U133A	C1D	nuclear DNA-binding protein	gb:NM_006333.1 /DEF=Homo sapiens nuclear DNA-binding protein (C1D), mRNA. /FEA=mRNA /GEN=C1D /PROD=nuclear DNA-binding protein /DB_XREF=gi:5453582 /UG=Hs.15164 nuclear DNA-binding protein /FL=gb:NM_006333.1
200068_s_at_HG-U133B	CANX	calnexin	gb:M94859.1 /DEF=Human calnexin mRNA, complete cds. /FEA=mRNA /PROD=calnexin /DB_XREF=gi:179831 /UG=Hs.155560 calnexin /FL=gb:NM_001746.1 gb:BC003552.1 gb:M94859.1 gb:M98452.1 gb:L10284.1 gb:L18887.1
200071_at_HG-U133A	SPF30	splicing factor 30, survival of motor neuron-related	Consensus includes gb:BF224259 /FEA=EST /DB_XREF=gi:11131523 /DB_XREF=est:7q85c09.x1 /CLONE=IMAGE:3705208 /UG=Hs.79968 splicing factor 30, survival of motor neuron-related /FL=gb:AF083385.1 gb:AF107463.1 gb:NM_005871.1
200072_s_at_HG-U133A	HNRPM	heterogeneous nuclear ribonucleoprotein M	gb:AF061832.1 /DEF=Homo sapiens M4 protein deletion mutant mRNA, complete cds. /FEA=mRNA /PROD=M4 protein deletion mutant /DB_XREF=gi:31238877 /UG=Hs.79024 heterogeneous nuclear ribonucleoprotein M /FL=gb:AF061832.1
200093_s_at_HG-U133A	HINT1	histidine triad nucleotide binding protein 1	Consensus includes gb:N32864 /FEA=EST /DB_XREF=gi:1153263 /DB_XREF=est:yw8sd08.s1 /CLONE=IMAGE:259311 /UG=Hs.256697 histidine triad nucleotide-binding protein 1
200094_s_at_HG-U133A	EEF2	eukaryotic translation elongation factor 2	Consensus includes gb:AI004246 /FEA=EST /DB_XREF=gi:3213756 /DB_XREF=est:ou03g06.x1 /CLONE=IMAGE:1625242 /UG=Hs.75309 eukaryotic translation elongation factor 2
200598_s_at_HG-U133A	TRA1	tumor rejection antigen (gp96) 1	Consensus includes gb:AI582238 /FEA=EST /DB_XREF=gi:4568135 /DB_XREF=est:tg65c10.x1 /CLONE=IMAGE:2213682 /UG=Hs.82689 tumor

			rejection antigen (gp96) 1 /FL=gb:NM_003299.1
200608_s_at_HG-U133A	RAD21	RAD21 homolog (S. pombe)	gb:NM_006265.1 /DEF=Homo sapiens RAD21 (S. pombe) homolog (RAD21, mRNA, /FEA=mRNA /GEN=RAD21 /PROD=RAD21 (S. pombe) homolog /DB_XREF=gi:5455393 /UG=Hs.81848 RAD21 (S. pombe) homolog /FL=gb:D38551.1 gb:NM_006265.1
200620_at_HG-U133A	C1orf8	chromosome 1 open reading frame 8	gb:NM_004872.1 /DEF=Homo sapiens chromosome 1 open reading frame 8 (C1ORF8), mRNA /FEA=mRNA /GEN=C1ORF8 /PROD=chromosome 1 open reading frame 8 /DB_XREF=gi:4758571 /UG=Hs.11441 chromosome 1 open reading frame 8 /FL=gb:BC003106.1 gb:AF290615.1 gb:AF047439.1
200625_s_at_HG-U133A	CAP	adenylyl cyclase-associated protein	gb:NM_006367.2 /DEF=Homo sapiens adenylyl cyclase-associated protein (CAP), mRNA /FEA=mRNA /GEN=CAP /PROD=adenylyl cyclase-associated protein /DB_XREF=gi:10938021 /UG=Hs.104125 adenylyl cyclase-associated protein /FL=gb:NM_006367.2 gb:L12168.1 gb:M98474.1
200630_x_at_HG-U133A	SET	SET translocation (myeloid leukemia-associated)	Consensus includes gb:AV702810 /FEA=EST /DB_XREF=gi:10719140 /DB_XREF=est:AV702810 /CLONE=ADBDGH01 /UG=Hs.145279 SET translocation (myeloid leukemia-associated) /FL=gb:U51924.1 gb:M93651.1
200631_s_at_HG-U133A	SET	SET translocation (myeloid leukemia-associated)	gb:NM_003011.1 /DEF=Homo sapiens SET translocation (myeloid leukemia-associated) (SET), mRNA, /FEA=mRNA /GEN=SET /PROD=SET translocation (myeloid leukemia-associated) /DB_XREF=gi:4506890 /UG=Hs.145279 SET translocation (myeloid leukemia-associated) /FL=gb:U51924.1 gb:M93651.1
200646_s_at_HG-U133A	NUCB1	nucleobindin 1	gb:NM_006184.1 /DEF=Homo sapiens nucleobindin 1 (NUCB1), mRNA /FEA=mRNA /GEN=NUCB1 /PROD=nucleobindin 1 /DB_XREF=gi:5453817 /UG=Hs.172609 nucleobindin 1 /FL=gb:BC002356.1 gb:M96824.1
200649_at_HG-U133A	NUCB1	nucleobindin 1	gb:BC002356.1 /DEF=Homo sapiens, nucleobindin 1, clone MGC:8479,

		mRNA, complete cds. /FEA=mRNA /PROD=nucleobindin 1 /DB_XREF=gi:12803104 /UG=Hs.172609 nucleobindin 1 /FL=gb:BC002356.1 gb:M96B24.1 gb:NM_006184.1
200650_s_at_HG-U133A	LDHA	gb:NM_005566.1 /DEF=Homo sapiens lactate dehydrogenase A (LDHA), mRNA. /FEA=mRNA /GEN=LDHA /PROD=LDHA /DB_XREF=gi:5031856 /UG=Hs.2795 lactate dehydrogenase A /FL=gb:BC001829.1 gb:NM_005566.1
200654_at_HG-U133A	P4HB	gb:J02783.1 /DEF=Human thyroid hormone binding protein (p55) mRNA, complete cds. /FEA=mRNA /GEN=P4HB /DB_XREF=gi:339646 /UG=Hs.75655 procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55) /FL=gb:J02783.1 gb:NM_000918.1
200655_s_at_HG-U133A	CALM1	gb:NM_006888.1 /DEF=Homo sapiens calmodulin 1 (phosphorylase kinase, delta) (CALM1), mRNA. /FEA=mRNA /GEN=CALM1 /PROD=calmodulin 1 (phosphorylase kinase, delta) /DB_XREF=gi:5901911 /UG=Hs.177656 calmodulin 1 (phosphorylase kinase, delta) /FL=gb:NM27319.1 gb:NM_006888.1
200656_s_at_HG-U133A	P4HB	gb:NM_000918.1 /DEF=Homo sapiens procollagen-proline, 2-oxoglutarate 4- dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55) (P4HB), mRNA. /FEA=mRNA /GEN=P4HB /PROD=procollagen-proline, 2-oxoglutarate 4- dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55) /DB_XREF=gi:4505566 /UG=Hs.75655 procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4- hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55) /FL=gb:J02783.1 gb:NM_000918.1
200659_s_at_HG-U133A	PHB	gb:NM_002634.2 /DEF=Homo sapiens prohibitin (PHB), mRNA. /FEA=mRNA /GEN=PHB /PROD=prohibitin /DB_XREF=gi:6031190 /UG=Hs.75323 prohibitin /FL=gb:NM_002634.2
200661_at_HG-U133A	PPGB	gb:NM_000308.1 /DEF=Homo sapiens protective protein for beta-

	(galactosialidosis)	galactosidase (galactosialidosis) (PPGB), mRNA, /FEA=mRNA /GEN=PPGB /PROD=protective protein for beta-galactosidase /DB_XREF=gi:4505988 /UG=Hs.118126 protective protein for beta-galactosidase (galactosialidosis) /FL=gb:BC000597.1 gb:M22960.1 gb:NM_000308.1
200665_s_at_HG-U133A	SPARC	secreted protein, acidic, cysteine-rich (osteonectin) gb:NM_003118.1 /DEF=Homo sapiens secreted protein, acidic, cysteine-rich (osteonectin) (SPARC), mRNA, /FEA=mRNA /GEN=SPARC /PROD=secreted protein, acidic, cysteine-rich(osteonectin) /DB_XREF=gi:4507170 /UG=Hs.111779 secreted protein, acidic, cysteine-rich (osteonectin) /FL=gb:BC004974.1 gb:J03040.1 gb:NM_003118.1
200673_at_HG-U133A	LAPTM4A	lysosomal-associated protein transmembrane 4 alpha gb:NM_014713.2 /DEF=Homo sapiens lysosomal-associated protein transmembrane 4 alpha (MBNT), mRNA, /FEA=mRNA /GEN=MBNT /PROD=lysosomal-associated protein transmembrane 4alpha /DB_XREF=gi:13518239 /UG=Hs.111894 lysosomal-associated protein transmembrane 4 alpha /FL=gb:BC000421.1 gb:NM_014713.2 gb:D14696.1
200675_at_HG-U133A	CD81	CD81 antigen (target of antiproliferative antibody 1) gb:NM_004356.1 /DEF=Homo sapiens CD81 antigen (target of antiproliferative antibody 1) (CD81), mRNA, /FEA=mRNA /GEN=CD81 /PROD=CD81 antigen (target of antiproliferativeantibody 1) /DB_XREF=gi:4757943 /UG=Hs.54457 CD81 antigen (target of antiproliferative antibody 1) /FL=gb:BC002978.1 gb:M33680.1 gb:NM_004356.1
200679_x_at_HG-U133A	HMG1	high-mobility group (nonhistone chromosomal) protein 1 Consensus includes gb:BE311760 /FEA=EST /DB_XREF=gi:9148272 /DB_XREF=est:601143587F1 /CLONE=IMAGE:3507284 /UG=Hs.274472 high-mobility group (nonhistone chromosomal) protein 1 /FL=gb:BC003378.1 gb:NM_002128.1 gb:D63874.1
200707_at_HG-U133A	PRKCSH	protein kinase C substrate 80K-H gb:NM_002743.1 /DEF=Homo sapiens protein kinase C substrate 80K-H (PRKCSH), mRNA, /FEA=mRNA /GEN=PRKCSH /PROD=protein kinase C substrate 80K-H /DB_XREF=gi:4506076 /UG=Hs.1432 protein kinase C substrate 80K-H /FL=gb:J03075.1 gb:NM_002743.1 gb:AF144075.1

200742_s_at_HG-U133A	CLN2	ceroid-lipofuscinosis, neuronal 2, late infantile (Jansky-Bielschowsky disease)	Consensus includes gb:BG231932 /FEA=EST /DB_XREF=gi:12727071 /DB_XREF=est:nat34b12.x1 /CLONE=IMAGE:4142926 /UG=Hs.20478 ceroid-lipofuscinosis, neuronal 2, late infantile (Jansky-Bielschowsky disease) /FL=gb:AF017456.1 gb:NM_000391.2
200743_s_at_HG-U133A	CLN2	ceroid-lipofuscinosis, neuronal 2, late infantile (Jansky-Bielschowsky disease)	gb:NM_000391.2 /DEF=Homo sapiens ceroid-lipofuscinosis, neuronal 2, late infantile (Jansky-Bielschowsky disease) (CLN2), mRNA, /FEA=mRNA /GEN=CLN2 /PROD=ceroid-lipofuscinosis, neuronal 2, late infantile (Jansky-Bielschowsky disease) /DB_XREF=gi:5597012 /UG=Hs.20478 ceroid-lipofuscinosis, neuronal 2, late infantile (Jansky-Bielschowsky disease) /FL=gb:AF017456.1 gb:NM_000391.2
200765_x_at_HG-U133A	CTNNNA1	catenin (cadherin-associated protein), alpha 1 (102kD)	- gb:NM_001903.1 /DEF=Homo sapiens catenin (cadherin-associated protein), alpha 1 (102kD) (CTNNNA1), mRNA, /FEA=mRNA /GEN=CTNNNA1 /PROD=catenin (cadherin-associated protein), alpha 1(102kD) /DB_XREF=gi:4503126 /UG=Hs.178452 catenin (cadherin-associated protein), alpha 1 (102kD) /FL=gb:1.23805.1 gb:NM_001903.1
200770_s_at_HG-U133A	LAMC1	laminin, gamma 1 (formerly LAMB2)	gb:J03202.1 /DEF=Human laminin B2 chain mRNA, complete cds. /FEA=mRNA /GEN=LAMB2 /DB_XREF=gi:186916 /UG=Hs.214982 laminin, gamma 1 (formerly LAMB2) /FL=gb:J03202.1 gb:NM_002293.2
200825_s_at_HG-U133A	ORP150	oxygen regulated protein (150kD)	- gb:NM_006389.2 /DEF=Homo sapiens oxygen regulated protein (150kD) (ORP150), mRNA, /FEA=mRNA /GEN=ORP150 /PROD=oxygen regulated protein precursor /DB_XREF=gi:13699861 /UG=Hs.277704 oxygen regulated protein (150kD) /FL=gb:NM_006389.2 gb:U65785.1
200829_x_at_HG-U133A	ZNF207	zinc finger protein 207	gb:NM_003457.1 /DEF=Homo sapiens zinc finger protein 207 (ZNF207), mRNA, /FEA=mRNA /GEN=ZNF207 /PROD=zinc finger protein 207 /DB_XREF=gi:4508016 /UG=Hs.62112 zinc finger protein 207 /FL=gb:AF046001.1 gb:NM_003457.1
200832_s_at_HG-U133A	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	gb:AB032261.1 /DEF=Homo sapiens Scd mRNA for stearoyl-CoA desaturase, complete cds. /FEA=mRNA /GEN=Scd /PROD=stearoyl-CoA desaturase

			/DB_XREF=gi:7415720 /UG=Hs.119597 stearoyl-CoA desaturase (delta-9-desaturase) /FL=gb:AF097514.1 gb:NM_005063.1 gb:AB032261.1
			Consensus includes gb:AL031685 /DEF=Human DNA sequence from clone RP5-963K23 on chromosome 20q13.11-13.2 Contains a KRT18 (Keratin type I, Cytoskeletal 18 (Cytokeratin 18, CK18,CYK18)) pseudogene, a gene for a novel protein, the gene for spermatogenesis associated protein PD1 (KIAA0... /FEA=mRNA_2 /DB_XREF=gi:9368423 /UG=Hs.10590 zinc finger protein 313 /FL=gb:AF265215.1 gb:NM_018683.1
			gb:NM_002966.1 /DEF=Homo sapiens S100 calcium-binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11)) (S100A10), mRNA. /FEA=mRNA /GEN=S100A10 /PROD=S100 calcium-binding protein A10 /DB_XREF=gi:4506760 /UG=Hs.119301 S100 calcium-binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11)) /FL=gb:M81457.1 gb:M38591.1 gb:NM_002966.1
			Consensus includes gb:AW006345 /FEA=EST /DB_XREF=gi:5855123 /DB_XREF=est:wI04d05.x1 /CLONE=IMAGE:2506473 /UG=Hs.250773 signal sequence receptor, alpha (translocon-associated protein alpha) /FL=gb:AF156965.1 gb:NM_003144.2
			Consensus includes gb:AK025843.1 /DEF=Homo sapiens cDNA: FLJ22190 fis, clone HRC01053. /FEA=mRNA /DB_XREF=gi:10438481 /UG=Hs.194431 palladin /FL=gb:AF077041.1 gb:AF151909.1 gb:NM_016081.1
			Consensus includes gb:AU157932 /FEA=EST /DB_XREF=gi:11019453 /DB_XREF=est:AU157932 /CLONE=PLACE1010217 /UG=Hs.194431 palladin /FL=gb:AF077041.1 gb:AF151909.1 gb:NM_016081.1
			Consensus includes gb:BG474541 /FEA=EST /DB_XREF=gi:13406818 /DB_XREF=est:602517313F1 /CLONE=IMAGE:4649162 /UG=Hs.75730 signal recognition particle receptor (docking protein) /FL=gb:BC0011162.1 gb:NM_003139.1
200867_at_HG-U133A		S100A10	S100 calcium binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11))
200872_at_HG-U133A		S100A10	signal sequence receptor, alpha (translocon-associated protein alpha)
200890_s_at_HG-U133A	SSR1		200906_s_at_HG-U133A
200907_s_at_HG-U133A	KIAA0992		200917_s_at_HG-U133A

200931_s_at_HG-U133A	VCL	vinculin	gb:NM_014000.1 /DEF=Homo sapiens vinculin (VCL), transcript variant meta-VCL, mRNA. /FEA=mRNA /GEN=VCL /PROD=vCL isoform meta-VCL /DB_XREF=gi:7669549 /UG=Hs.75350 vinculin /FL=gb:NM_014000.1
200935_at_HG-U133A	CALR	calreticulin	gb:NM_004343.2 /DEF=Homo sapiens calreticulin (CALR), mRNA. /FEA=mRNA /GEN=CALR /PROD=calreticulin precursor /DB_XREF=gi:5921996 /UG=Hs.16488 calreticulin /FL=gb:BC002500.1 gb:M84739.1 gb:M32294.1
200951_s_at_HG-U133A	CCND2	cyclin D2	Consensus includes gb:AW026491 /FEA=EST /DB_XREF=gi:5880021 /DB_XREF=est:tw14b06.x1 /CLONE=IMAGE:2529491 /UG=Hs.75586 cyclin D2 /FL=gb:NM90813.1 gb:D13639.1 gb:NM_001759.1
200952_s_at_HG-U133A	CCND2	cyclin D2	- Consensus includes gb:AI635187 /FEA=EST /DB_XREF=gi:4686517 /DB_XREF=est:z22b10.x1 /CLONE=IMAGE:2289307 /UG=Hs.75586 cyclin D2 /FL=gb:NM90813.1 gb:D13639.1 gb:NM_001759.1
200953_s_at_HG-U133A	CCND2	cyclin D2	gb:NM_001759.1 /DEF=Homo sapiens cyclin D2 (CCND2), mRNA. /FEA=mRNA /GEN=CCND2 /PROD=cyclin D2 /DB_XREF=gi:4502616 /UG=Hs.75586 cyclin D2 /FL=gb:NM90813.1 gb:D13639.1 gb:NM_001759.1
200967_at_HG-U133A	PPIB		gb:NM_000942.1 /DEF=Homo sapiens peptidyl/prolyl isomerase B (cyclophilin B) (PPIB), mRNA. /FEA=mRNA /GEN=PPIB /PROD=peptidyl/prolyl isomerase B (cyclophilin B) /DB_XREF=gi:4758949 /UG=Hs.699 peptidyl/prolyl isomerase B (cyclophilin B) /FL=gb:BC001125.1 gb:M60857.1 gb:M63573.1
200968_s_at_HG-U133A	PPIB		- peptidyl/prolyl isomerase B (cyclophilin B) /DB_XREF=gi:4758949 /UG=Hs.699 peptidyl/prolyl isomerase B (cyclophilin B) /FL=gb:BC001125.1 gb:M60857.1 gb:M63573.1
200984_s_at_HG-U133A	CD59		gb:NM_000942.1 /DEF=Homo sapiens peptidyl/prolyl isomerase B (cyclophilin B) (PPIB), mRNA. /FEA=mRNA /GEN=PPIB /PROD=peptidyl/prolyl isomerase B (cyclophilin B) /DB_XREF=gi:4758949 /UG=Hs.699 peptidyl/prolyl isomerase B (cyclophilin B) /FL=gb:BC001125.1 gb:M60857.1 gb:M63573.1
			gb:NM_000942.1 Consensus includes gb:X16447.1 /DEF=Human mRNA for CD59, an LY-6-like protein regulating complement membrane attack. /FEA=mRNA

	EJ30, EL32 and G344)	/PROD=precursor polypeptide (AA -25 to 103) /DB_XREF=gi:298805 /UG=Hs.119663 CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344) /FL=gb:NM_000611.1 gb:M34671.1
200985_s_at_HG-U133A	CD59	gb:NM_000611.1 /DEF=Homo sapiens CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344) /DB_XREF=gi:10835164 /UG=Hs.119663 CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344) /FL=gb:NM_000611.1 gb:M34671.1
200986_at_HG-U133A	SERPING1	gb:NM_00062.1 /DEF=Homo sapiens serine (or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member 1 (SERPING1), mRNA. /FEA=mRNA /GEN=SERPING1 /PROD=complement component 1 inhibitor precursor /DB_XREF=gi:4557378 /UG=Hs.151242 serine (or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member 1 /FL=gb:NM_13690.1 gb:M13656.1 gb:NM_000062.1
200996_at_HG-U133A	ACTR3	gb:NM_005721.2 /DEF=Homo sapiens ARP3 (actin-related protein 3, yeast) homolog (ACTR3), mRNA. /FEA=mRNA /GEN=ACTR3 /PROD=ARP3 (actin-related protein 3, yeast) homolog /DB_XREF=gi:7262289 /UG=Hs.5321 ARP3 (actin-related protein 3, yeast) homolog /FL=gb:AF006083.1 gb:NM_005721.2 Consensus includes gb:AW029619 /FEA=EST /DB_XREF=gi:5888375 /DB_XREF=est:wx14e05.x1 /CLONE=IMAGE:2543648 /UG=Hs.74368 transmembrane protein (63kD), endoplasmic reticulum/Golgi intermediate compartment /FL=gb:NM_006825.1
200998_s_at_HG-U133A	CKAP4	gb:NM_006280.1 /DEF=Homo sapiens signal sequence receptor, delta (translocon-associated protein delta) (SSR4), mRNA. /FEA=mRNA /GEN=SSR4 /PROD=signal sequence receptor, delta /DB_XREF=gi:5454089
201004_at_HG-U133A	SSR4	

			/UG=Hs.102135 signal sequence receptor, delta (translocon-associated protein delta) /FL=gb:BC003371.1 gb:NM_006280.1
201005_at_HG-U133A	CD9	CD9 antigen (p24)	gb:NM_001769.1 /DEF=Homo sapiens CD9 antigen (p24) (CD9), mRNA. /FEA=mRNA /GEN=CD9 /PROD=CD9 antigen (p24) /DB_XREF=gi:4502692 /UG=Hs.1244 CD9 antigen (p24) /FL=gb:NM3690.1 gb:NM_001769.1 gb:L34068.1
201008_s_at_HG-U133A	TXNIP	thioredoxin interacting protein	Consensus includes gb:AA812232 /FEA=EST /DB_XREF=gi:2881843 /DB_XREF=est:ob84n9.s1 /CLONE=IMAGE:1338113 /UG=Hs.179526 upregulated by 1,25-dihydroxyvitamin D-3 /FL=gb:NM_006472.1 gb:S73591.1
201012_at_HG-U133A	ANXA1	annexin A1	gb:NM_000700.1 /DEF=Homo sapiens annexin A1 (ANXA1), mRNA. /FEA=mRNA /GEN=ANXA1 /PROD=annexin I /DB_XREF=gi:4502100 /UG=Hs.78225 annexin A1 /FL=gb:BC001275.1 gb:NM_000700.1
201015_s_at_HG-U133A	JUP	junction plakoglobin	gb:NM_021991.1 /DEF=Homo sapiens junction plakoglobin (JUP), transcript variant 2, mRNA. /FEA=mRNA /GEN=JUP /PROD=junction plakoglobin isoform 1 /DB_XREF=gi:12056467 /UG=Hs.2340 junction plakoglobin /FL=gb:NM_021991.1 gb:BC000441.1
201029_s_at_HG-U133A	MIC2		gb:NM_002414.1 /DEF=Homo sapiens antigen identified by monoclonal antibodies 12E7, F21 and O13 (MIC2), mRNA. /FEA=mRNA /GEN=MIC2 /PROD=antigen identified by monoclonal antibodies12E7, F21 and O13 /DB_XREF=gi:4505182 /UG=Hs.177543 antigen identified by monoclonal antibodies 12E7, F21 and O13 /FL=gb:BC002584.1 gb:BC003147.1 gb:M16279.1 gb:U82164.1 gb:NM_002414.1
201034_at_HG-U133A	ADD3		Consensus includes gb:BE545756 /FEA=EST /DB_XREF=gi:9774401 /DB_XREF=est:601076920F1 /CLONE=IMAGE:3462940 /UG=Hs.8110 L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain /FL=gb:BC000306.1 gb:NM_005327.1
201061_s_at_HG-U133A	EPB72		gb:M81635.1 /DEF=Homo sapiens erythrocyte membrane protein band 7.2 complete cds. /FEA=mRNA /GEN=stomatin peptide /PROD=stomatin peptide

			/DB_XREF=gi:181183 /UG=Hs.160483 erythrocyte membrane protein band 7.2 (stomatin) /FL=gb:MB1635.1 gb:NM_004099.1
		MMP2	gb:NM_004530.1 /DEF=Homo sapiens matrix metalloproteinase 2 (gelatinase A, 72kD gelatinase, 72kD type IV collagenase) (MMP2), mRNA. /FEA=mRNA /GEN=MMP2 /PROD=matrix metalloproteinase 2 preproprotein /DB_XREF=gi:11342665 /UG=Hs.111301 matrix metalloproteinase 2 (gelatinase A, 72kD gelatinase, 72kD type IV collagenase) /FL=gb:NM_004530.1 gb:BC002576.1
201069_at_HG-U133A		SYNGR2	gb:NM_004710.1 /DEF=Homo sapiens synaptogyrin 2 (SYNGR2), mRNA. /FEA=mRNA /GEN=SYNGR2 /PROD=synaptogyrin 2 /DB_XREF=gi:4759201 /UG=Hs.5097 synaptogyrin 2 /FL=gb:BC000407.1 gb:NM_004710.1
201079_at_HG-U133A		LGALS1	gb:NM_002305.2 /DEF=Homo sapiens lectin, galactoside-binding, soluble 1 (galectin 1) (LGALS1), mRNA. /FEA=mRNA /GEN=LGALS1 /PROD=beta-galactosidase binding lectin precursor /DB_XREF=gi:60006015 /UG=Hs.227751 lectin, galactoside-binding, soluble, 1 (galactoside-binding lectin 1) /FL=gb:BC001693.1 gb:J04456.1 gb:NM_002305.2
201105_at_HG-U133A		ITGB5	gb:NM_0022213.1 /DEF=Homo sapiens integrin, beta 5 (ITGB5), mRNA. /FEA=mRNA /GEN=ITGB5 /PROD=integrin, beta 5 /DB_XREF=gi:4504772 /UG=Hs.149846 integrin, beta 5 /FL=gb:M35011.1 gb:J05633.1 gb:NM_0022213.1
201125_s_at_HG-U133A			gb:NM_002121.1 /DEF=Homo sapiens major histocompatibility complex, class II, DP beta 1 (HLA-DPB1), mRNA. /FEA=mRNA /GEN=HLA-DPB1 /PROD=major histocompatibility complex, class II, DPbeta 1 /DB_XREF=gi:4504404 /UG=Hs.814 major histocompatibility complex, class II, DP beta 1 /FL=gb:J03041.1 gb:MB3664.1 gb:NM_002121.1 gb:M28200.1 gb:M28202.1
201137_s_at_HG-U133A		MBNL	Consensus includes gb:N31913 /FEA=EST /DB_XREF=gi:1152312 /DB_XREF=eatty2f10.s1 /CLONE=IMAGE:271915 /UG=Hs.28578 muscleblind
201152_s_at_HG-U133A			

			(Drosophila)-like /FL=gb:NM_021038.1 gb:AB007888.1
201153_s_at_HG-U133A	MBNL	muscleblind-like (Drosophila)	gb:NM_021038.1 /DEF=Homo sapiens muscleblind (Drosophila)-like (MBNL), mRNA. /FEA=mRNA /GEN=MBNL /PROD=muscleblind (Drosophila)-like /DB_XREF=gi:10518339 /UG=Hs.28578 muscleblind (Drosophila)-like /FL=gb:NM_021038.1 gb:AB007888.1
201162_at_HG-U133A	IGFBP7	insulin-like growth factor binding protein 7	gb:NM_001553.1 /DEF=Homo sapiens insulin-like growth factor binding protein 7 (IGFBP7), mRNA. /FEA=mRNA /GEN=IGFBP7 /PROD=insulin-like growth factor binding protein 7 /DB_XREF=gi:4504618 /UG=Hs.119206 insulin-like growth factor binding protein 7 /FL=gb:1.19182.1 gb:NM_001553.1
201163_s_at_HG-U133A	IGFBP7	insulin-like growth factor binding protein 7	gb:NM_001553.1 /DEF=Homo sapiens insulin-like growth factor binding protein 7 (IGFBP7), mRNA. /FEA=mRNA /GEN=IGFBP7 /PROD=insulin-like growth factor binding protein 7 /DB_XREF=gi:4504618 /UG=Hs.119206 insulin-like growth factor binding protein 7 /FL=gb:1.19182.1 gb:NM_001553.1
201164_s_at_HG-U133A	PUM1	pumilio homolog 1 (Drosophila)	Consensus includes gb:BG474429 /FEA=EST /DB_XREF=gi:13406706 /DB_XREF=est602517152F1 /CLONE=IMAGE:4648765 /UG=Hs.153834 pumilio (Drosophila) homolog 1 /FL=gb:AF315592.1 gb:NM_014676.1
201189_s_at_HG-U133A	TPR3	inositol 1,4,5-triphosphate receptor, type 3	gb:NM_002224.1 /DEF=Homo sapiens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3), mRNA. /FEA=mRNA /GEN=ITPR3 /PROD=inositol 1,4,5-triphosphate receptor, type 3 /DB_XREF=gi:4504794 /UG=Hs.77515 inositol 1,4,5-triphosphate receptor, type 3 /FL=gb:D26351.1 gb:NM_002224.1 gb:U01062.1
201200_at_HG-U133A	CREG	cellular repressor of E1A-stimulated genes	gb:NM_003851.1 /DEF=Homo sapiens cellular repressor of E1A-stimulated genes (CREG), mRNA. /FEA=mRNA /GEN=CREG /PROD=cellular repressor of E1A-stimulated genes /DB_XREF=gi:4503036 /UG=Hs.5710 cellular repressor of E1A-stimulated genes /FL=gb:AF084523.1 gb:NM_003851.1
201247_at_HG-U133A	SREBF2	sterol regulatory element binding transcription factor 2	Consensus includes gb:BE513151 /FEA=EST /DB_XREF=gi:9720362 /DB_XREF=est601171940F1 /CLONE=IMAGE:3545697 /UG=Hs.1086689 sterol regulatory element binding transcription factor 2 /FL=gb:U02031.1

			gb:NM_004599.1
			gb:NM_003191.1 /DEF=Homo sapiens threonyl-tRNA synthetase (TARS), mRNA. /FEA=mRNA /GEN=TARS /PROD=threonyl-tRNA synthetase
201263_at_HG-U133A	TARS	threonyl-tRNA synthetase	/DB_XREF=gi:4507366 /UG=Hs.84131 threonyl-tRNA synthetase /FL=gb:BC000517.1 gb:M63180.1 gb:NM_003191.1
201278_at_HG-U133A	DAB2	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	Consensus includes: gb:N21202 /FEA=EST /DB_XREF=gi:1126372 /DB_XREF=est:xy41e12.s1 /CLONE=IMAGE:264334 /UG=Hs.81988 disabled (Drosophila) homolog 2 (mitogen-responsive phosphoprotein) /FL=gb:U39050.1 gb:U53446.1 gb:BC003064.1 gb:NM_001343.1
201281_at_HG-U133A	ADRM1	adhesion regulating molecule 1	gb:NM_007002.1 /DEF=Homo sapiens cell membrane glycoprotein, 110000M(r) (surface antigen) (GP110), mRNA. /FEA=mRNA /GEN=GP110 /PROD=cell membrane glycoprotein, 110000M(r) (surface antigen) /DB_XREF=gi:5901959 /UG=Hs.90107 cell membrane glycoprotein, 110000M(r) (surface antigen) /FL=gb:NM_007002.1 gb:D64154.1
201324_at_HG-U133A	EMP1	epithelial membrane protein 1	gb:NM_001423.1 /DEF=Homo sapiens epithelial membrane protein 1 (EMP1), mRNA. /FEA=mRNA /GEN=EMP1 /PROD=epithelial membrane protein 1 /DB_XREF=gi:4503558 /UG=Hs.79368 epithelial membrane protein 1 /FL=gb:U77085.1 gb:U43916.1 gb:NM_001423.1
201334_s_at_HG-U133A	ARHGEF12	Rho guanine nucleotide exchange factor (GEF) 12	Consensus includes: gb:AB002380.1 /DEF=Human mRNA for KIAA0382 gene, partial cds. /FEA=mRNA /GEN=KIAA0382 /DB_XREF=gi:2224704 /UG=Hs.65382 Rho guanine exchange factor (GEF) 12 /FL=gb:AF180681.1 gb:NM_015313.1
201338_x_at_HG-U133A	GTF3A	general transcription factor IIIA	gb:NM_002097.1 /DEF=Homo sapiens general transcription factor IIIA (GTF3A), mRNA. /FEA=mRNA /GEN=GTF3A /PROD=general transcription factor IIIA /DB_XREF=gi:4753158 /UG=Hs.75113 general transcription factor IIIA /FL=gb:D32257.1 gb:NM_002097.1
201352_at_HG-U133A	YME1L1	YME1-like 1 (S. cerevisiae)	gb:NM_014263.1 /DEF=Homo sapiens YME1 (S.cerevisiae)-like 1 (YME1L1), mRNA. /FEA=mRNA /GEN=YME1L1 /PROD=YME1 (S.cerevisiae)-like 1

			/DB_XREF=gi:7657688 /UG=Hs_206521 YME1 (S.cerevisiae)-like 1 /FL=gb:AF070656.1 gb:NM_014263.1
201358_s_at_HG-U133A	COPB	coatomer protein complex, subunit beta	gb:NM_016451.1 /DEF=Homo sapiens coatomer protein complex, subunit beta (COPB), mRNA. /FEA=mRNA /GEN=COPB /PROD=coatomer protein complex, subunit beta /DB_XREF=gi:7705368 /UG=Hs_3059 coatomer protein complex, subunit beta /FL=gb:AF084457.1 gb:NM_016451.1
201359_at_HG-U133A	COPB	coatomer protein complex, subunit beta	gb:NM_016451.1 /DEF=Homo sapiens coatomer protein complex, subunit beta (COPB), mRNA. /FEA=mRNA /GEN=COPB /PROD=coatomer protein complex, subunit beta /DB_XREF=gi:7705368 /UG=Hs_3059 coatomer protein complex, subunit beta /FL=gb:AF084457.1 gb:NM_016451.1
201360_at_HG-U133A	CST3	cystatin C (amyloid angiopathy and cerebral hemorrhage)	- gb:NM_000099.1 /DEF=Homo sapiens cystatin C (amyloid angiopathy and cerebral hemorrhage) (CST3), mRNA. /FEA=mRNA /GEN=CST3 /PROD=cystatin C (amyloid angiopathy and cerebral hemorrhage) /DB_XREF=gi:4503106 /UG=Hs_135084 cystatin C (amyloid angiopathy and cerebral hemorrhage) /FL=gb:NM_000099.1
201362_at_HG-U133A	NS1-BP	NS1-binding protein	gb:AF205218.1 /DEF=Homo sapiens NS1-binding protein-like protein mRNA, complete cds. /FEA=mRNA /PROD=NS1-binding protein-like protein /DB_XREF=gi:12003206 /UG=Hs_197293 NS1-binding protein /FL=gb:AF205218.1 gb:AB020657.1 gb:NM_016389.1
201377_at_HG-U133A	KIAA0144	KIAA0144 gene product	- gb:NM_014847.1 /DEF=Homo sapiens KIAA0144 gene product (KIAA0144), mRNA. /FEA=mRNA /GEN=KIAA0144 /PROD=KIAA0144 gene product /DB_XREF=gi:7661941 /UG=Hs_8127 KIAA0144 gene product /FL=gb:D63478.1 gb:NM_014847.1
201396_s_at_HG-U133A	SGT	small glutamine-rich tetra-tripeptide repeat (TPR)-containing	gb:NM_003021.2 /DEF=Homo sapiens small glutamine-rich tetra-tripeptide repeat (TPR)-containing (SGT), mRNA. /FEA=mRNA /GEN=SGT. /PROD=small glutamine-rich tetra-tripeptide /DB_XREF=gi:13259553 /UG=Hs_203910 small glutamine-rich tetra-tripeptide repeat (TPR)-containing /FL=gb:BC000390.1 gb:NM_003021.2 gb:BC005165.1 gb:AL050156.1

201416_at_HG-U133A	SOX4	SRY (sex determining region Y)-box 4	Consensus includes gb:BG528420 /FEA=EST /DB_XREF=gi:13519957 /DB_XREF=est:602379853F1 /CLONE=IMAGE:4719060 /UG=Hs.83484 SRY (sex determining region Y)-box 4 /FL=gb:NM_003107.1
201417_at_HG-U133A			Consensus includes gb:AL136179 /DEF=Human DNA sequence from clone RP3-322L4 on chromosome 6. Contains the SOX4 gene for SRY (sex determining region Y)-box 4, a pseudogene similar to predicted fly, worm and yeast genes, ESTs, STSs, GSSs and four CPG islands /FEA=mRNA /DB_XREF=gi:8649149 /UG=Hs.83484 SRY (sex determining region Y)-box 4 /FL=gb:NM_003107.1
201425_at_HG-U133A	ALDH2	aldehyde dehydrogenase 2 family (mitochondrial)	gb:NM_000690.1 /DEF=Homo sapiens aldehyde dehydrogenase 2, mitochondrial (ALDH2), mRNA. /FEA=mRNA /GEN=ALDH2 /PROD=aldehyde dehydrogenase 2, mitochondrial /DB_XREF=gi:4502032 /UG=Hs.195432 aldehyde dehydrogenase 2 family (mitochondrial) /FL=gb:BC002967.1 gb:NM_000690.1
201433_s_at_HG-U133A	PTDSS1	phosphatidylserine synthase 1	gb:NM_014754.1 /DEF=Homo sapiens phosphatidylserine synthase 1 (PTDSS1), mRNA. /FEA=mRNA /GEN=PTDSS1 /PROD=phosphatidylserine synthase 1 /DB_XREF=gi:7662646 /UG=Hs.77329 phosphatidylserine synthase 1 /FL=gb:BC004192.1 gb:BC004390.1 gb:D14694.1 gb:NM_014754.1
201437_s_at_HG-U133A	EIF4E	eukaryotic translation initiation factor 4E	gb:NM_001968.1 /DEF=Homo sapiens eukaryotic translation initiation factor 4E (EIF4E), mRNA. /FEA=mRNA /GEN=EIF4E /PROD=eukaryotic translation initiation factor 4E /DB_XREF=gi:4503534 /UG=Hs.79306 eukaryotic translation initiation factor 4E /FL=gb:M15353.1 gb:NM_001968.1
201462_at_HG-U133A	KIAA0193	KIAA0193 gene product	gb:NM_014766.1 /DEF=Homo sapiens KIAA0193 gene product (KIAA0193), mRNA. /FEA=mRNA /GEN=KIAA0193 /PROD=KIAA0193 gene product /DB_XREF=gi:7661983 /UG=Hs.75137 KIAA0193 gene product /FL=gb:D83777.1 gb:NM_014766.1
201463_s_at_HG-U133A	TALDO1	transaldolase 1	gb:NM_006755.1 /DEF=Homo sapiens transaldolase 1 (TALDO1), mRNA. /FEA=mRNA /GEN=TALDO1 /PROD=transaldolase 1 /DB_XREF=gi:5803186

		/UG=Hs.77290 transaldolase 1 /FL=gb:L19437.2 gb:NM_006755.1
		gb:NM_002826.2 /DEF=Homo sapiens quiescin Q6 (QSCN6), mRNA. /FEA=mRNA /GEN=QSCN6 /PROD=quiescin Q6 /DB_XREF=gi:13325074
201482_at_HG-U133A	QSCN6	/UG=Hs.77266 quiescin Q6 /FL=gb:L42379.1 gb:NM_002826.2
201485_s_at_HG-U133A	RCN2	gb:BC004892.1 /DEF=Homo sapiens, reticulocalbin 2, EF-hand calcium binding domain, clone MGC:1650, mRNA, complete cds. /FEA=mRNA /PROD=reticulocalbin 2, EF-hand calcium bindingdomain /DB_XREF=gi:13436151 /UG=Hs.79088 reticulocalbin 2, EF-hand calcium binding domain /FL=gb:BC004892.1 gb:NM_002902.1
201486_at_HG-U133A	RCN2	gb:NM_002902.1 /DEF=Homo sapiens reticulocalbin 2, EF-hand calcium binding domain (RCN2), mRNA. /FEA=mRNA /GEN=RCN2 /PROD=reticulocalbin 2, EF-hand calcium bindingdomain /DB_XREF=gi:4506456 /UG=Hs.79088 reticulocalbin 2, EF-hand calcium binding domain /FL=gb:BC004892.1 gb:NM_002902.1
201496_x_at_HG-U133A	MYH11	Consensus includes gb:S67238.1 /DEF=smooth muscle myosin heavy chain isoform SM2 human, umbilical cord, fetal aorta, mRNA Partial, 1078 nt. /FEA=mRNA /GEN=smooth muscle myosin heavy chain isoform SM2 /PROD=smooth muscle myosin heavy chain isoform SM2 /DB_XREF=gi:452982 /UG=Hs.78344 myosin, heavy polypeptide 11, smooth muscle /FL=gb:NM_022844.1
201497_x_at_HG-U133A	MYH11	gb:NM_022844.1 /DEF=Homo sapiens myosin, heavy polypeptide 11, smooth muscle (MYH11), transcript variant SM2, mRNA. /FEA=mRNA /GEN=MYH11 /PROD=smooth muscle myosin heavy chain 11, isoformSM2 /DB_XREF=gi:13124874 /UG=Hs.78344 myosin, heavy polypeptide 11, smooth muscle /FL=gb:NM_022844.1
201506_at_HG-U133A	TGFBI	gb:NM_000358.1 /DEF=Homo sapiens transforming growth factor, beta-induced, 68kD (TGFBI), mRNA. /FEA=mRNA /GEN=TGFBI /PROD=transforming growth factor, beta-induced, 68kD /DB_XREF=gi:4507466

			/UG=Hs.118787 transforming growth factor, beta-induced, 68kD /FL=gb:BC000097.1 gb:BC004972.1 gb:NM_000358.1
201530_x_at_HG-U133A	EIF4A1	eukaryotic translation initiation factor 4A, isoform 1	gb:NM_001416.1 /DEF=Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1), mRNA. /FEA=mRNA /GEN=EIF4A1 /PROD=eukaryotic translation initiation factor 4A,isoform 1 /DB_XREF=gi:4503328 /UG=Hs.129673 eukaryotic translation initiation factor 4A, isoform 1 /FL=gb:NM_001416.1
201537_s_at_HG-U133A	DUSP3	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	gb:BC002682.1 /DEF=Homo sapiens, dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related), clone MGC:3615, mRNA, complete cds. /FEA=mRNA /PROD=dual specificity phosphatase 3 (vaccinia virusphosphatase VH1-related) /DB_XREF=gi:12803692 /UG=Hs.181046 dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related) /FL=gb:BC002682.1 gb:L05147.1 gb:NM_004090.1
201540_at_HG-U133A	FHL1	four and a half LIM domains 1	gb:NM_001449.1 /DEF=Homo sapiens four and a half LIM domains 1 (FHL1), mRNA. /FEA=mRNA /GEN=FHL1 /PROD=four and a half LIM domains 1 /DB_XREF=gi:4503720 /UG=Hs.239069 four and a half LIM domains 1 /FL=gb:U29538.1 gb:U60115.1 gb:NM_001449.1
201548_s_at_HG-U133A	PLU-1	putative DNA/chromatin binding motif	Consensus includes gb:W02533 /FEA=EST /DB_XREF=gi:1274571 /DB_XREF=est:za51e06.r1 /CLONE=IMAGE:296098 /UG=Hs.143323 putative DNAChromatin binding motif /FL=gb:NM_006618.1
201564_s_at_HG-U133A	SNL	singed-like (fascin homolog, sea urchin) (Drosophila)	gb:NM_003088.1 /DEF=Homo sapiens singed (Drosophila)-like (sea urchin fascin homolog like) (SNL), mRNA. /FEA=mRNA /GEN=SNL /PROD=singed (Drosophila)-like (sea urchin fascinhomolog like) /DB_XREF=gi:4507114 /UG=Hs.118400 singed (Drosophila)-like (sea urchin fascin homolog like) /FL=gb:BC000521.1 gb:NM_003088.1 gb:U03057.1 gb:U09873.1
201585_s_at_HG-U133A	SFPQ	splicing factor proline/glutamine rich (polyprymidine tract binding protein associated)	Consensus includes gb:BG035151 /FEA=EST /DB_XREF=gi:12428997 /DB_XREF=est:602324851F1 /CLONE=IMAGE:4412917 /UG=Hs.180610 splicing factor prolineglutamine rich (polyprymidine tract-binding protein-

			(associated) /FL=gb:NM_005066.1
201592_at_HG-U133A	EIF3S3	eukaryotic translation initiation factor 3, subunit 3 (gamma, 40kD)	gb:NM_003756.1 /DEF=Homo sapiens eukaryotic translation initiation factor 3, subunit 3 (gamma, 40kD) (EIF3S3), mRNA. /FEA=mRNA /GEN=EIF3S3 /PROD=eukaryotic translation initiation factor 3, subunit 3 (gamma, 40kD) /DB_XREF=gi:4503514 /UG=Hs.58189 eukaryotic translation initiation factor 3, subunit 3 (gamma, 40kD) /FL=gb:BC000386.1 gb:U54559.1 gb:NM_003756.1
201595_s_at_HG-U133A	HT010	uncharacterized hypothalamus protein HT010	gb:NM_018471.1 /DEF=Homo sapiens uncharacterized hypothalamus protein HT010 (HT010), mRNA. /FEA=mRNA /GEN=HT010 /PROD=uncharacterized hypothalamus protein HT010 /DB_XREF=gi:8923807 /UG=Hs.6375 uncharacterized hypothalamus protein HT010 /FL=gb:AF220184.1 gb:NM_018471.1
201596_x_at_HG-U133A	KRT18	keratin 18	gb:NM_000224.1 /DEF=Homo sapiens keratin 18 (KRT18), mRNA. /FEA=mRNA /GEN=KRT18 /PROD=keratin 18 /DB_XREF=gi:4557887 /UG=Hs.65114 keratin 18 /FL=gb:BC000698.1 gb:BC000180.2 gb:BC004253.1 gb:M26326.1 gb:NM_000224.1
201602_s_at_HG-U133A	PPP1R12A	protein phosphatase 1, regulatory (inhibitor) subunit 12A	Consensus includes gb:BE/37620 /FEA=EST /DB_XREF=gi:10151612 /DB_XREF=est601572895F1 /CLONE=MAGE3839831 /UG=Hs.16533 myosin phosphatase, target subunit 1 /FL=gb:NM_002480.1
201640_x_at_HG-U133A	CLPTM1	cleft lip and palate associated cleft lip and palate associated transmembrane protein 1	gb:NM_001294.1 /DEF=Homo sapiens cleft lip and palate associated transmembrane protein 1 (CLPTM1), mRNA. /FEA=mRNA /GEN=CLPTM1 /PROD=cleft lip and palate associated transmembrane protein 1 /DB_XREF=gi:4502896 /UG=Hs.106671 cleft lip and palate associated transmembrane protein 1 /FL=gb:AF037339.1 gb:NM_001294.1
201644_at_HG-U133A	TSTA3	tissue specific transplantation antigen P35B	gb:NM_003313.2 /DEF=Homo sapiens tissue specific transplantation antigen P35B (TSTA3), mRNA. /FEA=mRNA /GEN=TSTA3 /PROD=tissue specific transplantation antigen P35B /DB_XREF=gi:6598326 /UG=Hs.264428 tissue specific transplantation antigen P35B /FL=gb:BC001941.1 gb:U58766.1 gb:NM_003313.2

		gb:NM_006837.1 /DEF=Homo sapiens COP9 (constitutive photomorphogenic, Arabidopsis, homolog) subunit 5 (COPSS5), mRNA. /FEA=mRNA /GEN=COPSS5 /PROD=COP9 (constitutive photomorphogenic,Arabidopsis, homolog) subunit 5 /DB_XREF=gi:5803045 /UG=Hs.198767 COP9 (constitutive photomorphogenic, Arabidopsis, homolog) subunit 5 /FL=gb:BC001187.1 gb:BC001185.1 gb:U65928.1 gb:U70734.1
201652_at_HG-U133A	COPSS5	COP9 constitutive photomorphogenic homolog subunit 5 (Arabidopsis) gb:NM_006837.1
201753_s_at_HG-U133A	ADD3	gb:NM_019903.1 /DEF=Homo sapiens adducin 3 (gamma) (ADD3), transcript variant 2, mRNA. /FEA=mRNA /GEN=ADD3 /PROD=adducin 3, isoform b /DB_XREF=gi:9951926 /UG=Hs.324470 adducin 3 (gamma) /FL=gb:D67031.1 gb:NM_019903.1
201761_at_HG-U133A	MTHFD2	gb:NM_006636.2 /DEF=Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=MTHFD2 /PROD=methylene tetrahydrofolate dehydrogenase (NAD+dependent), methenyltetrahydrofolate cyclohydrolase,precursor /DB_XREF=gi:13699899 /UG=Hs.154672 methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase /FL=gb:NM_006636.2
201810_s_at_HG-U133A	SH3BP5	Consensus includes gb:AL562152 /FEA=EST /DB_XREF=gi:12910291 /DB_XREF=est:AL562152 /CLONE=CS0DC001YK23 (3 prime) /UG=Hs.109150 SH3-domain binding protein 5 (BTK-associated) /FL=gb:AB005047.1 gb:NM_004844.1
201811_x_at_HG-U133A	SH3BP5	gb:NM_004844.1 /DEF=Homo sapiens SH3-domain binding protein 5 (BTK-associated) (SH3BP5), mRNA. /FEA=mRNA /GEN=SH3BP5 /PROD=SH3-domain binding protein 5 (BTK-associated) /DB_XREF=gi:4759507 /UG=Hs.109150 SH3-domain binding protein 5 (BTK-associated) /FL=gb:AB005047.1 gb:NM_004844.1

201812_s_at_HG-U133A	LOC54543	6.2 kd protein	gb:NM_019059.1 /DEF=Homo sapiens 6.2 kd protein (LOC54543), mRNA. /FEA=mRNA /GEN=LOC54543 /PROD=6.2 kd protein /DB_XREF=gi:9506858 /UG=Hs.112318 6.2 kd protein /FL=gb:BC001732.1 gb:AF150733.1 gb:NM_019059.1
201813_s_at_HG-U133A	KIAA0210	KIAA0210 gene product	Consensus includes gb:AI654161 /FEA=EST /DB_XREF=gi:4738140 /DB_XREF=est:ly62e04.x1 /CLONE=IMAGE:2283678 /UG=Hs.115740 KIAA0210 gene product /FL=gb:D86965.1 gb:NM_014744.1
201825_s_at_HG-U133A	LOC51097	CGI-49 protein	Consensus includes gb:AL572542 /FEA=EST /DB_XREF=gi:12930912 /DB_XREF=est:AL572542 /CLONE=CS0DI008YCO9 (3 prime) /UG=Hs.238126 CGI-49 protein /FL=gb:AF151807.1 gb:NM_016002.1
201828_x_at_HG-U133A	CXX1	CAAX box 1	gb:NM_003928.1 /DEF=Homo sapiens CAAX box 1 (CXX1), mRNA. /FEA=mRNA /GEN=CXX1 /PROD=CAAX box 1 /DB_XREF=gi:1503180 /UG=Hs.250708 CAAX box 1 /FL=gb:BC002385.1 gb:BC002410.1 gb:AF038168.1 gb:AF052096.1 gb:NM_003928.1
201829_at_HG-U133A	NET1	neuroepithelial cell transforming gene 1	Consensus includes gb:AW263232 /FEA=EST /DB_XREF=gi:6640048 /DB_XREF=est:xn79e03.x1 /CLONE=IMAGE:2700700 /UG=Hs.25155 neuroepithelial cell transforming gene 1 /FL=gb:NM_005863.1 gb:U02081.1
201830_s_at_HG-U133A	NET1	neuroepithelial cell transforming gene 1	gb:NM_005863.1 /DEF=Homo sapiens neuroepithelial cell transforming gene 1 (NET1), mRNA. /FEA=mRNA /GEN=NET1 /PROD=neuroepithelial cell transforming gene 1 /DB_XREF=gi:5031938 /UG=Hs.25155 neuroepithelial cell transforming gene 1 /FL=gb:NM_005863.1 gb:U02081.1
201851_at_HG-U133A	SH3GL1	SH3-domain GRB2-like 1	gb:NM_003025.1 /DEF=Homo sapiens SH3-domain GRB2-like 1 (SH3GL1), mRNA. /FEA=mRNA /GEN=SH3GL1 /PROD=SH3-domain GRB2-like 1 /DB_XREF=gi:4506928 /UG=Hs.97616 SH3-domain GRB2-like 1 /FL=gb:BC001270.1 gb:U65999.1 gb:NM_003025.1
201853_s_at_HG-U133A	CDC25B	cell division cycle 25B	gb:NM_021873.1 /DEF=Homo sapiens cell division cycle 25B (CDC25B), transcript variant 3, mRNA. /FEA=mRNA /GEN=CDC25B /PROD=cell division cycle 25B, isoform 3 /DB_XREF=gi:11641412 /UG=Hs.153752 cell division

			cycle 25B /FL=gb:NM_021873.1
201858_s_at_HG-U133A	PRG1	proteoglycan 1, secretory granule	gb:J03223.1 /DEF=Human secretory granule proteoglycan peptide core mRNA, complete cds. /FEA=mRNA /GEN=PRG1 /DB_XREF=gi:190419 /UG=Hs.1908 proteoglycan 1, secretory granule /FL=gb:J03223.1 gb:NM_002727.1
201874_at_HG-U133A	FLJ21047	hypothetical protein FLJ21047	Consensus includes gb:BF978611 /FEA=EST /DB_XREF=gi:12345826 /DB_XREF=est:602149061F1 /CLONE=IMAGE:4307822 /UG=Hs.14891 hypothetical protein FLJ21047 /FL=gb:NM_024569.1
201889_at_HG-U133A	GS3786	predicted osteoblast protein	gb:NM_014888.1 /DEF=Homo sapiens predicted osteoblast protein (GS3786), mRNA. /FEA=mRNA /GEN=GS3786 /PROD=predicted osteoblast protein /DB_XREF=gi:7661713 /UG=Hs.29882 predicted osteoblast protein /FL=gb:D87120.1 db:NM_014888.1
201922_at_HG-U133A	YR-29	hypothetical protein YR-29	gb:NM_014886.1 /DEF=Homo sapiens hypothetical protein (YR-29), mRNA. /FEA=mRNA /GEN=YR-29 /PROD=hypothetical protein /DB_XREF=gi:7662676 /UG=Hs.8170 hypothetical protein /FL=gb:AF077615.1 gb:BC005288.1 gb:NM_014886.1
201923_at_HG-U133A	PRDX4	peroxiredoxin 4	gb:NM_006406.1 /DEF=Homo sapiens thioredoxin peroxidase (antioxidant enzyme) (AOE372), mRNA. /FEA=mRNA /GEN=AOE372 /PROD=thioredoxin peroxidase /DB_XREF=gi:5453548 /UG=Hs.83383 thioredoxin peroxidase (antioxidant enzyme) /FL=gb:BC003609.1 gb:NM_006406.1 gb:U25182.1
201962_s_at_HG-U133A	SBB103	hypothetical SBB103 protein	gb:NM_005785.1 /DEF=Homo sapiens hypothetical SBB103 protein mRNA. /FEA=mRNA /GEN=SBB103 /PROD=hypothetical SBB103 protein /DB_XREF=gi:5032070 /UG=Hs.153639 hypothetical SBB103 protein /FL=gb:AF077599.1 gb:NM_005785.1
201968_s_at_HG-U133A	PGM1	phosphoglucomutase 1	gb:NM_002633.1 /DEF=Homo sapiens phosphoglucomutase 1 (PGM1), mRNA. /FEA=mRNA /GEN=PGM1 /PROD=phosphoglucomutase 1 /DB_XREF=gi:4505764 /UG=Hs.1869 phosphoglucomutase 1 /FL=gb:BC001756.1 gb:NM_002633.1

201974_s_at_HG-U133A	LOC51622	CGI-43 protein	gb:NM_015622.1 /DEF=Homo sapiens CGI-43 protein (LOC51622), mRNA. /FEA=mRNA /GEN=LOC51622 /PROD=DKFZP586I1023 protein /DB_XREF=gi:11056021 /UG=Hs.289112 CGI-43 protein /FL=gb:NM_015622.1
			gb:AF151801.1
201985_at_HG-U133A	KIAA0196	KIAA0196 gene product	gb:NM_014846.1 /DEF=Homo sapiens KIAA0196 gene product (KIAA0196), mRNA. /FEA=mRNA /GEN=KIAA0196 /PROD=KIAA0196 gene product /DB_XREF=gi:7661987 /UG=Hs.8294 KIAA0196 gene product /FL=gb:NM_014846.1
201988_s_at_HG-U133A	CREBL2	cAMP responsive element binding protein-like 2	Consensus includes gb:BF438056 /FEA=EST /DB_XREF=gi:11450573 /DB_XREF=est:7q63e01.x1 /CLONE=IMAGE:3703369 /UG=Hs.13313 cAMP responsive element binding protein-like 2 /FL=gb:AF039081.1
201998_at_HG-U133A	SIAT1	sialyltransferase 1 (beta-galactoside alpha-2,6-sialyltransferase)	gb:NM_001310.1
202016_at_HG-U133A	MEST	mesoderm specific transcript homolog (mouse)	Consensus includes gb:AI743792 /FEA=EST /DB_XREF=gi:5112080 /DB_XREF=est:wg53h11.x1 /CLONE=IMAGE:2368869 /UG=Hs.2554 sialyltransferase 1 (beta-galactoside alpha-2,6-sialyltransferase) /FL=gb:NM_003032.1
202018_s_at_HG-U133A	LTF	lactotransferrin	gb:NM_002402.1 /DEF=Homo sapiens mesoderm specific transcript (mouse) homolog (MEST), mRNA. /FEA=mRNA /GEN=MEST /PROD=mesoderm specific transcript (mouse) homolog /DB_XREF=gi:4505154 /UG=Hs.79284 mesoderm specific transcript (mouse) homolog /FL=gb:BC002413.1
202028_s_at_HG-U133A	RPL38	ribosomal protein L38	gb:D78611.1 gb:D87367.1 gb:NM_002402.1
			gb:NM_002343.1 /DEF=Homo sapiens lactotransferrin (LTF), mRNA. /FEA=mRNA /GEN=LTF /PROD=lactotransferrin /DB_XREF=gi:4505042 /UG=Hs.105938 lactotransferrin /FL=gb:AF332168.1 gb:M93150.1 gb:M83202.1
			gb:NM_002343.1
			Consensus includes gb:BC000603.1 /DEF=Homo sapiens, ribosomal protein L38, clone MGC:1637, mRNA, complete cds. /FEA=mRNA /PROD=ribosomal protein L38 /DB_XREF=gi:12653644 /UG=Hs.2017 ribosomal protein L38

			/FL=gb:BC000603.1 gb:NM_000999.1
202052_s_at_HG-U133A	RA14	retinoic acid induced 14	gb:NM_015577.1 /DEF=Homo sapiens novel retinal pigment epithelial gene (NORPEG), mRNA. /FEA=mRNA /GEN=NORPEG /PROD=DKFZP564G013 protein /DB_XREF=gi:13470085 /UG=Hs.15165 novel retinal pigment epithelial gene /FL=gb:NM_015577.1 gb:AF155135.1
202074_s_at_HG-U133A	OPTN	optineurin	gb:NM_021980.1 /DEF=Homo sapiens tumor necrosis factor alpha-inducible cellular protein containing leucine zipper domains; Huntingtin interacting protein L; transcription factor IIIA-interacting protein (FIP2), mRNA. /FEA=mRNA /GEN=FIP2 /PROD=tumor necrosis factor alpha-inducible cellular protein containing leucine zipper domains; Huntingtin interacting protein L; transcription factor IIIA-interacting protein /DB_XREF=gi:11415041 /UG=Hs.278898 tumor necrosis factor alpha-inducible cellular protein containing leucine zipper domains; Huntingtin interacting protein L; transcription factor IIIA-interacting protein /FL=gb:NM_021980.1
202080_s_at_HG-U133A	KIAA1042	KIAA1042 protein	gb:NM_014965.1 /DEF=Homo sapiens KIAA1042 protein (KIAA1042), mRNA. /FEA=mRNA /GEN=KIAA1042 /PROD=KIAA1042 protein /DB_XREF=gi:7662457 /UG=Hs.6705 KIAA1042 protein /FL=gb:AB028965.1
202085_at_HG-U133A	TJP2	tight junction protein 2 (zona occludens 2)	gb:NM_014965.1 /DEF=Homo sapiens tight junction protein 2 (zona occludens 2) (TJP2), mRNA. /FEA=mRNA /GEN=TJP2 /PROD=tight junction protein 2 (zona occludens 2) /DB_XREF=gi:4759341 /UG=Hs.75608 tight junction protein 2 (zona occludens 2) /FL=gb:NM_004817.1 gb:127476.1
202095_s_at_HG-U133A	BIRC5	baculoviral IAP repeat-containing 5 (survivin)	gb:NM_001168.1 /DEF=Homo sapiens baculoviral IAP repeat-containing 5 (survivin) /GEN=BIRC5 /PROD=baculoviral IAP (survivin) (BIRC5), mRNA. /FEA=mRNA /GEN=BIRC5 /PROD=baculoviral IAP repeat-containing protein 5 (survivin) /FL=gb:NM_001168.1 gb:AF077350.1
202101_s_at_HG-U133A	RALB	v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding)	gb:NM_002881.1 /DEF=Homo sapiens v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein) (RALB), mRNA. /FEA=mRNA

		protein)	/GEN=RALB /PROD=v-ral simian leukemia viral oncogene homolog B /DB_XREF=gi:4506404 /UG=Hs.250811 v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein) /FL=gb:NM35416.1 gb:NM_002881.1
202113_s_at_HG-U133A	SNX2	sorting nexin 2	gb:AF043453.1 /DEF=Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds. /FEA=mRNA /GEN=SNX2 /PROD=sorting nexin 2 /DB_XREF=gi:2827433 /UG=Hs.11183 sorting nexin 2 /FL=gb:BC003382.1 gb:AF043453.1 gb:AF065482.1 gb:NM_003100.1
202123_s_at_HG-U133A	ABL1	v-abl Abelson murine leukemia viral oncogene homolog 1	gb:NM_005157.2 /DEF=Homo sapiens v-abl Abelson murine leukemia viral oncogene homolog 1 (ABL1), transcript variant a, mRNA. /FEA=mRNA /GEN=ABL1 /PROD=v-abl Abelson murine leukemia viral oncogene homolog 1 isoform a /DB_XREF=gi:63882056 /UG=Hs.146355 v-abl Abelson murine leukemia viral oncogene homolog 1 /FL=gb:NM_005157.2 gb:NM_006624.1 /DEF=Homo sapiens adenovirus 5 E1A binding protein (BS69), mRNA. /FEA=mRNA /GEN=BS69 /PROD=adenovirus 5 E1A binding protein /DB_XREF=gi:5729745 /UG=Hs.301449 adenovirus 5 E1A binding protein /FL=gb:NM_006624.1
202137_s_at_HG-U133A	BS69	adenovirus 5 E1A binding protein	gb:NM_006907.1 /DEF=Homo sapiens pyrroline-5-carboxylate reductase 1 (PYCR1), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=PYCR1 /PROD=pyrroline-5-carboxylate reductase 1 /DB_XREF=gi:5902035 /UG=Hs.79217 pyrroline-5-carboxylate reductase 1 /FL=gb:NM77836.1 gb:NM_006907.1
202148_s_at_HG-U133A	PYCR1	pyrroline-5-carboxylate reductase 1	gb:U64317.1 /DEF=Human Crk-associated substrate related protein Cas-L mRNA, complete cds. /FEA=mRNA /PROD=Crk-associated substrate related protein Cas-L /DB_XREF=gi:1490786 /UG=Hs.80261 enhancer of filamentation 1 (cas-like docking; Crk-associated substrate related) /FL=gb:L43821.1 gb:U64317.1 gb:NM_006403.1
202150_s_at_HG-U133A	HEF1	enhancer of filamentation 1 (cas-like docking; Crk-associated substrate related)	Consensus includes gb:N36839 /FEA=EST /DB_XREF=gi:1157981
202156_s_at_HG-	CUGBP2	CUG triplet repeat, RNA binding protein	

U133A		2	/DB_XREF=est:yy35f07.s1 /CLONE=IMAGE:273253 /UG=Hs.211610 CUG triplet repeat, RNA-binding protein 2 /FL=gb:U69546.1 gb:AF036956.1 gb:AF090694.1 gb:NM_006561.1
			Consensus includes gb:AW450363 /FEA=EST /DB_XREF=gi:6991139 /DB_XREF=est:U1-H-BI3-akn-d-02-O-U1.s1 /CLONE=IMAGE:2734875 /UG=Hs.111554 ADP-ribosylation factor-like 7 /FL=gb:BC001051.1 gb:AB016811.1 gb:NM_005737.2
202206_at_HG-U133A	ARL7		ADP-ribosylation factor-like 7 /DB_XREF=est:AU146233 /CLONE=HEMBA1007223 /UG=Hs.110707 H326
202249_s_at_HG-U133A	H326	H326	Consensus includes gb:AB016811.1 gb:NM_015726.1 /FL=gb:U06631.1 gb:NM_015726.1
202254_at_HG-U133A	KIAA0440	KIAA0440 protein	Consensus includes gb:AB007900.1 /DEF=Homo sapiens KIAA0440 mRNA partial cds. /FEA=mRNA /GEN=KIAA0440 /DB_XREF=gi:2662160 /UG=Hs.172180 KIAA0440 protein /FL=gb:AF090990.1 gb:NM_015556.1
202262_x_at_HG-U133A	DDAH2		gb:NM_013974.1 /DEF=Homo sapiens dimethylarginine dimethylaminohydrolase 2 (DDAH2), mRNA. /FEA=mRNA /GEN=DDAH2 /PROD=dimethylarginine dimethylaminohydrolase 2 /DB_XREF=gi:7524353 /UG=Hs.247362 dimethylarginine dimethylaminohydrolase 2 /FL=gb:BC001435.1 gb:AF070667.1 gb:NM_013974.1
202265_at_HG-U133A	BMI1		gb:NM_005180.1 /DEF=Homo sapiens murine leukemia viral (bmi-1) oncogene homolog (BMI1), mRNA. /FEA=mRNA /GEN=BMI1 /PROD=murine leukemia viral (bmi-1) oncogene homolog /DB_XREF=gi:4885094 /UG=Hs.431 murine leukemia viral (bmi-1) oncogene homolog /FL=gb:L13689.1 gb:NM_005180.1
202283_at_HG-U133A	SERPINF1		gb:NM_002615.1 /DEF=Homo sapiens serine (or cysteine) proteinase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1 (SERPINF1), mRNA. /FEA=mRNA /GEN=SERPINF1 /PROD=serine serine (or cysteine) proteinase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1 /DB_XREF=gi:4505708 /UG=Hs.173594

		serine (or cysteine) proteinase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1 /FL=gb:NM_002615.1
		gb:BC000522.1 gb:M76979.1 gb:NM_002615.1
		gb:U88966.1 /DEF=Human protein rapamycin associated protein (FRAP2) gene, complete cds. /FEA=mRNA /GEN=FRAP2 /PROD=rapamycin associated protein FRAP2 /DB_XREF=gi:3282238 /UG=Hs.250723 FK506 binding protein 12-rapamycin associated protein 1 /FL=gb:U88966.1
		gb:NM_004958.1 gb:L34075.1
202288_at_HG-U133A	FRAP1	FK506 binding protein 12-rapamycin associated protein 1
		gb:NM_000296.1 /DEF=Homo sapiens polycystic kidney disease 1 (autosomal dominant) (PKD1), mRNA. /FEA=mRNA /GEN=PKD1 /PROD=polycystic kidney disease 1 (autosomal dominant) /DB_XREF=gi:4505832 /UG=Hs.75813 polycystic kidney disease 1 (autosomal dominant) /FL=gb:NM_000296.1
		gb:U24497.1 gb:L33243.1
		gb:NM_001894.1 /DEF=Homo sapiens casein kinase 1, epsilon (CSNK1E), mRNA. /FEA=mRNA /GEN=CSNK1E /PROD=casein kinase 1, epsilon /DB_XREF=gi:4503092 /UG=Hs.79658 casein kinase 1, epsilon /FL=gb:NM_001894.1 gb:AB024597.1 gb:L37043.1
202328_s_at_HG-U133A	PKD1	polycystic kidney disease 1 (autosomal dominant)
202332_at_HG-U133A	CSNK1E	casein kinase 1, epsilon
202340_x_at_HG-U133A	NR4A1	casein kinase 1, epsilon nuclear receptor subfamily 4, group A, member 1
202370_s_at_HG-U133A	CBFB	nuclear receptor subfamily 4, group A, member 1 /DB_XREF=gi:4504440 /UG=Hs.1119 nuclear receptor subfamily 4, group A, member 1 /FL=gb:L13740.1 gb:NM_002135.1
202371_at_HG-U133A	FLJ21174	gb:NM_001755.1 /DEF=Homo sapiens core-binding factor, beta subunit (CBFB), transcript variant 2, mRNA. /FEA=mRNA /GEN=CBFB /PROD=core-binding factor, beta subunit, isoform 2 /DB_XREF=gi:13124872 /UG=Hs.179881 core-binding factor, beta subunit /FL=gb:NM_001755.1
		gb:NM_024863.1 /DEF=Homo sapiens hypothetical protein FLJ21174 /PROD=hypothetical protein (FLJ21174), mRNA. /FEA=mRNA /GEN=FLJ21174 /PROD=hypothetical protein

		FLJ21174 /DB_XREF=gi:13376293 /UG=Hs.194329 hypothetical protein FLJ21174 /FL=gb:AF271783.1 gb:NM_024863.1
202377_at_HG-U133A	HSOBRGRP	leptin receptor gene-related protein Consensus includes gb:AV028535 /FEA=EST /DB_XREF=gi:5880065 /DB_XREF=est:ww14f10.x1 /CLONE=IMAGE:2529547 /UG=Hs.23581 leptin receptor gene-related protein /FL=gb:NM_017526.1
202382_s_at_HG-U133A	GNPI	glucosamine-6-phosphate isomerase gb:NM_005471.1 /DEF=Homo sapiens glucosamine-6-phosphate isomerase (GNPI), mRNA. /FEA=mRNA /GEN=GNPI /PROD=glucosamine-6-phosphate isomerase /DB_XREF=gi:13027377 /UG=Hs.278500 glucosamine-6-phosphate isomerase /FL=gb:NM_005471.1 gb:AF029914.1 gb:AF048826.1 gb:D31766.1
202391_at_HG-U133A	BASP1	glucosamine-6-phosphate isomerase brain abundant, membrane attached signal protein 1 gb:NM_006317.1 /DEF=Homo sapiens brain acid-soluble protein 1 (BASP1), mRNA. /FEA=mRNA /GEN=BASP1 /PROD=brain acid-soluble protein 1 /DB_XREF=gi:5453749 /UG=Hs.79516 brain abundant, membrane attached signal protein 1 /FL=gb:BC000518.1 gb:AF039656.1 gb:NM_006317.1
202406_s_at_HG-U133A	TIAL1	TIA1 cytotoxic granule-associated RNA binding protein-like 1 gb:NM_003252.2 /DEF=Homo sapiens TIA1 cytotoxic granule-associated RNA-binding protein-like 1 (TIAL1), transcript variant 1, mRNA. /FEA=mRNA /GEN=TIAL1 /PROD=TIA1 cytotoxic granule-associated RNA-binding protein-like 1, isoform 1 /DB_XREF=gi:13435392 /UG=Hs.182741 TIA1 cytotoxic granule-associated RNA-binding protein-like 1 /FL=gb:NM_003252.2 gb:M96954.1
202413_s_at_HG-U133A	USP1	ubiquitin specific protease 1 gb:NM_003368.1 /DEF=Homo sapiens ubiquitin specific protease 1 (USP1), mRNA. /FEA=mRNA /GEN=USP1 /PROD=ubiquitin specific protease 1 /DB_XREF=gi:4507850 /UG=Hs.35086 ubiquitin specific protease 1 /FL=gb:AB014458.1 gb:AF117386.1 gb:NM_003368.1 gb:AL11757.1
202421_at_HG-U133A	IGSF3	immunoglobulin superfamily, member 3 similar to <i>Caenorhabditis elegans</i> protein C42C1.9 gb:KIAA0466 protein, partial cds. /FEA=mRNA /GEN=KIAA0466 /PROD=KIAA0466 /FL=gb:AF031174.1 gb:NM_001542.1 immunoglobulin superfamily, member 3 /DB_XREF=gi:3413893 /UG=Hs.81234
202441_at_HG-U133A	KEO4	Consensus includes gb:AB007935.1 /DEF=Homo sapiens mRNA for immunoglobulin superfamily, member 3 /FL=gb:AF031174.1 gb:NM_001542.1 Consensus includes gb:AL568449 /FEA=EST /DB_XREF=gi:12922799 /DB_XREF=est:AL568449 /CLONE=CS0DE001YC12 (3 prime) /UG=Hs.285818

			similar to <i>Caenorhabditis elegans</i> protein C42C1.9 /FL=gb:AF064093.1 gb:NM_006459.1
202443_X_at_HG-U133A	NOTCH2	Notch homolog 2 (<i>Drosophila</i>)	Consensus includes gb:AA291203 /FEA=EST /DB_XREF=gi:1939386 /DB_XREF=est;z38h02.s1 /CLONE=IMAGE:724659 /UG=Hs.8121 Notch (<i>Drosophila</i>) homolog 2 /FL=gb:AF315356.1 gb:NM_024408.1
202477_s_at_HG-U133A	GCP2	gamma-tubulin complex protein 2	gb:NM_006659.1 /DEF=Homo sapiens gamma-tubulin complex protein 2 (GCP2), mRNA. /FEA=mRNA /GEN=GCP2 /PROD=gamma-tubulin complex protein 2 /DB_XREF=gi:5729839 /UG=Hs.13386 gamma-tubulin complex protein 2 /FL=gb:BC005011.1 gb:NM_006659.1
202479_s_at_HG-U133A	GS3955	GS3955 protein	gb:BC002637.1 /DEF=Homo sapiens GS3955 protein, clone MGC:3860, mRNA, complete cds. /FEA=mRNA /PROD=GS3955 protein /DB_XREF=gi:12803604 /UG=Hs.155418 GS3955 protein /FL=gb:NM_021643.1 gb:BC002637.1 gb:D87119.1
202481_at_HG-U133A	SDR1	short-chain dehydrogenase/reductase 1	gb:NM_004753.1 /DEF=Homo sapiens short-chain dehydrogenasereductase 1 (SDR1), mRNA. /FEA=mRNA /GEN=SDR1 /PROD=short-chain dehydrogenasereductase 1 /DB_XREF=gi:4759083 /UG=Hs.17144 short-chain dehydrogenasereductase 1 /FL=gb:BC002730.1 gb:AF061741.1. gb:NM_004753.1
202503_s_at_HG-U133A	KIAA0101	KIAA0101 gene product	gb:NM_014736.1 /DEF=Homo sapiens KIAA0101 gene product (KIAA0101), mRNA. /FEA=mRNA /GEN=KIAA0101 /PROD=KIAA0101 gene product /DB_XREF=gi:7661905 /UG=Hs.81892 KIAA0101 gene product /FL=gb:DI4657.1 gb:NM_014736.1
202519_at_HG-U133A	MONDOA	Mlx interactor	gb:NM_014938.1 /DEF=Homo sapiens KIAA0867 protein (MONDOA), mRNA. /FEA=mRNA /GEN=MONDOA /PROD=MondoA protein /DB_XREF=gi:7662347 /UG=Hs.52081 KIAA0867 protein /FL=gb:AB020674.1 gb:NM_014938.1
202524_s_at_HG-U133A	KIAA0275	KIAA0275 gene product	gb:NM_014767.1 /DEF=Homo sapiens KIAA0275 gene product (KIAA0275), mRNA. /FEA=mRNA /GEN=KIAA0275 /PROD=KIAA0275 gene product /DB_XREF=gi:7662035 /UG=Hs.74583 KIAA0275 gene product

			/FL=gb:D87465.1 gb:NM_014767.1
202530_at_HG-U133A	MAPK14	mitogen-activated protein kinase 14	gb:NM_001315.1 /DEF=Homo sapiens mitogen-activated protein kinase 14 /PROD=(MAPK14), mRNA. /FEA=mRNA /GEN=MAPK14 /PROD=mitogen-activated protein kinase 14 /DB_XREF=gi:4503068 /UG=Hs.79107 mitogen-activated protein kinase 14 /FL=gb:NM_001315.1 gb:L35263.1
202535_at_HG-U133A	FADD	Fas (TNFRSF6)-associated via death domain	gb:NM_003824.1 /DEF=Homo sapiens Fas (TNFRSF6)-associated via death domain (FADD), mRNA. /FEA=mRNA /GEN=FADD /PROD=Fas (TNFRSF6)-associated via death domain /DB_XREF=gi:4505228 /UG=Hs.86131 Fas (TNFRSF6)-associated via death domain /FL=gb:BC0000334.1 gb:NM_003824.1 gb:U24231.1
202545_at_HG-U133A	PRKCD	protein kinase C, delta	gb:NM_006254.1 /DEF=Homo sapiens protein kinase C, delta (PRKCD), mRNA. /FEA=mRNA /GEN=PRKCD /PROD=protein kinase C, delta /DB_XREF=gi:5463969 /UG=Hs.155342 protein kinase C, delta /FL=gb:L07860.1 gb:L07861.1 gb:D10495.1 gb:NM_006254.1 -
202551_s_at_HG-U133A	CRIM1	cysteine-rich motor neuron 1	Consensus includes gb:BG548884 /FEA=EST /DB_XREF=gi:13545549 /DB_XREF=est:602574066F1 /CLONE=IMAGE:4702049 /UG=Hs.19280 cysteine-rich motor neuron 1 /FL=gb:NM_016441.1 gb:AF167706.1
202552_s_at_HG-U133A	CRIM1	cysteine-rich motor neuron 1	gb:NM_016441.1 /DEF=Homo sapiens cysteine-rich motor neuron 1 (CRM1), mRNA. /FEA=mRNA /GEN=CRM1 /PROD=cysteine-rich motor neuron 1 /DB_XREF=gi:10092638 /UG=Hs.19280 cysteine-rich motor neuron 1 /FL=gb:NM_016441.1 gb:AF167706.1
202572_s_at_HG-U133A	KIAA0964	KIAA0964 protein	gb:NM_014902.1 /DEF=Homo sapiens KIAA0964 protein (KIAA0964), mRNA. /FEA=mRNA /GEN=KIAA0964 /PROD=KIAA0964 protein /DB_XREF=gi:7662411 /UG=Hs.177425 KIAA0964 protein /FL=gb:AB023181.1 gb:NM_014902.1
202580_x_at_HG-U133A	FOXM1	forkhead box M1	gb:NM_021953.1 /DEF=Homo sapiens forkhead box M1 (FOXM1), mRNA. /FEA=mRNA /GEN=FOXM1 /PROD=forkhead box M1 /DB_XREF=gi:11386144 /UG=Hs.239 forkhead box M1 /FL=gb:NM_021953.1 gb:U83113.1 gb:L16783.1

202589_at_HG-U133A	TYMS	thymidylate synthetase	gb:NM_001071.1 /DEF=Homo sapiens thymidylate synthetase (TYMS), mRNA. /FEA=mRNA /GEN=TYMS /PROD=thymidylate synthetase /DB_XREF=gi:4507750 /UG=Hs.82962 thymidylate synthetase /FL=gb:BC002567.1 gb:NM_001071.1
202600_s_at_HG-U133A	NRIP1	nuclear receptor interacting protein 1	Consensus includes gb:AI824012 /FEA=EST /DB_XREF=gi:5444683 /DB_XREF=est:wj29e06.x1 /CLONE=IMAGE:2404258 /UG=Hs.155017 nuclear receptor interacting protein 1 /FL=gb:NM_003489.1
202606_s_at_HG-U133A	TLK1	tousled-like kinase 1	gb:NM_012290.1 /DEF=Homo sapiens tousled-like kinase 1 (TLK1), mRNA. /FEA=mRNA /GEN=TLK1 /PROD=tousled-like kinase 1 /DB_XREF=gi:6912719 /UG=Hs.18895 tousled-like kinase 1 /FL=gb:AB004885.1 gb:NM_012290.1 gb:AF246219.1
202619_s_at_HG-U133A	PLOD2	procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2	Consensus includes gb:AI754404 /FEA=EST /DB_XREF=gi:5132668 /DB_XREF=est:cr24g06.x1 /CLONE=HBMSC_cr24g06 /UG=Hs.41270 procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2 /FL=gb:U84573.1 gb:NM_000935.1
202625_at_HG-U133A	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	Consensus includes gb:AI356412 /FEA=EST /DB_XREF=gi:4108033 /DB_XREF=est:qz26n02.x1 /CLONE=IMAGE:2028051 /UG=Hs.80887 v-yes-1 Yamaguchi sarcoma viral related oncogene homolog /FL=gb:NM_002350.1 gb:NM_002350.1 /DEF=Homo sapiens v-yes-1 Yamaguchi sarcoma viral related oncogene homolog (LYN), mRNA. /GEN=LYN /PROD=v- yes-1 Yamaguchi sarcoma viral related oncogenehomolog /DB_XREF=gi:4505054 /UG=Hs.80887 v-yes-1 Yamaguchi sarcoma viral related oncogene homolog /FL=gb:NM_002350.1
202626_s_at_HG-U133A	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	gb:NM_0006010.1 /DEF=Homo sapiens arginine-rich, mutated in early stage tumors (ARMET), mRNA. /GEN=ARMET /PROD=arginine-rich protein /DB_XREF=gi:5174392 /UG=Hs.75412 arginine-rich, mutated in early stage tumors /FL=gb:MB3751.1 gb:NM_006010.1 gb:NM_004701.2 /DEF=Homo sapiens cyclin B2 (CCNB2), mRNA.

		/FEA=mRNA /GEN=CCNB2 /PROD=cyclin B2 /DB_XREF=gi:10938017 /UG=Hs.194698 cyclin B2 /FL=gb:NM_004701.2 gb:AF002822.1 gb:AB02981.1 gb:AL080146.1
202709_at_HG-U133A	FMOD	fibromodulin insulin-like growth factor binding protein 2 (36kD)
202718_at_HG-U133A	IGFBP2	insulin-like growth factor binding protein 2 (36kD) /DB_XREF=gi:10835156 /UG=Hs.162 insulin-like growth factor binding protein 2(36kD) /FL=gb:NM_000597.1 gb:BC004312.1 gb:M35410.1
202723_s_at_HGU133A	FOXO1A	forkhead box O1A (rhabdomyosarcoma) latent transforming growth factor beta binding protein 1
202729_s_at_HGU133A	LTPB1	latent transforming growth factor beta binding protein 1 /FL=gb:M34057.1 gb:NM_000627.1
202746_at_HG-U133A		Consensus includes gb:AL021786 /DEF=Human DNA sequence from PAC 696H22 on chromosome Xq21.1-21.2. Contains a mouse E25 like gene, a Kinesin like pseudogene and ESTs /FEA=mRNA /DB_XREF=gi:2853186 /UG=Hs.17109 integral membrane protein 2A /FL=gb:AF038953.1 gb:NM_004867.1
202747_s_at_HGU133A	ITM2A	integral membrane protein 2A /DB_XREF=gi:4758223 /UG=Hs.17109 integral membrane protein 2A /DB_XREF=gi:4758223 /UG=Hs.17109 integral membrane protein 2A

			/FL=gb:AF038953.1 gb:NM_004867.1
202761_s_at_HG-U133A	SYNE-2	synaptic nuclei expressed gene 2	gb:NM_015180.1 /DEF=Homo sapiens synaptic nuclei expressed gene 2; KIAA1011 protein (KIAA1011), mRNA. /FEA=mRNA /GEN=KIAA1011 /PROD=KIAA1011 protein /DB_XREF=gi:11056019 /UG=Hs.57749 synaptic nuclei expressed gene 2; KIAA1011 protein /FL=gb:NM_015180.1 gb:AL080133.1
202819_s_at_HG-U133A	TCEB3	transcription elongation factor B (SIII), polypeptide 3 (110kD, elongin A)	gb:NM_003198.1 /DEF=Homo sapiens transcription elongation factor B (SIII), polypeptide 3 (110kD, elongin A) (TCEB3), mRNA. /FEA=mRNA /GEN=TCEB3 /PROD=elongin A /DB_XREF=gi:4507388 /UG=Hs.155202 transcription elongation factor B (SIII), polypeptide 3 (110kD, elongin A) /FL=gb:BC002883.1 gb:NM_003198.1 gb:l:47345.1
202822_at_HG-U133A	LPP	LIM domain containing preferred translocation partner in lipoma	Consensus includes gb:BF221852 /FEA=EST /DB_XREF=gi:11129029 /DB_XREF=est:p37ff11.x1 /CLONE=IMAGE:3648141 /UG=Hs.180398 LIM domain-containing preferred translocation partner in lipoma /FL=gb:NM_005578.1
202823_at_HG-U133A	TCEB1	transcription elongation factor B (SIII), polypeptide 1 (15kD, elongin C)	Consensus includes gb:N89607 /DEF=EST /DB_XREF=gi:1442934 /DB_XREF=est:zb08h02.s1 /CLONE=IMAGE:301491 /UG=Hs.184693 transcription elongation factor B (SIII), polypeptide 1 (15kD, elongin C) /FL=gb:NM_005648.1 gb:L34587.1
202853_s_at_HG-U133A	RYK	RYK receptor-like tyrosine kinase	gb:NM_02958.1 /DEF=Homo sapiens RYK receptor-like tyrosine (RYK), mRNA. /FEA=mRNA /GEN=RYK /PROD=RYK receptor-like tyrosine kinase precursor /DB_XREF=gi:11863158 /UG=Hs.79350 RYK receptor-like tyrosine kinase /FL=gb:NM_002958.1
202862_at_HG-U133A	FAH	fumarylacetoacetate hydrolase (fumarylacetoacetate)	gb:NM_000137.1 /DEF=Homo sapiens fumarylacetoacetate (FAH), mRNA. /FEA=mRNA /GEN=FAH /PROD=fumarylacetoacetate /DB_XREF=gi:4557586 /UG=Hs.73875 fumarylacetoacetate /FL=gb:BC002527.1 gb:M55150.1
202863_at_HG-U133A	SP100	nuclear antigen Sp100	gb:NM_003113.1 /DEF=Homo sapiens nuclear antigen Sp100 (SP100),

		mRNA. /FEA=mRNA /GEN=SP100 /PROD=nuclear antigen Sp100 /DB_XREF=gi:4507164 /UG=Hs.77617 nuclear antigen Sp100 /FL=gb:M60618.1 gb:NM_003113.1
202980_s_at_HG-U133A	PSCD1	gb:NM_004762.1 /DEF=Homo sapiens pleckstrin homology, Sec7 and coiledcoil domains 1 (cytohesin 1) (PSCD1), transcript variant 1, mRNA. /FEA=mRNA /GEN=PSCD1 /PROD=cytohesin 1, isoform 1 /DB_XREF=gi:4758963 /UG=Hs.1050 pleckstrin homology, Sec7 and coiledcoil domains 1 (cytohesin 1) /FL=gb:NM_004762.1 gb:NM_017456.1 Consensus includes gb:T79584 /FEA=EST /DB_XREF=gi:698093
202983_s_at_HG-U133A	PPP2R1B	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform /FL=gb:NM_002716.1 gb:AF162473.1 gb:NM65254.1 gb:AF087438.1
202926_at_HG-U133A	NAG	gb:NM_015909.1 /DEF=Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA. /GEN=LOC51594 /PROD=neuroblastoma-amplified protein /DB_XREF=gi:7706239 /UG=Hs.15430 neuroblastoma-amplified protein /FL=gb:AF056195.1 gb:NM_015909.1 gb:NM_000262.1 /DEF=Homo sapiens N-acetylgalactosaminidase, alpha-(NAGA), mRNA. /FEA=mRNA /GEN=NAGA /PROD=alpha-N-acetylgalactosaminidase precursor /DB_XREF=gi:4557780 /UG=Hs.75372 N-acetylgalactosaminidase, alpha-. /FL=gb:BC000095.1 gb:M62783.1 gb:M38083.1 gb:NM_000262.1
202944_at_HG-U133A	NAGA	gb:NM_004957.1 /DEF=Homo sapiens folypolyglutamate synthase (FPGS), mRNA. /FEA=mRNA /GEN=FPGS /PROD=folypolyglutamate synthase /DB_XREF=gi:4826727 /UG=Hs.754 folypolyglutamate synthase /FL=gb:NM98045.1 gb:NM_004957.1
202945_at_HG-U133A	FPGS	gb:NM_006421.2 /DEF=Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA. /FEA=mRNA /GEN=BIG1 /PROD=brefeldin A-inhibited guanine nucleotide-exchange protein 1
202956_at_HG-U133A	BIG1	

		/DB_XREF=gi:6715588 /UG=Hs.94631 brefeldin A-inhibited guanine nucleotide-exchange protein 1 /FL=gb:AF084520.1 gb:AF11162.1 gb:NM_006421.2
202973_x_at_HG-U133A	KIAA0914	gb:NM_014883.1 /DEF=Homo sapiens KIAA0914 gene product (KIAA0914), mRNA. /FEA=mRNA /GEN=KIAA0914 /PROD=KIAA0914 gene product /DB_XREF=gi:7662375 /UG=Hs.177664 KIAA0914 gene product /FL=gb:AB020721.1 gb:NM_014883.1
203005_at_HG-U133A	LTBR	gb:NM_002342.1 /DEF=Homo sapiens lymphotoxin beta receptor (TNFR superfamily, member 3 (LTBR), mRNA. /FEA=mRNA /GEN=LTR /PROD=lymphotoxin B receptor /DB_XREF=gi:4505038 /UG=Hs.1116 lymphotoxin beta receptor (TNFR superfamily, member 3 /FL=gb:LO4270.1 gb:NM_002342.1
203007_x_at_HG-U133A		gb:AF07198.1 /DEF=Homo sapiens lysophospholipase mRNA, complete cds. /FEA=mRNA /PROD=lysophospholipase /DB_XREF=gi:4679009 /UG=Hs.12540 lysophospholipase 1 /FL=gb:AF081281.1 gb:NM_006330.1 gb:AF291053.1
203020_at_HG-U133A	KIAA0471	gb:NM_014857.1 /DEF=Homo sapiens KIAA0471 gene product (KIAA0471), mRNA. /FEA=mRNA /GEN=KIAA0471 /PROD=KIAA0471 gene product /DB_XREF=gi:7662143 /UG=Hs.242271 KIAA0471 gene product /FL=gb:AB007940.1 gb:NM_014857.1
203021_at_HG-U133A	SLPI	gb:NM_003064.1 /DEF=Homo sapiens secretory leukocyte protease inhibitor (antileukoproteinase) (SLPI), mRNA. /FEA=mRNA /GEN=SLPI /PROD=secretory leukocyte protease inhibitor(antileukoproteinase) /DB_XREF=gi:4507064 /UG=Hs.251754 secretory leukocyte protease inhibitor (antileukoproteinase) /FL=gb:NM_003066.1 gb:AF114471.1 gb:NM_003064.1
203026_at_HG-U133A	KIAA0354	gb:NM_014872.1 /DEF=Homo sapiens KIAA0354 gene product (KIAA0354), mRNA. /FEA=mRNA /GEN=KIAA0354 /PROD=KIAA0354 gene product /DB_XREF=gi:7662073 /UG=Hs.36682 KIAA0354 gene product

			/FL=gb:AB002352.1 gb:NM_014872.1
203037_s_at_HG-U133A	KIAA0429	KIAA0429 gene product	gb:NM_014751.1 /DEF=Homo sapiens KIAA0429 gene product (KIAA0429). mRNA. /FEA=mRNA /GEN=KIAA0429 /PROD=KIAA0429 gene product /DB_XREF=gi:7662113 /UG=Hs.77694 KIAA0429 gene product /FL=gb:AB007889.1 gb:NM_014751.1
203041_s_at_HG-U133A	LAMP2	lysosomal-associated membrane protein 2	gb:J04183.1 /DEF=Homo sapiens lysosomal membrane glycoprotein-2 (LAMP2), complete cds. /FEA=mRNA /GEN=LAMP2 /PROD=lysosomal membrane glycoprotein-2 /DB_XREF=gi:186929 /UG=Hs.8262 lysosomal-associated membrane protein 2 /FL=gb:J04183.1 gb:NM_002294.1
203053_at_HG-U133A	BCAS2	breast carcinoma amplified sequence 2	gb:NM_005872.1 /DEF=Homo sapiens BCAS2 /PROD=breast carcinoma (BCAS2), mRNA. /FEA=mRNA /GEN=BCAS2 /PROD=breast carcinoma amplified sequence 2 /DB_XREF=gi:5031652 /UG=Hs.22960 breast carcinoma amplified sequence 2 /FL=gb:BC005285.1 gb:AF081788.1 gb:AB020623.1 gb:NM_005872.1
203057_s_at_HG-U133A	PRDM2	PR domain containing 2, with ZNF domain	Consensus includes gb:AV724783 /FEA=EST /DB_XREF=gi:10829513 /DB_XREF=est:AV724783 /CLONE=HTBCEG11 /UG=Hs.26719 zinc-finger DNA-binding protein /FL=gb:D45132.1 gb:NM_015866.1
203074_at_HG-U133A	ANXA8	annexin A8	gb:NM_001630.1 /DEF=Homo sapiens annexin A8 (ANXA8), mRNA. /FEA=mRNA /GEN=ANXA8 /PROD=annexin VIII /DB_XREF=gi:4502112 /UG=Hs.87268 annexin A8 /FL=gb:BC004376.1 gb:NM81844.1 gb:NM_001630.1
203092_at_HG-U133A	TIMM44		gb:AF026030.1 /DEF=Homo sapiens putative mitochondrial inner membrane protein import receptor (hTIM44) mRNA, nuclear gene encoding mitochondrial protein, complete cds. /FEA=mRNA /GEN=hTIM44 /PROD=putative mitochondrial inner membrane protein import receptor /DB_XREF=gi:4103601 /UG=Hs.123178 translocase of inner mitochondrial membrane 44 (yeast) homolog /FL=gb:AF026030.1 gb:NM_006351.1
203104_at_HG-U133A	CSF1R		gb:NM_005211.1 /DEF=Homo sapiens colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog

	(v-fms) oncogene homolog	(CSF1R), mRNA. /FEA=mRNA /GEN=CSF1R /PROD=colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog /DB_XREF=gi:4885158 /UG=Hs.174142 colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog /FL=gb:NM_005211.1
203110_at_HG-U133A	PTK2B	protein tyrosine kinase 2 beta /DEF=Human cell adhesion kinase beta (CAKbeta) mRNA, complete cds. /FEA=mRNA /GEN=CAKbeta /PROD=cell adhesion kinase beta /DB_XREF=gi:1165218 /UG=Hs.20313 protein tyrosine kinase 2 beta /FL=gb:L49207.1 gb:U43522.1 gb:NM_004103.1 gb:U33284.1
203133_at_HG-U133A	SEC61B	protein translocation complex beta /DEF=Homo sapiens protein translocation complex beta (SEC61B), mRNA. /FEA=mRNA /GEN=SEC61B /PROD=protein translocation complex beta /DB_XREF=gi:5803164 /UG=Hs.77028 protein translocation complex beta /FL=gb:BC001734.1 gb:L25085.1 gb:NM_006808.1 Consensus includes gb:T79953 /FEA=EST /DB_XREF=gi:698462 /DB_XREF=est:yd85c11.s1 /CLONE=IMAGE:115028 /UG=Hs.158282 KIAA0040 gene product /FL=gb:D25539.1 gb:NM_014656.1
203143_s_at_HG-U133A	KIAA0040	KIAA0040 gene product /DEF=Homo sapiens transcription factor 6-like 1 (mitochondrial transcription factor 1-like) (TCF6L1), mRNA. /FEA=mRNA /GEN=TCF6L1 /PROD=transcription factor 6-like 1 (mitochondrial transcription factor 1-like) /DB_XREF=gi:4507400 /UG=Hs.75133 transcription factor 6-like 1 (mitochondrial transcription factor 1-like) /FL=gb:M62810.1 gb:NM_003201.1
203177_x_at_HG-U133A	TFAM	transcription factor A, mitochondrial /DEF=Homo sapiens i-beta-1,3-N-acetylglucosaminyltransferase (BETA3GNTI), mRNA. /FEA=mRNA /GEN=BETA3GNTI /PROD=i-beta-1,3-N-acetylglucosaminyltransferase /DB_XREF=gi:5802983 /UG=Hs.8526 i-beta-1,3-N-acetylglucosaminyltransferase /FL=gb:AF029893.1 gb:NM_006876.1
203188_at_HG-U133A	B3GNT6	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6 /DEF=Homo sapiens sialyltransferase 9 (CMP-sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase) (SIAT9),
203217_s_at_HG-U133A	SIAT9	

	sialyltransferase; GM3 synthase)	mRNA. /FEA=mRNA /GEN=SIAT9 /PROD=sialyltransferase 9 (CMP-NeuAc: lactosylceramidealpha-2,3-sialyltransferase; GM3 synthase) /DB_XREF=gi:4506654 /UG=Hs.225939 sialyltransferase 9 (CMP-NeuAc: lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase) /FL=gb:AB018356.1 gb:NM_003896.1 gb:AF119415.1
203233_at_HG-U133A	IL4R	interleukin 4 receptor gb:NM_000418.1 /DEF=Homo sapiens interleukin 4 receptor (IL4R), mRNA /FEA=mRNA /GEN=IL4R /PROD=interleukin 4 receptor precursor /DB_XREF=gi:4557668 /UG=Hs.75545 interleukin 4 receptor /FL=gb:NM_000418.1
203241_at_HG-U133A	UVRAG	UV radiation resistance associated gene gb:NM_003369.1 /DEF=Homo sapiens UV radiation resistance associated gene (UVRAG), mRNA /FEA=mRNA /GEN=UVRAG /PROD=UV radiation resistance associated gene /DB_XREF=gi:4507860 /UG=Hs.13137 UV radiation resistance associated gene /FL=gb:NM_003369.1 gb:AB012958.1
203288_at_HG-U133A	KIAA0355	KIAA0355 gene product gb:NM_014686.1 /DEF=Homo sapiens KIAA0355 gene product (KIAA0355), mRNA. /FEA=mRNA /GEN=KIAA0355 /PROD=KIAA0355 gene product /DB_XREF=gi:7662075 /UG=Hs.186840 KIAA0355 gene product /FL=gb:AB002353.1 gb:NM_014686.1
203345_s_at_HG-U133A	M96	putative DNA binding protein Consensus includes gb:AI566096 /FEA=EST /DB_XREF=gi:4524548 /DB_XREF=est:tn53d02.x1 /CLONE=IMAGE:2172099 /UG=Hs.31016 putative DNA binding protein /FL=gb:AF072814.1 gb:NM_007358.1
203355_s_at_HG-U133A	KIAA0942	KIAA0942 protein gb:NM_015310.1 /DEF=Homo sapiens KIAA0942 protein (KIAA0942), mRNA. /FEA=mRNA /GEN=KIAA0942 /PROD=KIAA0942 protein /DB_XREF=gi:7662395 /UG=Hs.6763 KIAA0942 protein /FL=gb:AF243495.2 gb:NM_015310.1
203367_at_HG-U133A	DUSP14	dual specificity phosphatase 14 gb:NM_007026.1 /DEF=Homo sapiens MKP-1 like protein tyrosine phosphatase (MKP-L), mRNA /GEN=MKP-L /PROD=MKP-1 like protein tyrosine phosphatase /DB_XREF=gi:5902001 /UG=Hs.91448 MKP-1 like protein tyrosine phosphatase /FL=gb:BC000370.1 gb:BC001894.1

			gb:BC004448.1 /DEF=Homo sapiens enigma (LIM domain protein) gb:NM_005451.2 /PROD=enigma protein (ENIGMA), mRNA, /GEN=mRNA /PROD=enigma protein /DB_XREF=gi:11496884 /UG=Hs.102948 enigma (LIM domain protein) /FL=gb:NM_005451.2 gb:BC001093.1 gb:AF265209.1
203370_s_at_HG-U133A	ENIGMA	enigma (LIM domain protein)	gb:AB004903.1 /DEF=Homo sapiens mRNA for STAT induced STAT inhibitor-2, complete cds. /FEA=mRNA /PROD=STAT induced STAT inhibitor-2 /DB_XREF=gi:2443360 /UG=Hs.110776 STAT induced STAT inhibitor-2 /FL=gb:AB004903.1 gb:AB006966.1 gb:AF037989.1 gb:AF020590.1
203372_s_at_HG-U133A	STAT12	STAT induced STAT inhibitor-2	gb:NM_003877.1 /DEF=Homo sapiens STAT induced STAT inhibitor-2 (STAT12), mRNA, /FEA=mRNA /GEN=STAT12 /PROD=STAT induced STAT inhibitor-2 /DB_XREF=gi:4507262 /UG=Hs.110776 STAT induced STAT inhibitor-2 /FL=gb:AB004903.1 gb:AB006966.1 gb:AF037989.1 gb:AF020590.1
203373_at_HG-U133A	STAT12	STAT induced STAT inhibitor-2	gb:NM_003877.1 /DEF=Homo sapiens splicing factor, arginineserine-rich 5 (SFRS5), mRNA, /FEA=mRNA /GEN=SFRS5 /PROD=splicing factor, arginineserine-rich 5 /DB_XREF=gi:55902077 /UG=Hs.166975 splicing factor, arginineserine-rich 5 /FL=gb:U30827.1 gb:NM_006925.1
203380_x_at_HG-U133A	SFRS5	splicing factor, arginine/serine-rich 5	gb:NM_001345.1 /DEF=Homo sapiens diacylglycerol kinase, alpha (80kD) (DGKA), mRNA, /FEA=mRNA /GEN=DGKA /PROD=diacylglycerol kinase, alpha (80kD) /DB_XREF=gi:11415023 /UG=Hs.172690 diacylglycerol kinase, alpha (80kD) /FL=gb:NM_001345.1 gb:AF064770.1
203385_at_HG-U133A	DGKA	diacylglycerol kinase, alpha (80kD)	Consensus includes gb:AI650848 /FEA=EST /DB_XREF=gi:4734827 /DB_XREF=est:wa95d04.x1 /CLONE=IMAGE:2303911 /UG=Hs.173802 KIAA0603 gene product /FL=gb:AB011175.1 gb:NM_014832.1
203386_at_HG-U133A	KIAA0603	KIAA0603 gene product	gb:NM_014832.1 /DEF=Homo sapiens KIAA0603 gene product (KIAA0603), mRNA, /FEA=mRNA /GEN=KIAA0603 /PROD=KIAA0603 gene product
203387_s_at_HG-U133A	KIAA0603	KIAA0603 gene product	

			/DB_XREF=gi:7662197 /UG=Hs.173802 KIAA0603 gene product -
			/FL=gb:AB011175.1 gb:NM_014832.1
203394_s_at_HG-U133A	HRY	hairy homolog (Drosophila)	Consensus includes gb:BE973687 /FEA=EST /DB_XREF=gi:10587023
			/DB_XREF=est:601680868F1 /CLONE=IMAGE:3951041 /UG=Hs.250666 hairy (Drosophila)-homolog /FL=gb:AF264785.1 gb:NM_005524.2
203535_at_HG-U133A	\$100A9	S100 calcium binding protein A9 (calgranulin B)	gb:NM_002965.2 /DEF=Homo sapiens S100 calcium-binding protein A9 (calgranulin B) (S100A9), mRNA, /GEN=S100A9 /PROD=S100 calcium-binding protein A9 (calgranulin B) /FL=gb:M25311.1 gb:NM_002965.2
203544_s_at_HG-U133A	STAM	signal transducing adaptor molecule (SH3 domain and ITAM motif) 1	gb:NM_003473.1 /DEF=Homo sapiens signal transducing adaptor molecule (SH3 domain and ITAM motif) 1 (STAM), mRNA, /FEA=mRNA /GEN=STAM /PROD=signal transducing adaptor molecule (SH3 domain and ITAM motif) 1 /DB_XREF=gi:4507248 /UG=Hs.153487 signal transducing adaptor molecule (SH3 domain and ITAM motif) 1 /FL=gb:U43899.1 gb:NM_003473.1
203556_at_HG-U133A	KIAA0854	KIAA0854 protein	gb:NM_014943.1 /DEF=Homo sapiens KIAA0854 protein (KIAA0854), mRNA, /FEA=mRNA /GEN=KIAA0854 /PROD=KIAA0854 protein /DB_XREF=gi:7662341 /UG=Hs.30209 KIAA0854 protein /FL=gb:AB020661.1
203593_at_HG-U133A	CD2AP	CD2-associated protein	gb:NM_014943.1 /DEF=Homo sapiens CD2-associated protein (CD2AP), mRNA, /FEA=mRNA /GEN=CD2AP /PROD=CD2-associated protein /DB_XREF=gi:11321633 /UG=Hs.265561 CD2-associated protein /FL=gb:NM_012120.1 gb:AF146277.1 gb:AF164377.1
203602_s_at_HG-U133A	ZNF151	zinc finger protein 151 (pHZ-67)	gb:NM_003443.1 /DEF=Homo sapiens zinc finger protein 151 (pHZ-67) (ZNF151), mRNA, /FEA=mRNA /GEN=ZNF151 /PROD=zinc finger protein 151 (pHZ-67) /DB_XREF=gi:4507996 /UG=Hs.33532 zinc finger protein 151 (pHZ-67) /FL=gb:NM_003443.1
203607_at_HG-U133A	SAC2	Sac domain-containing inositol phosphatase 2	gb:NM_014937.1 /DEF=Homo sapiens KIAA0966 protein (KIAA0966), mRNA, /FEA=mRNA /GEN=KIAA0966 /PROD=KIAA0966 protein

			/DB_XREF=gi:7662413 /UG=Hs.52463 KIAA0966 protein /FL=gb:AF113227.1 gb:AB023183.1 gb:NM_014937.1
			gb:NM_004244.1 /DEF=Homo sapiens CD163 antigen (CD163), mRNA. /FEA=mRNA /GEN=CD163 /PROD=CD163 antigen /FL=gb:NM_004244.1 /UG=Hs.74076 CD163 antigen /FL=gb:NM_004244.1
203645_s_at_HG-U133A	CD163	CD163 antigen	gb:NM_008858.1 /DEF=Homo sapiens putative T1ST2 receptor binding protein (IL1RL1LG), mRNA. /FEA=mRNA /GEN=IL1RL1LG /PROD=putative T1ST2 receptor binding protein /DB_XREF=gi:5803039 /UG=Hs.54411 putative T1ST2 receptor binding protein /FL=gb:U41804.1 gb:BC002443.1
203679_at_HG-U133A	IL1RL1LG		gb:NM_008858.1 putative T1/ST2 receptor binding protein
203685_at_HG-U133A	BCL2	B-cell CLL/lymphoma 2	gb:NM_000633.1 /DEF=Homo sapiens B-cell CLLlymphoma 2 (BCL2), nuclear gene encoding mitochondrial protein, transcript variant alpha, mRNA. /FEA=mRNA /GEN=BCL2 /PROD=B-cell lymphoma protein 2 alpha /DB_XREF=gi:4557354 /UG=Hs.79241 B-cell CLLlymphoma 2 /FL=gb:NM_13994.1 gb:NM_000633.1
203725_at_HG-U133A	GADD45A		gb:NM_001924.2 /DEF=Homo sapiens growth arrest and DNA-damage-inducible, alpha (GADD45A), mRNA. /FEA=mRNA /GEN=GADD45A /PROD=growth arrest and DNA-damage-inducible, alpha /DB_XREF=gi:9790904 /UG=Hs.80409 growth arrest and DNA-damage-inducible, alpha /FL=gb:NM_001924.2
203729_at_HG-U133A	EMP3		gb:NM_001425.1 /DEF=Homo sapiens epithelial membrane protein 3 (EMP3), mRNA. /FEA=mRNA /GEN=EMP3 /PROD=epithelial membrane protein 3 /DB_XREF=gi:4503562 /UG=Hs.9999 epithelial membrane protein 3 /FL=gb:U52101.1 gb:U87947.1 gb:NM_001425.1
203731_s_at_HG-U133A	ZFP95		gb:NM_014569.1 /DEF=Homo sapiens zinc finger protein homologous to Zfp95 in mouse (ZFP95), mRNA. /FEA=mRNA /GEN=ZFP95 /PROD=zinc finger protein homologous to Zfp95 in mouse /UG=Hs.110839 zinc finger protein homologous to Zfp95 in mouse

			/FL=gb:NM_014569.1 /gb:AB023232.1
			gb:NM_003199.1 /DEF=Homo sapiens transcription factor 4 (TCF4), mRNA /FEA=mRNA /GEN=TCF4 /PROD=transcription factor 4, isoform b
203753_at_HG-U133A	TCF4	transcription factor 4	/DB_XREF=gi:4507398 /UG=Hs.326198 transcription factor 4 /FL=gb:NM_003199.1
203757_s_at_HG-U133A	CEACAM6	carinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)	gb:BC005008.1 /DEF=Homo sapiens, carinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen), clone MGC:10467, mRNA, complete cds. /FEA=mRNA /PROD=carinoembryonic antigen-related cell adhesionmolecule 6 (non-specific cross reacting antigen) /DB_XREF=gi:13477106 /UG=Hs.73848 carinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen) /FL=gb:BC005008.1 gb:M18216.1 gb:NM29541.1 gb:NM_002483.1
203787_at_HG-U133A	SSBP2	single-stranded DNA binding protein 2	gb:NM_012446.1 /DEF=Homo sapiens single-stranded-DNA-binding protein (SSBP2), mRNA. /FEA=mRNA /GEN=SSBP2 /PROD=single-stranded-DNA-binding protein /DB_XREF=gi:7106422 /UG=Hs.169833 single-stranded-DNA-binding protein /FL=gb:AL080076.1 gb:AF161465.1 gb:NM_012446.1
203795_s_at_HG-U133A	BCL7A	B-cell CLL/lymphoma 7A	gb:NM_020993.1 /DEF=Homo sapiens B-cell CLLlymphoma 7A (BCL7A), mRNA. /FEA=mRNA /GEN=BCL7A /PROD=B-cell CLLlymphoma 7A /DB_XREF=gi:10337612 /UG=Hs.211563 B-cell CLLlymphoma 7A /FL=gb:NM_020993.1
203796_s_at_HG-U133A	BCL7A	B-cell CLL/lymphoma 7A	Consensus includes gb:AI950380 /FEA=EST /DB_XREF=gi:5742690 /DB_XREF=est:wp10g03.x1 /CLONE=IMAGE:2464468 /UG=Hs.211563 B-cell CLLlymphoma 7A /FL=gb:NM_020993.1
203808_at_HG-U133A	AKT2	v-akt murine thymoma viral oncogene homolog 2	Consensus includes gb:M95936.1 /DEF=human protein-serinethreonine (AKT2) mRNA, complete cds. /FEA=mRNA /GEN=AKT2 /PROD=protein serinethreonine kinase /DB_XREF=gi:178325 /UG=Hs.326445 v-akt murine thymoma viral oncogene homolog 2 /FL=gb:NM05936.1 gb:NM_001626.2
203818_s_at_HG-	SF3A3	splicing factor 3a, subunit 3, 60kD	gb:NM_006802.1 /DEF=Homo sapiens splicing factor 3a, subunit 3, 60kD

U133A			(SF3A3), mRNA. /FEA=mRNA /GEN=SF3A3 /PROD=splicing factor 3a, subunit 3, 60kD /DB_XREF=gi:5803166 /UG=Hs.77897 splicing factor 3a, subunit 3, 60kD /FL=gb:BC002395.1 gb:NM_006802.1
203857_s_at_HG-U133A	PDIR	for protein disulfide isomerase-related	gb:NM_006810.1 /DEF=Homo sapiens for protein disulfide isomerase-related (PDIR), mRNA. /FEA=mRNA /GEN=PDIR /PROD=for protein disulfide isomerase-related /DB_XREF=gi:5803120 /UG=Hs.76901 for protein disulfide isomerase-related /FL=gb:D49490.1 gb:NM_006810.1
203859_s_at_HG-U133A	PALM	paralemmin	gb:NM_002579.1 /DEF=Homo sapiens paralemmin (PALM), mRNA. /FEA=mRNA /GEN=PALM /PROD=paralemmin /DB_XREF=gi:4557041 /UG=Hs.78482 paralemmin /FL=gb:NM_002579.1
203881_s_at_HG-U133A	DMD	dystrophin (muscular dystrophy, Duchenne and Becker types)	gb:NM_004010.1 /DEF=Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427p2, mRNA. /FEA=mRNA /GEN=DMD /PROD=dystrophin Dp427p2 isoform /DB_XREF=gi:5032314 /UG=Hs.169470 dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 /FL=gb:NM_004010.1
203897_at_HG-U133A	LOC57149	hypothetical protein A-211C6.1	Consensus includes gb:BE963444 /FEA=EST /DB_XREF=gi:11766863 /DB_XREF=est6016577224R1 /CLONE=IMAGE:3866357 /UG=Hs.288607 hypothetical protein A-211C6.1 /FL=gb:NM_020424.1
203904_x_at_HG-U133A	KAI1	kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4))	gb:NM_002231.2 /DEF=Homo sapiens kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4)) (KAI1), mRNA. /FEA=mRNA /GEN=KAI1 /PROD=kangai 1 /DB_XREF=gi:13259537 /UG=Hs.323949 kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4)) /FL=gb:BC000726.1 gb:BC001821.1 gb:NM_002231.2 gb:U20770.1

203910_at_HG-U133A	PARG1	PTPL1-associated RhoGAP 1	gb:NM_004815.1 /DEF=Homo sapiens PTPL1-associated RhoGAP - (PARG1), mRNA, /FEA=mRNA /GEN=PARG1 /PROD=PTPL1-associated RhoGAP 1 /DB_XREF=gi:4758881 /UG=Hs.70983 PTPL1-associated RhoGAP 1 /FL=gb:U90920.1 gb:NM_004815.1
203932_at_HG-U133A	HLA-DMB	major histocompatibility complex; class II, DM beta	gb:NM_002118.1 /DEF=Homo sapiens major histocompatibility complex, class II, DM beta (HLA-DMB), mRNA, /FEA=mRNA /GEN=HLA-DMB /PROD=major histocompatibility complex, class II, DM beta /DB_XREF=gi:4504398 /UG=Hs.1162 major histocompatibility complex, class II, DM beta /FL=gb:NM_002118.1 gb:U15085.1
203936_s_at_HG-U133A	MMP9	matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase)	gb:NM_004994.1 /DEF=Homo sapiens matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase) /GEN=MMP9, mRNA, /FEA=mRNA /PROD=matrix metalloproteinase 9 preprotein /DB_XREF=gi:4826835 /UG=Hs.151738 matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase) /FL=gb:J05070.1 gb:NM_004994.1
203939_at_HG-U133A	NT5E	5'-nucleotidase, ecto (CD73)	gb:NM_002526.1 /DEF=Homo sapiens 5 nucleotidase (CD73) (NT5), mRNA, /FEA=mRNA /GEN=NT5 /PROD=5 nucleotidase /DB_XREF=gi:4505466 /UG=Hs.153952 5 nucleotidase (CD73) /FL=gb:NM_002526.1 /UG=Hs.1817 myeloperoxidase mRNA, complete cds. /DB_XREF=gi:189039
203948_s_at_HG-U133A	MPO	myeloperoxidase	gb:NM_002694.1 /DEF=Human myeloperoxidase mRNA, complete cds. /GEN=MPO /PROD=myeloperoxidase /DB_XREF=gi:J02694.1 /UG=Hs.19507.1 gb:J02694.1 gb:NM_00250.1
203949_at_HG-U133A	MPO	myeloperoxidase	gb:NM_000250.1 /DEF=Homo sapiens myeloperoxidase (MPO), nuclear gene encoding mitochondrial protein, mRNA, /FEA=mRNA /GEN=MPO /PROD=myeloperoxidase /DB_XREF=gi:4557758 /UG=Hs.1817 myeloperoxidase /FL=gb:M19507.1 gb:J02694.1 gb:NM_000250.1
203973_s_at_HG-U133A	CEBPD	CCAAT/enhancer binding protein (C/EBP), delta	gb:NM_005195.1 /DEF=Homo sapiens CCAAT/enhancer binding protein (CEBP), delta (CEBPD), mRNA, /FEA=mRNA /GEN=CEBPD

			/PROD=CCAATenhancer binding protein (CEBP), delta /DB_XREF=gi:4885130 /UG=Hs.76722 CCAATenhancer binding protein (CEBP), delta /FL=gb:MS3667.1 gb:NM_005195.1
204000_at_HG-U133A	GNB5	guanine nucleotide binding protein (G protein), beta 5	gb:NM_016194.1 /DEF=Homo sapiens hypothetical protein (DKTp586O1922). mRNA. /FEA=mRNA /GEN=DKTp586O1922 /PROD=hypothetical protein /DB_XREF=gi:7705366 /UG=Hs.155090 hypothetical protein /FL=gb:AL117471.1 gb:NM_016194.1
204030_s_at_HG-U133A	SCHIP1	schwannomin interacting protein 1	gb:NM_04575.1 /DEF=Homo sapiens schwannomin interacting protein 1 (SCHIP-1). mRNA. /FEA=mRNA /GEN=SCHIP-1 /PROD=schwannomin interacting protein 1 /DB_XREF=gi:7657539 /UG=Hs.61490 schwannomin interacting protein 1 /FL=gb:AF145713.1 gb:NM_014575.1
204044_at_HG-U133A	QPRT	quinolinate phosphoribosyltransferase (nicotinate-nucleotide pyrophosphorylase (carboxylating))	gb:NM_014298.2 /DEF=Homo sapiens quinolinate phosphoribosyltransferase (nicotinate-nucleotide pyrophosphorylase (carboxylating)) (QPRT), mRNA. /FEA=mRNA /GEN=QPRT /PROD=quinolinate phosphoribosyltransferase /DB_XREF=gi:9257236 /UG=Hs.8935 quinolinate phosphoribosyltransferase (nicotinate-nucleotide pyrophosphorylase (carboxylating)) /FL=gb:D78177.1
204057_at_HG-U133A	ICSBP1	interferon consensus sequence binding protein 1	gb:BC005060.1 gb:NM_014298.2 Consensus includes gb:AI07394 /FEA=EST /DB_XREF=gi:34006328 /DB_XREF=est066c05.x1 /CLONE=IMAGE:1670792 /UG=Hs.14453 interferon consensus sequence binding protein 1 /FL=gb:M91196.1 gb:NM_002163.1
204069_at_HG-U133A	MEIS1	Meis1, myeloid ecotropic viral integration site 1 homolog (mouse)	gb:NM_002398.1 /DEF=Homo sapiens Meis1 (mouse) homolog (MEIS1), mRNA. /FEA=mRNA /GEN=MEIS1 /PROD=Meis1 homolog /DB_XREF=gi:4505150 /UG=Hs.170177 Meis1 (mouse) homolog /FL=gb:U85707.1 gb:NM_002398.1
204075_s_at_HG-U133A	KIAA0562	KIAA0562 gene product	gb:NM_014704.1 /DEF=Homo sapiens KIAA0562 gene product (KIAA0562), mRNA. /FEA=mRNA /GEN=KIAA0562 /PROD=KIAA0562 gene product /DB_XREF=gi:7662179 /UG=Hs.200595 KIAA0562 gene product /FL=gb:AB011134.1 gb:NM_014704.1

204082_at_HG-U133A	PBX3	pre-B-cell leukemia transcription factor 3	gb:NM_006195.1 /DEF=Homo sapiens pre-B-cell leukemia transcription factor 3 (PBX3), mRNA. /FEA=mRNA /GEN=PBX3 /PROD=pre-B-cell leukemia transcription factor 3 /DB_XREF=gi:5453851 /UG=Hs.294101 pre-B-cell leukemia transcription factor 3 /FL=gb:NM_006195.1
204101_at_HG-U133A	MTM1	myotubular myopathy 1	gb:NM_000252.1 /DEF=Homo sapiens myotubular myopathy 1 (MTM1), mRNA. /FEA=mRNA /GEN=MTM1 /PROD=myotubular myopathy 1 /DB_XREF=gi:4557895 /UG=Hs.75302 myotubular myopathy 1 /FL=gb:U46024.1 gb:NM_000252.1
204112_s_at_HG-U133A	HNMT	histamine N-methyltransferase	gb:NM_006895.1 /DEF=Homo sapiens histamine N-methyltransferase mRNA. /FEA=mRNA /GEN=HNMT /PROD=histamine N-methyltransferase /DB_XREF=gi:5901969 /UG=Hs.81182 histamine N-methyltransferase /FL=gb:U08092.1 gb:D16224.1 gb:NM_006895.1
204116_at_HG-U133A	IL2RG	interleukin 2 receptor, gamma (severe combined immunodeficiency)	gb:NM_000206.1 /DEF=Homo sapiens interleukin 2 receptor, gamma (severe combined immunodeficiency) (IL2RG), mRNA. /FEA=mRNA /GEN=IL2RG /PROD=interleukin 2 receptor, gamma chain, precursor /DB_XREF=gi:4557881 /UG=Hs.84 interleukin 2 receptor, gamma (severe combined immunodeficiency) /FL=gb:NM_000206.1
204118_at_HG-U133A	CD48	CD48 antigen (B-cell membrane protein)	gb:NM_001778.1 /DEF=Homo sapiens CD48 antigen (B-cell membrane protein) (CD48), mRNA. /FEA=mRNA /GEN=CD48 /PROD=CD48 antigen (B-cell membrane protein) /DB_XREF=gi:4502674 /UG=Hs.901 CD48 antigen (B-cell membrane protein) /FL=gb:M59904.1 gb:NM_001778.1
204150_at_HG-U133A	STAB1	stabin 1	gb:NM_015136.1 /DEF=Homo sapiens KIAA0246 protein (KIAA0246), mRNA /FEA=mRNA /GEN=KIAA0246 /PROD=KIAA0246 protein /DB_XREF=gi:12225239 /UG=Hs.301989 KIAA0246 protein /FL=gb:NM_015136.1
204163_at_HG-U133A	EMILIN	elastin microfibril interface located protein	gb:NM_007046.1 /DEF=Homo sapiens elastin microfibril interface located protein (EMILIN), mRNA. /FEA=mRNA /GEN=EMILIN /PROD=elastin microfibril interface located protein /DB_XREF=gi:5901943 /UG=Hs.63348

		elastin microfibril interface located protein /FL=gb:AF088916.1 gb:NM_007046.1
		gb:NM_001629.1 /DEF=Homo sapiens arachidonate 5-lipoxygenase-activating protein (ALOX5AP), mRNA. /FEA=mRNA /GEN=ALOX5AP /PROD=arachidonate 5-lipoxygenase-activating protein /DB_XREF=gi:4502058 /UG=Hs.100194 arachidonate 5-lipoxygenase-activating protein /FL=gb:NM_001629.1
204174_at_HG-U133A	ALOX5AP	arachidonate 5-lipoxygenase-activating protein gb:NM_001774.1 /DEF=Homo sapiens CD37 antigen (CD37), mRNA. /FEA=mRNA /GEN=CD37 /PROD=CD37 antigen /DB_XREF=gi:4502662 /UG=Hs.153053 CD37 antigen /FL=gb:NM_001774.1
204192_at_HG-U133A	CD37	CD37 antigen gb:NM_014636.1 /DEF=Homo sapiens Ral guanine nucleotide exchange factor RalGPS1A (RalGPS1A), mRNA. /FEA=mRNA /GEN=RalGPS1A /PROD=Ral guanine nucleotide exchange factor RalGPS1A /DB_XREF=gi:7662069 /UG=Hs.170307 Ral guanine nucleotide exchange factor RalGPS1A /FL=gb:AB002349.1 gb:NM_014636.1
204199_at_HG-U133A	RALGPS1A	Ral guanine nucleotide exchange factor RalGPS1A gb:NM_021822.1 /DEF=Homo sapiens phorbolin-like protein MDS019 (MDS019), mRNA. /FEA=mRNA /GEN=MDS019 /PROD=phorbolin-like protein MDS019 /DB_XREF=gi:13399333 /UG=Hs.250619 phorbolin-like protein MDS019 /FL=gb:AF182420.1 gb:NM_021822.1
204205_at_HG-U133A	MDS019	phorbolin-like protein MDS019 gb:NM_003800.1 /DEF=Homo sapiens RNA guanylyltransferase and 5-phosphatase (RNGTT), mRNA /GEN=RNGTT /PROD=RNA guanylyltransferase and 5-phosphatase /DB_XREF=gi:4506562 /UG=Hs.27345 RNA guanylyltransferase and 5-phosphatase /FL=gb:AF025654.1 gb:AB012142.1 gb:AB009022.1 gb:NM_003800.1
204208_at_HG-U133A	RNGTT	RNA guanylyltransferase and 5'-phosphatase gb:NM_006834.1 /DEF=Homo sapiens RAB32, member RAS oncogene family (RAB32), mRNA. /FEA=mRNA /GEN=RAB32 /PROD=RAB32, member RAS oncogene family /DB_XREF=gi:5803132 /UG=Hs.32217 RAB32, member RAS oncogene family /FL=gb:U71127.1 gb:NM_006834.1
204214_s_at_HG-U133A	RAB32	RAB32, member RAS oncogene family

		gb:NM_024315.1 /DEF=Homo sapiens hypothetical protein MGC4175 (MGC4175), mRNA. /FEA=mRNA /GEN=MGC4175 /PROD=hypothetical protein MGC4175 /DB_XREF=gi:13236556 /UG=Hs.322404 hypothetical protein MGC4175 /FL=gb:BC002837.1 gb:NM_024315.1
204215_at_HG-U133A	MGC4175	hypothetical protein MGC4175
204225_at_HG-U133A	HDAC4	histone deacetylase 4
204227_s_at_HG-U133A	TK2	thymidine kinase 2, mitochondrial thymidine kinase 2, mitochondrial
204249_s_at_HG-U133A	LMO2	LIM domain only 2 (rhombotin-like 1)
204269_at_HG-U133A	PIM2	pim-2 oncogene
204285_s_at_HG-U133A	PMAP1	phorbol-12-myristate-13-acetate-induced protein 1
204306_s_at_HG-U133A	CD151	CD151 antigen
204319_s_at_HG-U133A	RGS10	regulator of G-protein signalling 10

			signalling 10 /DB_XREF=gi:11184225 /UG=Hs.82280 regulator of G-protein signalling 10 /FL=gb:NM_002925.2 gb:AF045229.1
			gb:NM_007267.2 /DEF=Homo sapiens expressed in activated TLAK lymphocytes (LAK-4P), mRNA, /FEA=mRNA /GEN=LAK-4P /PROD=expressed in activated TLAK lymphocytes /DB_XREF=gi:7305226 /UG=Hs.16165 expressed in activated TLAK lymphocytes /FL=gb:AB002405.2
204328_at_HG-U133A	LAK-4P		expressed in activated TLAK lymphocytes
204348_s_at_HG-U133A	AK3	adenylylate kinase 3	gb:NM_013410.1 /DEF=Homo sapiens adenylylate kinase 3 (AK3), nuclear gene encoding mitochondrial protein, mRNA, /FEA=mRNA /GEN=AK3 /PROD=adenylylate kinase 3 /DB_XREF=gi:8051578 /UG=Hs.274691 adenylylate kinase 3 /FL=gb:NM_013410.1
204351_at_HG-U133A	S100P		gb:NM_005980.1 /DEF=Homo sapiens S100 calcium-binding protein P (S100P), mRNA, /FEA=mRNA /GEN=S100P /PROD=S100 calcium-binding protein P /DB_XREF=gi:5174662 /UG=Hs.29662 S100 calcium-binding protein P /FL=gb:NM_005980.1
204352_at_HG-U133A	TRAF5	TNF receptor-associated factor 5	gb:NM_004619.1 /DEF=Homo sapiens TNF receptor-associated factor 5 (TRAF5), mRNA, /FEA=mRNA /GEN=TRAF5 /PROD=TNF receptor-associated factor 5 /DB_XREF=gi:11321602 /UG=Hs.29736 TNF receptor-associated factor 5 /FL=gb:NM_004619.1 gb:AB000509.1
204401_at_HG-U133A	KCNN4		gb:NM_002250.1 /DEF=Homo sapiens potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4 (KCNN4), mRNA, /FEA=mRNA /GEN=KCNN4 /PROD=potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4 /DB_XREF=gi:4504858 /UG=Hs.10082 potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4 /FL=gb:AF000972.1 gb:AF033021.1 gb:AF022150.1 gb:AF022797.1
204422_s_at_HG-	FGF2	fibroblast growth factor 2 (basic)	gb:NM_002006.1 /DEF=Homo sapiens fibroblast growth factor 2 (basic)

U133A			(FGF2), mRNA, /FEA=mRNA /GEN=FGF2 /PROD=fibroblast growth factor 2 (basic) /DB_XREF=gi:4503698 /UG=Hs.284244 fibroblast growth factor 2 (basic) /FL=gb:M27968.1 gb:NM_002006.1
204425_at_HG-U133A	ARHGAP4	Rho GTPase activating protein 4	gb:NM_001666.1 /DEF=Homo sapiens Rho GTPase activating protein 4 (ARHGAP4), mRNA, /FEA=mRNA /GEN=ARHGAP4 /PROD=Rho GTPase activating protein 4 /DB_XREF=gi:11386132 /UG=Hs.3109 Rho GTPase activating protein 4 /FL=gb:NM_001666.1
204446_s_at_HG-U133A	ALOX5	arachidonate 5-lipoxygenase	gb:NM_000698.1 /DEF=Homo sapiens arachidonate 5-lipoxygenase (ALOX5), mRNA, /FEA=mRNA /GEN=ALOX5 /PROD=arachidonate 5-lipoxygenase /DB_XREF=gi:4502056 /UG=Hs.89499 arachidonate 5-lipoxygenase /FL=gb:J03600.1 gb:J03571.1 gb:NM_000698.1
204484_at_HG-U133A	PIK3C2B	phosphoinositide-3-kinase, class 2, beta polypeptide	gb:NM_002646.1 /DEF=Homo sapiens phosphoinositide-3-kinase, class 2, beta polypeptide (PIK3C2B), mRNA, /FEA=mRNA /GEN=PIK3C2B /PROD=phosphoinositide-3-kinase, class 2, betapolypeptide /DB_XREF=gi:11136637 /UG=Hs.132463 phosphoinositide-3-kinase, class 2, beta polypeptide /FL=gb:NM_002646.1
204495_s_at_HG-U133A	DKFZP434H132	DKFZP434H132 protein	gb:NM_015492.1 /DEF=Homo sapiens DKFZP434H132 protein (DKFZP434H132), mRNA, /FEA=mRNA /GEN=DKFZP434H132 /PROD=DKFZP434H132 protein /DB_XREF=gi:7661575 /UG=Hs.17936 DKFZP434H132 protein /FL=gb:BC000540.1 gb:NM_015492.1
204501_at_HG-U133A	NOV	nephroblastoma overexpressed gene	gb:NM_002514.1 /DEF=Homo sapiens nephroblastoma overexpressed gene (NOV), mRNA, /FEA=mRNA /GEN=NOV /PROD=nephroblastoma overexpressed gene /DB_XREF=gi:4505422 /UG=Hs.235935 nephroblastoma overexpressed gene /FL=gb:NM_002514.1
204511_at_HG-U133A	KIAA0793	KIAA0793 gene product	gb:NM_014808.1 /DEF=Homo sapiens KIAA0793 gene product (KIAA0793), mRNA, /FEA=mRNA /GEN=KIAA0793 /PROD=KIAA0793 gene product /DB_XREF=gi:7662309 /UG=Hs.301283 KIAA0793 gene product /FL=gb:AB018336.1 gb:NM_014808.1

		gb:NM_002114.1 /DEF=Homo sapiens human immunodeficiency virus type 1 enhancer-binding protein 1 (HIVEP1), mRNA. /FEA=mRNA /GEN=HIVEP1 /PROD=human immunodeficiency virus type enhancer-binding protein 1 /DB_XREF=gi:4504388 /UG=Hs.306 human immunodeficiency virus type 1 enhancer-binding protein 1 /FL=gb:NM_002114.1
204512_at_HG-U133A	HIVEP1	human immunodeficiency virus type 1 enhancer binding protein 1
204562_at_HG-U133A	IRF4	interferon regulatory factor 4
204563_at_HG-U133A	SELL	selectin L (lymphocyte adhesion molecule 1)
204604_at_HG-U133A	PFTK1	PFTAIRE protein kinase 1
204638_at_HG-U133A	ACP5	acid phosphatase 5, tartrate resistant
204647_at_HG-U133A	HOMER-3	Homer, neuronal immediate early gene, 3
204661_at_HG-U133A	CDW52	CDW52 antigen (CAMPATH-1 antigen)

			(CAMPATH-1 antigen) /DB_XREF=gi:4502760 /UG=Hs.276770 CDW52
			antigen (CAMPATH-1 antigen) /FL=gb:BC000644.1 gb:NM_001803.1
204663_at_HG-U133A	ME3	mitochondrial malic enzyme 3, NADP(+)-dependent	gb:NM_006680.1 /DEF=Homo sapiens malic enzyme 3, NADP(+)-dependent mitochondrial (ME3), mRNA. /FEA=mRNA /GEN=ME3 /PROD=malic enzyme 3, NADP(+)-dependent,mitochondrial /DB_XREF=gi:5729919 /UG=Hs.2838
204670_x_at_HG-U133A	HLA-DRB5	major histocompatibility complex, class II, DR beta 5	gb:NM_002125.1 /DEF=Homo sapiens major histocompatibility complex, class II, DR beta 5 (HLA-DRB5), mRNA. /FEA=mRNA /GEN=HLA-DRB5 /PROD=major histocompatibility complex, class II, DRbeta 5 /DB_XREF=gi:4504412 /UG=Hs.308026 major histocompatibility complex, class II, DR beta 5 /FL=gb:M11867.1 gb:NM20430.1 gb:NM_002125.1
204672_s_at_HG-U133A	ANKRD6	ankyrin repeat domain 6	gb:NM_014942.1 /DEF=Homo sapiens KIAA0957 protein (KIAA0957), mRNA /FEA=mRNA /GEN=KIAA0957 /PROD=KIAA0957 protein /DB_XREF=gi:7662405 /UG=Hs.30991 KIAA0957 protein /FL=gb:AB023174.1
204674_at_HG-U133A	LRMP	- lymphoid-restricted membrane protein	gb:NM_006152.1 /DEF=Homo sapiens lymphoid-restricted membrane protein (LRMP), mRNA. /FEA=mRNA /GEN=LRMP /PROD=lymphoid-restricted membrane protein /DB_XREF=gi:5453723 /UG=Hs.40202 lymphoid-restricted membrane protein /FL=gb:U10485.1 gb:NM_006152.1
204703_at_HG-U133A	TG737	Probe hTg737 (polycystic kidney disease, autosomal recessive, in)	gb:NM_006531.1 /DEF=Homo sapiens Probe hTg737 (polycystic kidney disease, autosomal recessive, in) (TG737), mRNA. /FEA=mRNA /GEN=TG737 /PROD=Tg737 protein /DB_XREF=gi:5729799 /UG=Hs.2291 Probe hTg737 (polycystic kidney disease, autosomal recessive, in) /FL=gb:NM_006531.1 gb:U20362.1
204731_at_HG-U133A	TGFBR3	transforming growth factor, beta receptor III (betaglycan, 300kD)	gb:NM_003243.1 /DEF=Homo sapiens transforming growth factor, beta receptor III (betaglycan, 300kD) (TGFBR3), mRNA. /FEA=mRNA /GEN=TGFBR3 /PROD=transforming growth factor, beta receptor III (betaglycan, 300kD) /DB_XREF=gi:4507470 /UG=Hs.79059 transforming

		growth factor, beta receptor III (betaglycan, 300kD) /FL=gb:NM_003243.1 gb:L07594.1
204776_at_HG-U133A	THBS4	gb:NM_003248.1 /DEF=Homo sapiens thrombospondin 4 (THBS4), mRNA. /FEA=mRNA /GEN=THBS4 /PROD=thrombospondin 4 /DB_XREF=gi:4507488 /UG=Hs.75774 thrombospondin 4 /FL=gb:NM_003248.1
204793_at_HG-U133A	KIAA0443	gb:NM_014710.1 /DEF=Homo sapiens KIAA0443 gene product (KIAA0443), mRNA. /FEA=mRNA /GEN=KIAA0443 /PROD=KIAA0443 gene product /DB_XREF=gi:7662129 /UG=Hs.113082 KIAA0443 gene product /FL=gb:AB007903.1 gb:NM_014710.1
204798_at_HG-U133A	MYB	gb:NM_005375.1 /DEF=Homo sapiens v-myb avian myeloblastosis viral oncogene homolog (MYB), mRNA. /FEA=mRNA /GEN=MYB /PROD=v-myb avian myeloblastosis viral oncogenehomolog /DB_XREF=gi:4885496 /UG=Hs.1334 v-myb avian myeloblastosis viral oncogene homolog /FL=gb:NM_015024.1 gb:AF104863.1 gb:NM_005375.1
204811_s_at_HG-U133A	CACNA2D2	gb:NM_006030.1 /DEF=Homo sapiens calcium channel, voltage-dependent, alpha 2delta subunit 2 (CACNA2D2), mRNA. /FEA=mRNA /GEN=CACNA2D2 /PROD=calcium channel, voltage-dependent, alpha2delta subunit 2 /DB_XREF=gi:5174402 /UG=Hs.127436 calcium channel, voltage-dependent, alpha 2delta subunit 2 /FL=gb:AF040709.1 gb:NM_006030.1
204858_s_at_HG-U133A	ECGF1	gb:NM_001953.2 /DEF=Homo sapiens endothelial cell growth factor 1 (platelet-derived) (ECGF1), mRNA. /FEA=mRNA /GEN=ECGF1 /PROD=endothelial cell growth factor 1(platelet-derived) /DB_XREF=gi:7669488 /UG=Hs.73946 endothelial cell growth factor 1 (platelet-derived) /FL=gb:NM_001953.2
204882_at_HG-U133A	KIAA0053	gb:NM_014882.1 /DEF=Homo sapiens KIAA0053 gene product (KIAA0053), mRNA. /FEA=mRNA /GEN=KIAA0053 /PROD=KIAA0053 gene product /DB_XREF=gi:7661881 /UG=Hs.1528 KIAA0053 gene product /FL=gb:D29642.1 gb:NM_014882.1

204891_s_at_HG-U133A	LCK	lymphocyte-specific protein tyrosine kinase	gb:NM_005356.1 /DEF=Homo sapiens lymphocyte-specific protein tyrosine kinase (LCK), mRNA /FEA=mRNA /GEN=LCK /PROD=lymphocyte-specific protein tyrosine kinase /DB_XREF=gi:4885448 /UG=Hs.1765 lymphocyte-specific protein tyrosine kinase /FL=gb:M36881.1 gb:U07236.1
204922_at_HG-U133A	FLJ22531	hypothetical protein FLJ22531	gb:NM_024650.1 /DEF=Homo sapiens hypothetical protein FLJ22531 /PROD=hypothetical protein (FLJ22531), mRNA /FEA=mRNA /GEN=FLJ22531 /UG=Hs.13375894 /DB_XREF=gi:13375894 /UG=Hs.55613 hypothetical protein
204951_at_HG-U133A	ARHH	ras homolog gene family, member H	gb:NM_004310.1 /DEF=Homo sapiens ras homolog gene family, member H (ARHH), mRNA /FEA=mRNA /GEN=ARHH /PROD=ras homolog gene family, member H /DB_XREF=gi:4757769 /UG=Hs.109918 ras homolog gene family, member H /FL=gb:NM_004310.1
204992_s_at_HG-U133A	PFN2	profilin 2	gb:NM_002628.1 /DEF=Homo sapiens profilin 2 (PFN2), mRNA /FEA=mRNA /GEN=PFN2 /PROD=profilin 2 /DB_XREF=gi:4505750 /UG=Hs.91747 profilin 2 /FL=gb:L10678.1 gb:NM_002628.1
205019_s_at_HG-U133A	VIPR1	vasoactive intestinal peptide receptor 1	gb:NM_004624.1 /DEF=Homo sapiens vasoactive intestinal peptide receptor 1 (VIPR1), mRNA /FEA=mRNA /GEN=VIPR1 /PROD=vasoactive intestinal peptide receptor 1 /DB_XREF=gi:4759307 /UG=Hs.198726 vasoactive intestinal peptide receptor 1 /FL=gb:NM_004624.1
205040_at_HG-U133A	ORM1	orosomucoid 1	gb:NM_000607.1 /DEF=Homo sapiens orosomucoid 1 (ORM1), mRNA /FEA=mRNA /GEN=ORM1 /PROD=orosomucoid 1 precursor /DB_XREF=gi:9257231 /UG=Hs.572 orosomucoid 1 /FL=gb:M13692.1
205041_s_at_HG-U133A	ORM1	orosomucoid 1	gb:NM_000607.1 /DEF=Homo sapiens orosomucoid 1 (ORM1), mRNA /FEA=mRNA /GEN=ORM1 /PROD=orosomucoid 1 precursor /DB_XREF=gi:9257231 /UG=Hs.572 orosomucoid 1 /FL=gb:M13692.1

205049_s_at_HG-U133A	CD79A	CD79A antigen (immunoglobulin-associated alpha) gb:NM_001783.1	/DEF=Homo sapiens CD79A antigen (immunoglobulin-associated alpha) (CD79A), transcript variant 1, mRNA. /FEA=mRNA /GEN=CD79A /PROD=CD79A antigen, isoform 1 precursor /DB_XREF=gi:4502684 /UG=Hs.79630 CD79A antigen (immunoglobulin-associated alpha) /FL=gb:NM80462.1 gb:M86921.1 gb:M74721.1 gb:NM_001783.1
205051_s_at_HG-U133A	KIT	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	gb:NM_000222.1 /DEF=Homo sapiens v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog (KIT), mRNA. /FEA=mRNA /GEN=KIT /PROD=v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog precursor /DB_XREF=gi:4557694 /UG=Hs.81665 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog /FL=gb:NM_000222.1
205055_at_HG-U133A	ITGAE	integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; alpha mucosal lymphocyte antigen 1; alpha polypeptide)	gb:NM_002208.3 /DEF=Homo sapiens integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; alpha polypeptide) (ITGAE), mRNA. /FEA=mRNA /GEN=ITGAE /PROD=integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; alpha polypeptide) /DB_XREF=gi:6007850 /UG=Hs.851 integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; alpha polypeptide) /FL=gb:L25851.2 gb:NM_002208.3
205059_s_at_HG-U133A	IDUA	iduronidase, alpha-L-	gb:NM_000203.1 /DEF=Homo sapiens iduronidase, alpha-L- (IDUA), mRNA /FEA=mRNA /GEN=IDUA /PROD=alpha-L-iduronidase precursor /DB_XREF=gi:4557660 /UG=Hs.89560 iduronidase, alpha-L- /FL=gb:M74715.1 gb:NM_000203.1
205074_at_HG-U133A	SLC22A5	solute carrier family 22 (organic cation transporter), member 5	gb:NM_003060.1 /DEF=Homo sapiens solute carrier family 22 (organic cation transporter), member 5 (SLC22A5), mRNA. /FEA=mRNA /GEN=SLC22A5 /PROD=solute carrier family 22 (organic cation transporter), member 5 /DB_XREF=gi:4507004 /UG=Hs.15813 solute carrier family 22 (organic cation transporter), member 5 /FL=gb:AB015050.1 gb:AF057164.1 gb:NM_003060.1
205076_s_at_HG-U133A	CRA	cisplatin resistance associated	gb:NM_006697.1 /DEF=Homo sapiens cisplatin resistance associated (CRA), mRNA. /FEA=mRNA /GEN=CRA /PROD=cisplatin resistance associated

			/DB_XREF=gi:5870890 /UG=Hs.166066 cisplatin resistance associated /FL=gb:U78557.1 gb:NM_006697.1
205101_at_HG-U133A	MHC2TA	MHC class II transactivator	gb:NM_00246.1 /DEF=Homo sapiens MHC class II transactivator (MHC2TA), mRNA, /FEA=mRNA /GEN=MHC2TA /PROD=MHC class II transactivator /DB_XREF=gi:4557748 /UG=Hs.3076 MHC class II transactivator /FL=gb:NM_000246.1 gb:U18259.1
205105_at_HG-U133A	MAN2A1	mannosidase, alpha, class 2A, member 1	gb:NM_002372.1 /DEF=Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA, /FEA=mRNA /GEN=MAN2A1 /PROD=mannosidase, alpha, class 2A, member 1 /DB_XREF=gi:4758697 /UG=Hs.32965 mannosidase, alpha, class 2A, member 1 /FL=gb:U31520.1 gb:NM_002372.1 gb:D63998.1
205110_s_at_HG-U133A	FGF13	fibroblast growth factor 13	gb:NM_004114.1 /DEF=Homo sapiens fibroblast growth factor 13 (FGF13), mRNA, /FEA=mRNA /GEN=FGF13 /PROD=fibroblast growth factor 13 /DB_XREF=gi:4758365 /UG=Hs.6540 fibroblast growth factor 13 /FL=gb:U66198.1 gb:AF100143.1 gb:NM_004114.1
205131_x_at_HG-U133A	SCGF	stem cell growth factor; lymphocyte secreted C-type lectin	gb:NM_002975.1 /DEF=Homo sapiens stem cell growth factor; lymphocyte secreted C-type lectin (SCGF), mRNA, /FEA=mRNA /GEN=SCGF /PROD=stem cell growth factor; lymphocyte secreted C-type lectin /DB_XREF=gi:4506802 /UG=Hs.105927 stem cell growth factor; lymphocyte secreted C-type lectin /FL=gb:AF020044.1 gb:AB009244.1 gb:NM_002975.1
205145_s_at_HG-U133A	MYL5	myosin, light polypeptide 5, regulatory	gb:NM_002477.1 /DEF=Homo sapiens myosin, light polypeptide 5, regulatory (MYL5), mRNA, /FEA=mRNA /GEN=MYL5 /PROD=myosin, light polypeptide 5, regulatory /DB_XREF=gi:4505304 /UG=Hs.170482 myosin, light polypeptide 5, regulatory /FL=gb:L03785.1 gb:NM_002477.1
205192_at_HG-U133A	MAP3K14	mitogen-activated protein kinase kinase kinase 14	gb:NM_003954.1 /DEF=Homo sapiens mitogen-activated protein kinase kinase 14 (MAP3K14), mRNA, /FEA=mRNA /GEN=MAP3K14 /PROD=mitogen-activated protein kinase kinase kinase 14 /DB_XREF=gi:4505396 /UG=Hs.47007 mitogen-activated protein kinase kinase 14

			kinase 14 /FL=gb:NM_003954.1
205223_at_HG-U133A	KIAA0645	KIAA0645 gene product	gb:NM_014662.1 /DEF=Homo sapiens KIAA0645 gene product (KIAA0645), mRNA, /FEA=mRNA /GEN=KIAA0645 /PROD=KIAA0645 gene product /DB_XREF=gi:7662221 /UG=Hs.155987 KIAA0645 gene product /FL=gb:AB014545.1 gb:NM_014662.1
205225_at_HG-U133A	ESR1	estrogen receptor 1	gb:NM_000125.1 /DEF=Homo sapiens estrogen receptor 1 (ESR1), mRNA, /FEA=mRNA /GEN=ESR1 /PROD=estrogen receptor 1 /DB_XREF=gi:4503602 /UG=Hs.1657 estrogen receptor 1 /FL=gb:NM_000125.1
205267_at_HG-U133A	POU2AF1	POU domain, class 2, associating factor 1	gb:NM_006235.1 /DEF=Homo sapiens POU domain, class 2, associating factor 1 (POU2AF1), mRNA, /FEA=mRNA /GEN=POU2AF1 /PROD=POU domain, class 2, associating factor 1 /DB_XREF=gi:5453933 /UG=Hs.2407 POU domain, class 2, associating factor 1 /FL=gb:NM_006235.1
205306_x_at_HG-U133A	KMO	kyurenine 3-monooxygenase (kyurenine 3-hydroxylase)	Consensus includes gb:AI074145 /FEA=EST /DB_XREF=gi:3400789 /DB_XREF=estov13a06.x1 /CLONE=IMAGE:1637170 /UG=Hs.107318 kyurenine 3-monooxygenase (kyurenine 3-hydroxylase) /FL=gb:NM_006235.1
205308_at_HG-U133A	LOC51101	CGI-62 protein	gb:NM_003679.1
205312_at_HG-U133A	SP1	spleen focus forming virus (SFFFV) proviral integration oncogene sp1	gb:NM_016010.1 /DEF=Homo sapiens CGI-62 protein (LOC51101), mRNA, /FEA=mRNA /GEN=LOC51101 /PROD=CGI-62 protein /DB_XREF=gi:7705774 /UG=Hs.118821 CGI-62 protein /FL=gb:AF151820.1 gb:NM_016010.1
205316_at_HG-U133A	SLC15A2	solute carrier family 15 (H ⁺ /peptide transporter), member 2	gb:NM_003120.1 /DEF=Homo sapiens spleen focus forming virus (SFFFV) proviral integration oncogene sp1 (SP1), mRNA, /FEA=mRNA /GEN=SP1 /PROD=spleen focus forming virus (SFFFV) proviral integration oncogene sp1 /DB_XREF=gi:4507174 /UG=Hs.157441 spleen focus forming virus (SFFFV) proviral integration oncogene sp1 /FL=gb:NM_003120.1
205349_at_HG-U133A	GNA15	guanine nucleotide binding protein (G	Consensus includes gb:BF223679 /FEA=EST /DB_XREF=gi:11130857 /DB_XREF=est:7q78g05.x1 /CLONE=IMAGE:3704625 /UG=Hs.182575 solute carrier family 15 (H ⁺ /peptide transporter), member 2 /FL=gb:NM_021082.1

		protein), alpha 15 (Gq class) (GNA15), mRNA. /FEA=mRNA /GEN=GNA15
		/PROD=guanine nucleotide binding protein (G protein),alpha 15 (Gq class) /DB_XREF=gi:4504038 /UG=Hs.73797 guanine nucleotide binding protein (G protein), alpha 15 (Gq class) /FL=gb:M63904.1 gb:NM_002068.1
		gb:NM_001609.1 /DEF=Homo sapiens acyl-Coenzyme A dehydrogenase, shortbranched chain (ACADS), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=ACADS /PROD=acyl-Coenzyme A dehydrogenase, shortbranchedchain precursor /DB_XREF=gi:4501858
		dehydrogenase, shortbranchedchain precursor /DB_XREF=gi:4501858 /UG=Hs.81934 acyl-Coenzyme A dehydrogenase, shortbranched chain /FL=gb:NM_001609.1 gb:U12778.1
205355_at_HG-U133A	ACADS	acyl-Coenzyme A dehydrogenase, shortbranched chain /FL=gb:NM_018952.1 /DEF=Homo sapiens homeo box B6 (HOXB6), mRNA. /FEA=mRNA /GEN=HOXB6 /PROD=homeo box B6 /DB_XREF=gi:9506792
205366_s_at_HG-U133A	HOXB6	homeo box B6 /UG=Hs.98428 homeo box B6 /FL=gb:NM_018952.1
205380_at_HG-U133A	PDZK1	PDZ domain containing 1 /FL=gb:AF012281.1 /DEF=Homo sapiens PDZ domain containing 1 (PDZK1), mRNA. /FEA=mRNA /GEN=PDZK1 /PROD=PDZ domain containing 1 /DB_XREF=gi:4505702 /UG=Hs.15456 PDZ domain containing 1 /FL=gb:NM_002614.1
205382_s_at_HG-U133A	DF	D component of complement (adipsin) /FL=gb:NM_001928.1 /DEF=Homo sapiens D component of complement (adipsin) (DF), mRNA. /FEA=mRNA /GEN=DF /PROD=adipsincomplement factor D precursor /DB_XREF=gi:4503308 /UG=Hs.155597 D component of complement (adipsin) /FL=gb:NM_001928.1
205383_s_at_HG-U133A	ZNF288	zinc finger protein 288 /FL=gb:AL050276.1 gb:NM_015642.1
205414_s_at_HG-U133A	KIAA0672	KIAA0672 gene product /FL=gb:NM_014859.1 /DEF=Homo sapiens KIAA0672 gene product (KIAA0672), mRNA. /FEA=mRNA /GEN=KIAA0672 /PROD=KIAA0672 gene product /DB_XREF=gi:7662241 /UG=Hs.6336 KIAA0672 gene product

			/FL=gb:AB014572.1 gb:NM_014859.1
			gb:NM_000288.1 /DEF=Homo sapiens peroxisomal biogenesis factor 7 (PEX7), mRNA, /FEA=mRNA /GEN=PEX7 /PROD=peroxisomal biogenesis factor 7 /DB_XREF=gi:4505730 /UG=Hs.79993 peroxisomal biogenesis factor 7 /FL=gb:U76560.1 gb:U88871.1 gb:NM_000288.1
205420_at_HG-U133A	PEX7	peroxisomal biogenesis factor 7	gb:NM_002105.1 /DEF=Homo sapiens H2A histone family, member X (H2AFX), mRNA, /FEA=mRNA /GEN=H2AFX /PROD=H2A histone family, member X /DB_XREF=gi:4504252 /UG=Hs.147097 H2A histone family, member X /FL=gb:BC004915.1 gb:NM_002105.1
205436_s_at_HG-U133A	H2AFX	H2A histone family, member X	gb:NM_002145.1 /DEF=Homo sapiens homeo box B2 (HOXB2), mRNA, /FEA=mRNA /GEN=HOXB2 /PROD=homeo box B2 /DB_XREF=gi:4504464 /UG=Hs.2733 homeo box B2 /FL=gb:NM_002145.1
205453_at_HG-U133A	HOXB2	homeo box B2	Consensus includes gb:AW772082 /FEA=EST /DB_XREF=gi:7704144 /DB_XREF=est:hn67b07.x1 /CLONE=IMAGE:3032917 /UG=Hs.63931 dachshund (Drosophila) homolog /FL=gb:NM_004392.1 gb:AF102546.1
205471_s_at_HG-U133A	DACH	dachshund homolog (Drosophila)	gb:NM_004392.1 /DEF=Homo sapiens dachshund (Drosophila) homolog (DACH), mRNA, /FEA=mRNA /GEN=DACH /PROD=dachshund (Drosophila) homolog /DB_XREF=gi:4758113 /UG=Hs.63931 dachshund (Drosophila) homolog /FL=gb:NM_004392.1 gb:AF102546.1
205472_s_at_HG-U133A	DACH	dachshund homolog (Drosophila)	gb:NM_000061.1 /DEF=Homo sapiens Bruton agammaglobulinemia tyrosine kinase (BTK), mRNA, /FEA=mRNA /GEN=BTK /PROD=Bruton agammaglobulinemia tyrosine kinase /DB_XREF=gi:4557376 /UG=Hs.159494 Bruton agammaglobulinemia tyrosine kinase /FL=gb:NM_000061.1 /UG=Hs.153756.1 gb:AF153757.1 gb:AF153758.1 gb:AF153759.1 gb:AF153760.1 gb:AF153761.1 gb:AF153762.1 gb:AF153364.1
205504_at_HG-U133A	BTK		gb:NM_001062.1 /DEF=Homo sapiens transcobalamin I (vitamin B12 binding protein, R binder family) (TCN1), mRNA, /FEA=mRNA /GEN=TCN1 /PROD=transcobalamin I (vitamin B12 binding protein, R binder family)
205513_at_HG-U133A	TCN1		

		/DB_XREF=gi:4507406 /UG=Hs.2012 transcobalamin 1 (vitamin B12 binding protein, R binder family) /FL=gb:NM_001062.1
205528_s_at_HG-U133A	CBFA2T1	Consensus includes gb:X799901 /DEF=H.sapiens ETO mRNA. /FEA=mRNA /GEN=ETO /DB_XREF=gi:510523 /UG=Hs.31551 core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related /FL=gb:NM_004349.1 gb:D43638.1
205529_s_at_HG-U133A	CBFA2T1	core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related /FL=gb:NM_004349.1 /DEF=Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1), mRNA. /FEA=mRNA /GEN=CBFA2T1 /PROD=core-binding factor, runt domain, alpha subunit2; translocated to, 1; cyclin D-related /DB_XREF=gi:4757915 /UG=Hs.31551 core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related /FL=gb:NM_004349.1 gb:D43638.1
205541_s_at_HG-U133A	GSPT2	core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related /FL=gb:NM_004349.1 /DEF=Homo sapiens hypothetical protein FLJ10441 /mRNA. /FEA=mRNA /GEN=FLJ10441 /PROD=hypothetical protein FLJ10441 /DB_XREF=gi:8922423 /UG=Hs.59523 hypothetical protein FLJ10441 /FL=gb:NM_018094.1
205547_s_at_HG-U133A	TAGLN	G1 to S phase transition 2 /FL=gb:NM_003186.2 /DEF=Homo sapiens transgelin (TAGLN), mRNA. /FEA=mRNA /GEN=TAGLN /PROD=transgelin /DB_XREF=gi:12621918 /UG=Hs.75777 transgelin /FL=gb:NM_003186.2 gb:M195787.1 gb:D17409.1
205557_at_HG-U133A	BPI	bactericidal/permeability-increasing protein (BPI), mRNA. /FEA=mRNA /GEN=BPI /PROD=bactericidal/permeability-increasing protein precursor /DB_XREF=gi:4502446 /UG=Hs.89535 bactericidal/permeability-increasing protein /FL=gb:AF322588.1 gb:J04739.1 /gb:NM_001725.1
205599_at_HG-U133A	TRAF1	TNF receptor-associated factor 1 /FL=gb:NM_005658.1 gb:U19261.1

205600_x_at_HG-U133A	HOXB5	homeo box B5	Consensus includes gb:AI052747 /FEA=EST /DB_XREF=gi:3308738 /DB_XREF=est:o227d05.x1 /CLONE=IMAGE:1676553 /UG=Hs.22554 homeobox B5 /FL=gb:M92299.1 gb:NM_002147.1
205601_s_at_HG-U133A	HOXB5	homeo box B5	gb:NM_002147.1 /DEF=Homo sapiens homeo box B5 (HOXB5), mRNA /FEA=mRNA /GEN=HOXB5 /PROD=homeo box B5 /DB_XREF=gi:4504468 /UG=Hs.22554 homeo box B5 /FL=gb:M92299.1 gb:NM_002147.1
205607_s_at_HG-U133A	LOC57147	hypothetical protein LOC57147	gb:NM_020423.1 /DEF=Homo sapiens hypothetical protein LOC57147 /PROD=hypothetical protein LOC57147 /DB_XREF=gi:9967093 /UG=Hs.24243 hypothetical protein LOC57147 /FL=gb:NM_020423.1
205613_at_HG-U133A	LOC51760	B/K protein	gb:NM_016524.1 /DEF=Homo sapiens BK protein (LOC51760), mRNA /FEA=mRNA /GEN=LOC51760 /PROD=BK protein /DB_XREF=gi:7706558 /UG=Hs.26971 BK protein /FL=gb:BC004518.1 gb:AF220560.1 gb:NM_016524.1
205614_x_at_HG-U133A	MST1		gb:NM_020998.1 /DEF=Homo sapiens macrophage stimulating 1 (hepatocyte growth factor-like) (MST1), mRNA /FEA=mRNA /GEN=MST1 /PROD=macrophage stimulating 1 (hepatocyte growthfactor-like) /DB_XREF=gi:10337614 /UG=Hs.278657 macrophage stimulating 1 (hepatocyte growth factor-like) /FL=gb:NM_020998.1 gb:M74178.1 gb:L11924.1
205624_at_HG-U133A	CPA3	carboxypeptidase A3 (mast cell)	gb:NM_001870.1 /DEF=Homo sapiens carboxypeptidase A3 (mast cell) /FL=gb:M27717.1 gb:NM_001870.1
205627_at_HG-U133A	CDA	cytidine deaminase	gb:NM_001785.1 /DEF=Homo sapiens cytidine deaminase (CDA), mRNA /FEA=mRNA /GEN=CDA /PROD=cytidine deaminase /DB_XREF=gi:11386156 /UG=Hs.72924 cytidine deaminase /FL=gb:NM_001785.1 gb:L27943.1
205640_at_HG-U133A	ALDH3B1	aldehyde dehydrogenase 3 family, member B1	gb:NM_000694.1 /DEF=Homo sapiens aldehyde dehydrogenase 3 family, member B1 (ALDH3B1), mRNA /FEA=mRNA /GEN=ALDH3B1

			/PROD=aldehyde dehydrogenase 3B1 /DB_XREF=gi:4502042 /UG=Hs.83155 aldehyde dehydrogenase 3 family, member B1 /FL=gb:NM_000694.1 gb:U10868.1
205653_at_HG-U133A	CTSG	cathepsin G	gb:NM_001911.1 /DEF=Homo sapiens cathepsin G (CTSG), mRNA. /FEA=mRNA /GEN=CTSG /PROD=cathepsin G /DB_XREF=gi:4503148 /UG=Hs.100764 cathepsin G /FL=gb:NM_001911.1
205663_at_HG-U133A	PCBP3	poly(rC) binding protein 3	gb:NM_020528.1 /DEF=Homo sapiens poly(rC)-binding protein 3 (PCBP3), mRNA. /FEA=mRNA /GEN=PCBP3 /PROD=poly(rC)-binding protein 3 /DB_XREF=gi:10092616 /UG=Hs.121241 poly(rC)-binding protein 3 /FL=gb:NM_020528.1 gb:AF176329.1
205668_at_HG-U133A	LY75	lymphocyte antigen 75	gb:NM_002349.1 /DEF=Homo sapiens lymphocyte antigen 75 (LY75), mRNA. /FEA=mRNA /GEN=LY75 /PROD=lymphocyte antigen 75 /DB_XREF=gi:4505052 /UG=Hs.153563 lymphocyte antigen 75 /FL=gb:AF011333.1 gb:AF064827.1 gb:NM_002349.1
205671_s_at_HG-U133A	HLA-DOB	major histocompatibility complex, class II, DO beta	gb:NM_002120.1 /DEF=Homo sapiens major histocompatibility complex, class II, DO beta (HLA-DOB), mRNA. /FEA=mRNA /GEN=HLA-DOB /PROD=major histocompatibility complex, class II, DO beta /DB_XREF=gi:4504402 /UG=Hs.1802 major histocompatibility complex, class II, DO beta /FL=gb:NM_002120.1 gb:NM_002120.1
205674_X_at_HG-U133A	FXYD2	FXYD domain-containing ion transport regulator 2	gb:NM_001680.2 /DEF=Homo sapiens FXYD domain-containing ion transport regulator 2 (FXYD2), transcript variant a, mRNA. /FEA=mRNA /GEN=FXYD2 /PROD=FXYD domain-containing ion transport regulator2, isoform 1 /DB_XREF=gi:11125765 /UG=Hs.19520 FXYD domain-containing ion transport regulator 2 /FL=gb:NM_001680.2 gb:AF241236.1 gb:U50743.1
205690_s_at_HG-U133A	G10	maternal G10 transcript	gb:NM_003910.1 /DEF=Homo sapiens maternal G10 transcript (G10), mRNA. /FEA=mRNA /GEN=G10 /PROD=maternal G10 transcript /DB_XREF=gi:4503836 /UG=Hs.330310 maternal G10 transcript /FL=gb:NM_003910.1 gb:U11861.1

205691_at_HG-U133A	SYNGR3	synaptotyrosin 3	gb:NM_004209.2 /DEF=Homo sapiens synaptotyrosin 3 (SYNGR3), mRNA. /FEA=mRNA /GEN=SYNGR3 /PROD=synaptotyrosin 3 /DB_XREF=gi:6631111 /UG=Hs.6467
205718_at_HG-U133A	ITGB7	integrin, beta 7	gb:NM_000889.1 /DEF=Homo sapiens integrin, beta 7 (ITGB7), mRNA. /FEA=mRNA /GEN=ITGB7 /PROD=integrin, beta 7 /DB_XREF=gi:4504776 /UG=Hs.1741
205790_at_HG-U133A	SCAP1	src family associated phosphoprotein 1	gb:NM_000889.1 /DEF=Homo sapiens src kinase-associated phosphoprotein of 55 kDa (SKAP55), mRNA /FEA=mRNA /GEN=SKAP55 /PROD=src kinase-associated phosphoprotein of 55 kDa /DB_XREF=gi:4506964 /UG=Hs.19126
205801_s_at_HG-U133A	GRP3	guanine nucleotide exchange factor for Rap1	gb:NM_015376.1 /DEF=Homo sapiens KIAA0846 protein (KIAA0846), mRNA. /FEA=mRNA /GEN=KIAA0846 /PROD=KIAA0846 protein /DB_XREF=gi:7662333 /UG=Hs.24024
205805_s_at_HG-U133A	ROR1	receptor tyrosine kinase-like orphan receptor 1	gb:NM_015376.1 /DEF=Homo sapiens receptor tyrosine kinase-like orphan receptor 1 (ROR1), mRNA /GEN=ROR1 /PROD=receptor tyrosine kinase-like orphan receptor 1 /DB_XREF=gi:4826867 /UG=Hs.274243 receptor tyrosine kinase-like orphan receptor 1 /FL=gb:M97675.1
205821_at_HG-U133A	D12S2489E		gb:NM_007360.1 /DEF=Homo sapiens DNA segment on chromosome 12 (unique) 2489 expressed sequence (D12S2489E), mRNA. /FEA=mRNA /GEN=D12S2489E /PROD=NKG2-D type II integral membrane protein /DB_XREF=gi:6679051 /UG=Hs.74085 DNA segment on chromosome 12 (unique) 2489 expressed sequence /FL=gb:NM_007360.1 gb:AF260135.1
205837_s_at_HG-	GYPA	glycophorin A (includes MN blood group)	gb:BC005319.1 /DEF=Homo sapiens, Similar to glycophorin A (includes MN

U133A			blood group), clone MGc:12403, mRNA, complete cds. /FEA=mRNA /PROD=Similar to glycoprotein A (includes MN bloodgroup) /DB_XREF=gi:13529076 /UG=Hs.108694 glycoprotein A (includes MN bloodgroup) /FL=gb:BC005319.1 gb:U00177.1 gb:U1860.1 gb:NM_002099.2
205841_at_HG-U133A	JAK2	Janus kinase 2 (a protein tyrosine kinase)	gb:NM_004972.2 /DEF=Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA. /FEA=mRNA /GEN=JAK2 /PROD=Janus kinase 2 (JAK2) /DB_XREF=gi:13325062 /UG=Hs.115541 Janus kinase 2 (a protein tyrosine kinase) /FL=gb:NM_004972.2 gb:AF005216.1 gb:AF058925.1 gb:AF001362.1
205849_s_at_HG-U133A	UQCRB	ubiquinol-cytochrome c reductase binding protein	gb:NM_006294.1 /DEF=Homo sapiens ubiquinol-cytochrome c reductase binding protein (UQCRB), mRNA. /FEA=mRNA /GEN=UQCRB /PROD=ubiquinol-cytochrome c reductase bindingprotein /DB_XREF=gi:5454151 /UG=Hs.131255 ubiquinol-cytochrome c reductase binding protein /FL=gb:M22348.1 gb:NM_006294.1
205855_at_HG-U133A	ZNF197	zinc finger protein 197	gb:NM_006991.2 /DEF=Homo sapiens zinc finger protein 197 (ZNF197), mRNA. /FEA=mRNA /GEN=ZNF197 /PROD=zinc finger protein 197 /DB_XREF=gi:12056483 /UG=Hs.170341 zinc finger protein 197 /FL=gb:NM_006991.2 gb:AF011573.1
205863_at_HG-U133A	S100A12	S100 calcium binding protein A12 (calgranulin C)	gb:NM_005621.1 /DEF=Homo sapiens S100 calcium-binding protein A12 (calgranulin C) (S100A12), mRNA. /FEA=mRNA /GEN=S100A12 /PROD=S100 calcium-binding protein A12 /DB_XREF=gi:5032058 /UG=Hs.19413 S100 calcium-binding protein A12 (calgranulin C) /FL=gb:D083664.1 gb:D49549.1
205899_at_HG-U133A	CCNA1	cyclin A1	gb:NM_003914.1 /DEF=Homo sapiens cyclin A1 (CCNA1), mRNA. /FEA=mRNA /GEN=CCNA1 /PROD=cyclin A1 /DB_XREF=gi:4502610 /UG=Hs.79378 cyclin A1 /FL=gb:U68638.1 gb:NM_003914.1
205901_at_HG-U133A	PNOC	pronociceptin	gb:NM_006228.2 /DEF=Homo sapiens pronociceptin (PNOC), mRNA. /FEA=mRNA /GEN=PNOC /PROD=pronociceptin /DB_XREF=gi:11079650 /UG=Hs.89040 pronociceptin /FL=gb:NM_006228.2 gb:U48263.1

205911_at_HG-U133A	PTHR1	parathyroid hormone receptor 1	gb:NM_000316.1 /DEF=Homo sapiens parathyroid hormone receptor 1 (PTHR1), mRNA. /FEA=mRNA /GEN=PTHR1 /PROD=parathyroid hormone receptor 1 /DB_XREF=gi:4506270 /UG=Hs.1019 parathyroid hormone receptor 1 /FL=gb:L04308.1 gb:NM_000316.1 gb:U17418.1
205933_at_HG-U133A	SETBP1	SET binding protein 1	gb:NM_015559.1 /DEF=Homo sapiens KIAA0437 protein (KIAA0437), mRNA. /FEA=mRNA /GEN=KIAA0437 /PROD=KIAA0437 protein /DB_XREF=gi:7662121 /UG=Hs.151717 KIAA0437 protein /FL=gb:AB022660.1 gb:NM_015559.1
205945_at_HG-U133A	IL6R	interleukin 6 receptor	gb:NM_000565.1 /DEF=Homo sapiens interleukin 6 receptor (IL6R), mRNA. /FEA=mRNA /GEN=IL6R /PROD=interleukin 6 receptor /DB_XREF=gi:4504672 /UG=Hs.193400 interleukin 6 receptor /FL=gb:NM_000565.1
205997_at_HG-U133A	ADAM28		gb:NM_021778.1 /DEF=Homo sapiens a disintegrin and metalloproteinase domain 28 (ADAM28), transcript variant 2, mRNA. /FEA=mRNA /GEN=ADAM28 /PROD=a disintegrin and metalloproteinase domain 28, isoform 2 preprotein /DB_XREF=gi:1496995 /UG=Hs.174030 a disintegrin and metalloproteinase domain 28 /FL=gb:NM_021778.1 gb:AF137334.1 gb:NM_014265.1
206009_at_HG-U133A	ITGA9	integrin, alpha 9	gb:NM_002207.1 /DEF=Homo sapiens integrin, alpha 9 (ITGA9), mRNA. /FEA=mRNA /GEN=ITGA9 /PROD=integrin, alpha 9 /DB_XREF=gi:11321594 /UG=Hs.2222 integrin, alpha 9 /FL=gb:NM_002207.1 gb:D25303.1
206090_s_at_HG-U133A	DISC1		gb:NM_018662.1 /DEF=Homo sapiens disrupted in schizophrenia 1 (DISC1), mRNA. /FEA=mRNA /GEN=DISC1 /PROD=disrupted in schizophrenia 1 /DB_XREF=gi:11037064 /UG=Hs.26985 disrupted in schizophrenia 1 /FL=gb:NM_018662.1 gb:AF222980.1
206111_at_HG-U133A	RNASE2		gb:NM_002934.1 /DEF=Homo sapiens ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin) (RNASE2), mRNA. /FEA=mRNA /GEN=RNASE2 /PROD=ribonuclease, RNase A family, 2 (liver,eosinophil-derived neurotoxin) /DB_XREF=gi:4506548 /UG=Hs.728 ribonuclease, RNase

			A family, 2 (liver, eosinophil-derived neurotoxin) /FL=gb:M24157-1 gb:NM_002934.1 gb:M28129.1
		Burkitt lymphoma receptor 1, GTP binding protein	gb:NM_001716.1 /DEF=Homo sapiens Burkitt lymphoma receptor 1, GTP-binding protein (BLR1), mRNA. /FEA=mRNA /GEN=BLR1 /PROD=Burkitt lymphoma receptor 1, GTP-binding protein /DB_XREF=gi:4502414 /UG=Hs.113916 Burkitt lymphoma receptor 1, GTP-binding protein /FL=gb:NM_001716.1
206126_at_HG-U133A	BLR1		gb:NM_014682.1 /DEF=Homo sapiens KIAA0535 gene product (KIAA0535), mRNA. /FEA=mRNA /GEN=KIAA0535 /PROD=KIAA0535 gene product /DB_XREF=gi:7662167 /UG=Hs.151449 KIAA0535 gene product /FL=gb:AB011107.1 gb:NM_014682.1
206135_at_HG-U133A	KIAA0535	KIAA0535 gene product	gb:NM_001242.1 /DEF=Homo sapiens tumor necrosis factor receptor superfamily, member 7 (TNFRSF7), mRNA. /FEA=mRNA /GEN=TNFRSF7 /PROD=CD27 antigen /DB_XREF=gi:4507586 /UG=Hs.180841 tumor necrosis factor receptor superfamily, member 7 /FL=gb:NM_001242.1
206150_at_HG-U133A	TNFRSF7	tumor necrosis factor receptor superfamily, member 7	gb:NM_000045.2 /DEF=Homo sapiens arginase, liver (ARG1), mRNA. /FEA=mRNA /GEN=ARG1 /PROD=arginase, type I /DB_XREF=gi:10947138 /UG=Hs.289057 arginase, liver /FL=gb:NM_000045.2 gb:M14502.1
206177_s_at_HG-U133A	ARG1	arginase, liver	gb:NM_000929.1 /DEF=Homo sapiens phospholipase A2, group V (PLA2G5), mRNA. /FEA=mRNA /GEN=PLA2G5 /PROD=phospholipase A2, group V /DB_XREF=gi:4505852 /UG=Hs.290 phospholipase A2, group V /FL=gb:NM_000929.1 gb:U03090.1
206178_at_HG-U133A	PLA2G5	phospholipase A2, group V	gb:NM_001828.3 /DEF=Homo sapiens Charot-Leyden crystal protein (CLC), mRNA. /FEA=mRNA /GEN=CLC /PROD=Charot-Leyden crystal protein /DB_XREF=gi:6325464 /UG=Hs.889 Charot-Leyden crystal protein /FL=gb:L01664.1 gb:NM_001828.3
206207_at_HG-U133A	CLC	Charot-Leyden crystal protein	gb:NM_002269.1 /DEF=Homo sapiens karyopherin alpha 5 (importin alpha 6) (KPNA5), mRNA. /FEA=mRNA /GEN=KPNA5 /PROD=karyopherin alpha 5
206241_at_HG-U133A	KPNA5	karyopherin alpha 5 (importin alpha 6)	

			(importin alpha 6) /DB_XREF=gi:4504902 /UG=Hs.182971 karyopherin alpha 5 (importin alpha 6) /FL=gb:AF005361.1 gb:NM_002269.1
206245_s_at_HG-U133A	NS1-BP	NS1-binding protein	gb:NM_006469.1 /DEF=Homo sapiens NS1-binding protein (NS1-BP), mRNA. /FEA=mRNA /GEN=NS1-BP /PROD=NS1-binding protein /DB_XREF=gi:5453803 /UG=Hs.197298 NS1-binding protein /FL=gb:NM_006469.1
206255_at_HG-U133A	BLK	B lymphoid tyrosine kinase	gb:NM_001715.1 /DEF=Homo sapiens B lymphoid tyrosine kinase (BLK), mRNA. /FEA=mRNA /GEN=BLK /PROD=B lymphoid tyrosine kinase /DB_XREF=gi:4502412 /UG=Hs.2243 B lymphoid tyrosine kinase /FL=gb:NM_001715.1
206295_at_HG-U133A	IL18	interleukin 18 (interferon-gamma-inducing factor)	gb:NM_001562.1 /DEF=Homo sapiens interleukin-18 (interferon-gamma-inducing factor) (IL18), mRNA. /FEA=mRNA /GEN=IL18 /PROD=interleukin 18 /DB_XREF=gi:4504652 /UG=Hs.83077 interleukin 18 (interferon-gamma-inducing factor) /FL=gb:D49950.1 gb:AF077611.1 gb:NM_001562.1
206302_s_at_HG-U133A	NUDT4	nudix (nucleoside diphosphate linked moiety X)-type motif 4	gb:NM_019094.1 /DEF=Homo sapiens nudix (nucleoside diphosphate linked moiety X)-type motif 4 (NUDT4), mRNA. /FEA=mRNA /GEN=NUDT4 /PROD=nudix (nucleoside diphosphate linked moiety X)-type motif 4 /DB_XREF=gi:10800135 /UG=Hs.92281 nudix (nucleoside diphosphate linked moiety X)-type motif 4 /FL=gb:NM_019094.1 gb:AF191650.1 gb:AF191653.1
206337_at_HG-U133A	CCR7	chemokine (C-C motif) receptor 7	gb:NM_001838.1 /DEF=Homo sapiens chemokine (C-C motif) receptor 7 (CCR7), mRNA. /FEA=mRNA /GEN=CCR7 /PROD=chemokine (C-C motif) receptor 7 /DB_XREF=gi:4502640 /UG=Hs.1652 chemokine (C-C motif) receptor 7 /FL=gb:108176.1 gb:NM_001838.1 gb:L31581.1
206380_s_at_HG-U133A	PFC	properdin P factor, complement	gb:NM_002621.1 /DEF=Homo sapiens properdin P factor, complement (PFC), mRNA. /FEA=mRNA /GEN=PFC /PROD=properdin P factor, complement /DB_XREF=gi:4505736 /UG=Hs.53155 properdin P factor, complement /FL=gb:NM_002621.1 gb:M83652.1

206398_s_at_HG-U133A	CD19	CD19 antigen	gb:NM_001770.1 /DEF=Homo sapiens CD19 antigen (CD19), mRNA. /FEA=mRNA /GEN=CD19 /PROD=CD19 antigen /DB_XREF=gi:10835052 /UG=Hs.96023 CD19 antigen /FL=gb:NM_001770.1 gb:M21097.1 qb:M28170.1
206438_x_at_HG-U133A	FLJ12975	hypothetical protein FLJ12975	gb:NM_024809.1 /DEF=Homo sapiens hypothetical protein FLJ12975 (FLJ12975), mRNA, /FEA=mRNA /GEN=FLJ12975 /PROD=hypothetical protein FLJ12975 /DB_XREF=gi:13376192 /UG=Hs.167165 hypothetical protein FLJ12975 /FL=gb:NM_024809.1
206440_at_HG-U133A	VEL11	Vertebrate LIN7 homolog 1, Tax interaction protein 33	gb:NM_004664.1 /DEF=Homo sapiens Vertebrate LIN7 homolog 1, Tax interaction protein 33 (VEL11), mRNA, /FEA=mRNA /GEN=VEL11 /PROD=Vertebrate LIN7 homolog 1, Tax interactionprotein 33 /DB_XREF=gi:4759305 /UG=Hs.178215 Vertebrate LIN7 homolog 1, Tax interaction protein 33 /FL=gb:AF087693.1 qb:NM_004664.1 qb:AF173081.1
206461_x_at_HG-U133A	MT1H	metallothionein 1H	gb:NM_005951.1 /DEF=Homo sapiens metallothionein 1H (MT1H), mRNA. /FEA=mRNA /GEN=MT1H /PROD=metallothionein 1H /DB_XREF=gi:10835084 /UG=Hs.2667 metallothionein 1H /FL=gb:NM_005951.1
206488_s_at_HG-U133A	CD36	CD36 antigen (collagen type I receptor, thrombospondin receptor)	gb:NM_000072.1 /DEF=Homo sapiens CD36 antigen (collagen type I receptor, thrombospondin receptor) (CD36), mRNA, /FEA=mRNA /GEN=CD36 /PROD=CD36 antigen (collagen type I receptor,thrombospondin receptor) /DB_XREF=gi:4557418 /UG=Hs.75613 CD36 antigen (collagen type I receptor, thrombospondin receptor) /FL=gb:M24795.1 qb:M98398.1 gb:LO6850.1 qb:NM_000072.1
206513_at_HG-U133A	AIM2	absent in melanoma 2	gb:NM_0046833.1 /DEF=Homo sapiens absent in melanoma 2 (AIM2), mRNA. /FEA=mRNA /GEN=AIM2 /PROD=absent in melanoma 2 /DB_XREF=gi:4757733 /UG=Hs.105115 absent in melanoma 2 /FL=gb:AF024714.1 qb:NM_004833.1
206515_at_HG-U133A	CYP4F3	cytochrome P450, subfamily IVF, polypeptide 3 (leukotriene B4 omega hydroxylase) (CYP4F3), mRNA /GEN=CYP4F3 /PROD=cytochrome P450, subfamily IVF, hydroxylase)	gb:NM_000896.1 /DEF=Homo sapiens cytochrome P450, subfamily IVF, polypeptide 3 (leukotriene B4 omega hydroxylase) (CYP4F3), mRNA /FEA=mRNA /GEN=CYP4F3 /PROD=cytochrome P450, subfamily IVF,

		polypeptide 3 /DB_XREF=gi:4503240 /UG=Hs.106242 cytochrome P450, subfamily IVF, polypeptide 3 (leukotriene B4 omega hydroxylase) /FL=gb:AB002454.1 gb:D12620.1 gb:NM_000896.1
206519_x_at_HG-U133A	SIGLEC6	gb:D86358.1 /DEF=Homo sapiens mRNA for CD33L1, complete cds. /FEA=mRNA /PROD=CD33L1 /DB_XREF=gi:2913994 /UG=Hs.117992 sialic acid binding Ig-like lectin 6 /FL=gb:U71382.1 gb:D86358.1 gb:NM_001245.1
206530_at_HG-U133A	RAB30	gb:NM_01488.1 /DEF=Homo sapiens RAB30, member RAS oncogene family (RAB30), mRNA. /FEA=mRNA /GEN=RAB30 /PROD=RAB30, member RAS oncogene family /DB_XREF=gi:7657493 /UG=Hs.159505 RAB30, member RAS oncogene family /FL=gb:NM_014488.1
206530_s_at_HG-U133A	NUP155	gb:NM_004298.1 /DEF=Homo sapiens nucleoporin 155kD (NUP155), mRNA /FEA=mRNA /GEN=NUP155 /PROD=nucleoporin 155kD /DB_XREF=gi:4758843 /UG=Hs.23255 nucleoporin 155kD /FL=gb:AB018334.1
206550_s_at_HG-U133A	CEACAM1	gb:NM_004298.1 /DEF=Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1), mRNA. /FEA=mRNA /GEN=CEACAM1 /PROD=carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) /DB_XREF=gi:4502404
206576_s_at_HG-U133A		carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) /UG=Hs.50964 carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) /FL=gb:NM_001712.1
206622_at_HG-U133A	TRH	gb:NM_007117.1 /DEF=Homo sapiens thyrotropin-releasing hormone (TRH), mRNA. /FEA=mRNA /GEN=TRH /PROD=thyrotropin-releasing hormone /DB_XREF=gi:6005919 /UG=Hs.182231 thyrotropin-releasing hormone /FL=gb:NM_007117.1
206633_at_HG-U133A	CHRNA1	gb:NM_000079.1 /DEF=Homo sapiens cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle) (CHRNA1), mRNA. /FEA=mRNA /GEN=CHRNA1 /PROD=cholinergic receptor, nicotinic, alphapolypeptide 1 (muscle) precursor /DB_XREF=gi:4557456 /UG=Hs.2266 cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle)

			polypeptide 1 (muscle) /FL=gb:NM_000079.1
206634_at_HG-U133A	SIX3	sine oculis homeobox homolog 3 (Drosophila)	gb:NM_005413.1 /DEF=Homo sapiens sine oculis homeobox (Drosophila) homolog 3 /mRNA, mRNA /FEA=mRNA /GEN=SIX3 /PROD=sine oculis homeobox (Drosophila) homolog 3 /DB_XREF=gi:4885596 /UG=Hs.227277
206676_at_HG-U133A	CEACAM8	carcinoembryonic antigen-related cell adhesion molecule 8	gb:M3326.1 /DEF=Human nonspecific cross-reacting complete cds. /FEA=mRNA /GEN=NCA /PROD=non-specific cross reacting antigen /DB_XREF=gi:189101 /UG=Hs.41 carcinoembryonic antigen-related cell adhesion molecule 8 /FL=gb:NM3326.1 db:NM_001816.1
206748_s_at_HG-U133A	SPAG9	sperm associated antigen 9	gb:NM_003971.1 /DEF=Homo sapiens sperm associated antigen 9 (SPAG9), mRNA. /FEA=mRNA /GEN=SPAG9 /PROD=sperm associated antigen 9 /DB_XREF=gi:4504524 /UG=Hs.129872 sperm associated antigen 9 /FL=gb:NM_003971.1
206759_at_HG-U133A	FCER2	Fc fragment of IgE, low affinity II, receptor for (CD23A)	gb:NM_002002.1 /DEF=Homo sapiens Fc fragment of IgE, low affinity II, receptor for (CD23A) (FCER2), mRNA. /FEA=mRNA /GEN=FCER2 /PROD=Fc fragment of IgE, low affinity II, receptor for (CD23A) /DB_XREF=gi:4503678 /UG=Hs.1416 Fc fragment of IgE, low affinity II, receptor for (CD23A) /FL=gb:NM15059.1 gb:NM_002002.1
206760_s_at_HG-U133A	FCER2	Fc fragment of IgE, low affinity II, receptor for (CD23A)	gb:NM_002002.1 /DEF=Homo sapiens Fc fragment of IgE, low affinity II, receptor for (CD23A) (FCER2), mRNA. /FEA=mRNA /GEN=FCER2 /PROD=Fc fragment of IgE, low affinity II, receptor for (CD23A) /DB_XREF=gi:4503678 /UG=Hs.1416 Fc fragment of IgE, low affinity II, receptor for (CD23A) /FL=gb:NM15059.1 gb:NM_002002.1
206761_at_HG-U133A	TACTILE	T cell activation, increased late expression	gb:NM_005816.1 /DEF=Homo sapiens T cell activation, increased late expression (TACTILE), mRNA. /FEA=mRNA /GEN=TACTILE /PROD=T cell activation, increased late expression /DB_XREF=gi:5032140 /UG=Hs.142023
206772_at_HG-U133A	PTHR2	parathyroid hormone receptor 2	T cell activation, increased late expression /FL=gb:M88282.1 gb:NM_005816.1

		(PTHR2), mRNA, /FEA=mRNA /GEN=PTHR2 /PROD=parathyroid hormone receptor 2 /DB_XREF=gi:4826953 /UG=Hs.159499 parathyroid hormone receptor 2 /FL=gb:NM_005048.1 gb:U25128.1
206781_at_HG-U133A	DNAJC4	gb:NM_005528.1 /DEF=Homo sapiens heat shock 40kD protein 2 (HSPF2), mRNA, /FEA=mRNA /GEN=HSPF2 /PROD=heat shock 40kD protein 2 /DB_XREF=gi:5031770 /UG=Hs.172847 Dnaj (Hsp40) homolog, subfamily C, member 4 /FL=gb:AF012106.1 gb:NM_005528.1
206804_at_HG-U133A	CD3G	gb:NM_000073.1 /DEF=Homo sapiens CD3G antigen, gamma polypeptide (TTT3 complex) (CD3G), mRNA, /FEA=mRNA /GEN=CD3G /PROD=CD3G gamma precursor /DB_XREF=gi:4557428 /UG=Hs.2259 CD3G antigen, gamma polypeptide (TTT3 complex) /FL=gb:NM_000073.1
206847_s_at_HG-U133A	HOXA7	gb:AF026397.1 /DEF=Homo sapiens homeobox transcription factor HOXA7 (HOXA7) mRNA, complete cds, /FEA=mRNA /GEN=HOXA7 /PROD=homeobox transcription factor HOXA7 /DB_XREF=gi:2739070 /UG=Hs.70954 homeo box A7 /FL=gb:AF026397.1 gb:NM_006896.1
206850_at_HG-U133A	RRP22	gb:NM_006477.1 /DEF=Homo sapiens RAS-related on chromosome 22 (RRP22), mRNA, /FEA=mRNA /GEN=RRP22 /PROD=RAS-related on chromosome 22 /DB_XREF=gi:5454029 /UG=Hs.73088 RAS-related on chromosome 22 /FL=gb:NM_006477.1
206871_at_HG-U133A	ELA2	gb:NM_001972.1 /DEF=Homo sapiens elastase 2, neutrophil (ELA2), mRNA /FEA=mRNA /GEN=ELA2 /PROD=elastase 2, neutrophil /DB_XREF=gi:4503548 /UG=Hs.99863 elastase 2, neutrophil /FL=gb:NM_001972.1
206940_s_at_HG-U133A	POU4F1	gb:NM_006237.1 /DEF=Homo sapiens POU domain, class 4, transcription factor 1 (POU4F1), mRNA, /FEA=mRNA /GEN=POU4F1 /PROD=POU domain, class 4, transcription factor 1 /DB_XREF=gi:5453937 /UG=Hs.211588
206956_at_HG-U133A	BGLAP	gb:NM_000711.1 /DEF=Homo sapiens bone gamma-carboxyglutamate (gla)

		protein (osteocalcin) (BGLAP), mRNA. /FEA=mRNA /GEN=BGLAP /PROD=bone gamma-carboxyglutamate (gla) protein(osteocalcin) /DB_XREF=gi:4502400 /UG=Hs.2558 bone gamma-carboxyglutamate (gla)
206995_x_at_HG-U133A	SREC	protein (osteocalcin) /FL=gb:NM_000711.1 gb:NM_003633.1 /DEF=Homo sapiens acetyl LDL receptor, SREC=scavenger receptor expressed by endothelial cells (SREC), mRNA. /FEA=mRNA /GEN=SREC /PROD=acetyl LDL receptor, SREC=scavenger receptor expressed by endothelial cells /DB_XREF=gi:4507202 /UG=Hs.57735 acetyl LDL receptor, SREC /FL=gb:D63483.1 gb:D86864.1 gb:NM_003693.1
207000_s_at_HG-U133A	PPP3CC	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma) (PPP3CC), mRNA. /FEA=mRNA /GEN=PPP3CC /PROD=protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma) /DB_XREF=gi:5031988 /UG=Hs.75206 protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma) /FL=gb:NM_005605.1 gb:AY007249.1
207030_s_at_HG-U133A	CSRP2	protein 2 /FL=gb:BC000992.2 gb:U57646.1 gb:NM_001321.1
207057_at_HG-U133A	SLC16A7	cysteine and glycine-rich protein 2 - solute carrier family 16 (monocarboxylic acid transporters), member 7 /FL=gb:AF058056.1 gb:NM_004731.1
207076_s_at_HG-U133A	ASS	argininosuccinate synthetase mRNA. /FEA=mRNA /GEN=ASS /PROD=argininosuccinate synthetase

			/DB_XREF=gi:4557336 /UG=Hs.160786 argininosuccinate synthetase /FL=gb:NM_000050.1
207168_s_at_HG-U133A	H2AFY	H2A histone family, member Y	gb:NM_004893.1 /DEF=Homo sapiens H2A histone family, member Y (H2AFY), mRNA. /FEA=mRNA /GEN=H2AFY /PROD=H2A histone family, member Y /DB_XREF=gi:4758495 /UG=Hs.75258 H2A histone family, member Y /FL=gb:AF054174.1 gb:NM_004893.1
207194_s_at_HG-U133A	ICAM4	intercellular adhesion molecule 4, Landsteiner-Wiener blood group	gb:NM_001544.2 /DEF=Homo sapiens intercellular adhesion molecule 4, Landsteiner-Wiener blood group (ICAM4), transcript variant 1, mRNA. /FEA=mRNA /GEN=ICAM4 /PROD=intercellular adhesion molecule 4, isoform 1 precursor /DB_XREF=gi:12545400 /UG=Hs.108287 intercellular adhesion molecule 4, Landsteiner-Wiener blood group /FL=gb:NM_001544.2 gb:L27671.1
207224_s_at_HG-U133A	SIGLEC7	sialic acid binding Ig-like lectin 7	gb:NM_016543.1 /DEF=Homo sapiens D-siglec precursor, (LOC51766), mRNA. /FEA=mRNA /GEN=LOC51766 /PROD=D-siglec precursor, /DB_XREF=gi:7706570 /UG=Hs.149250 D-siglec precursor, /FL=gb:AF178981.1 gb:NM_016543.1
207269_at_HG-U133A	DEFA4	defensin, alpha 4, corticostatin	gb:NM_001925.1 /DEF=Homo sapiens defensin, alpha 4, corticostatin (DEFA4), mRNA. /FEA=mRNA /GEN=DEFA4 /PROD=defensin, alpha 4, preproprotein /DB_XREF=gi:4503302 /UG=Hs.2582 defensin, alpha 4, corticostatin /FL=gb:NM_001925.1
207384_at_HG-U133A	PGLYRP	peptidoglycan recognition protein	gb:NM_005091.1 /DEF=Homo sapiens peptidoglycan recognition protein (PGLYRP), mRNA. /FEA=mRNA /GEN=PGLYRP /PROD=peptidoglycan recognition protein /DB_XREF=gi:4827035 /UG=Hs.137583 peptidoglycan recognition protein /FL=gb:AF076483.1 gb:NM_005091.1 gb:AF242517.1
207403_at_HG-U133A	IRS4	insulin receptor substrate 4	gb:NM_003604.1 /DEF=Homo sapiens insulin receptor substrate 4 (IRS4), mRNA. /FEA=mRNA /GEN=IRS4 /PROD=insulin receptor substrate 4 /DB_XREF=gi:4504732 /UG=Hs.159609 insulin receptor substrate 4 /FL=gb:AF007567.1 gb:NM_003604.1

207520_at_HG-U133A		Consensus includes gb:BG494940 /FEA=EST /DB_XREF=gi:13456455 /DB_XREF=st:602540961F1 /CLONE=IMAGE:4671854 /UG=Hs.554 Sjogren syndrome antigen A2 (60kD, ribonucleoprotein autoantigen SS-ARO) /FL=gb:J04137.1 gb:NM_004600.1
207543_s_at_HG-U133A	P4HA1	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I /GEN=P4HA1 /PROD=procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I /DB_XREF=gi:4505564 /UG=Hs.76768 procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I /FL=gb:NM_000917.1
207616_s_at_HG-U133A	TANK	TRAF family member-associated NFKB activator /FL=gb:U63830.1 gb:NM_004180.1 /DEF=Homo sapiens TRAF family member-associated NFKB activator (TANK), mRNA, /FEA=mRNA /GEN=TANK /PROD=TRAF family member-associated NFKB activator /DB_XREF=gi:4759249 /UG=Hs.146847
207641_at_HG-U133A	TAC1	transmembrane activator and CAML interactor /FL=gb:AF023614.1 gb:NM_012452.1 /DEF=Homo sapiens transmembrane activator and CAML interactor (TAC1), mRNA, /FEA=mRNA /GEN=TAC1 /PROD=transmembrane activator and CAML interactor /DB_XREF=gi:6912693 /UG=Hs.158341
207654_x_at_HG-U133A	DR1	down-regulator of transcription 1, TBP-binding (negative cofactor 2) /FL=gb:M97388.1 gb:NM_001938.1 gb:NM_013314.1 /DEF=Homo sapiens B cell linker protein (SLP65), mRNA, /FEA=mRNA /GEN=SLP65 /PROD=B cell linker protein /DB_XREF=gi:7019334 /UG=Hs.167746 B cell linker protein
207655_s_at_HG-U133A	BLNK	B-cell linker

			/FL=gb:AF068180.1 /gb:NM_013314.1
			gb:NM_005874.1 /DEF=Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2 (LILRB2), mRNA. /FEA=mRNA /GEN=LILRB2 /PROD=leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2
207697_x_at_HG-U133A	LILRB2		/DB_XREF=gi:5031910 /UG=Hs.22405 leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2 /FL=gb:AF025528.1
207700_s_at_HG-U133A	NCOA3		gb:NM_005874.1
207734_at_HG-U133A	FLJ20340		gb:NM_005874.1 /DEF=Homo sapiens nuclear receptor coactivator 3 (NCOA3), mRNA. /FEA=mRNA /GEN=NCOA3 /PROD=nuclear receptor coactivator 3 /DB_XREF=gi:5729725 /UG=Hs.225977 nuclear receptor coactivator 3 /FL=gb:AF036892.1 gb:NM_006534.1
207760_s_at_HG-U133A	NCOR2		gb:NM_017773.1 /DEF=Homo sapiens hypothetical protein FLJ20340 (FLJ20340), mRNA. /FEA=mRNA /GEN=FLJ20340 /PROD=hypothetical protein FLJ20340 /DB_XREF=gi:8923315 /UG=Hs.272794 hypothetical protein FLJ20340 /FL=gb:NM_017773.1
207777_s_at_HG-U133A	SP140		gb:NM_006312.1 /DEF=Homo sapiens nuclear receptor co-repressor 2 (NCOR2), mRNA. /FEA=mRNA /GEN=NCOR2 /PROD=nuclear receptor co-repressor 2 /DB_XREF=gi:5454073 /UG=Hs.287994 nuclear receptor co-repressor 2 /FL=gb:AF113003.1 gb:NM_006312.1
207801_s_at_HG-U133A	RNF10		gb:NM_007237.1 /DEF=Homo sapiens nuclear body protein Sp140 (SP140), mRNA. /FEA=mRNA /GEN=SP140 /PROD=nuclear body protein Sp140 /DB_XREF=gi:6005879 /UG=Hs.309943 nuclear body protein Sp140
			/FL=gb:U63420.1 gb:NM_007237.1
			gb:NM_014868.1 /DEF=Homo sapiens ring finger protein 10 (RNF10), mRNA. /FEA=mRNA /GEN=RNF10 /PROD=ring finger protein 10
			/DB_XREF=gi:7662652 /UG=Hs.5094 ring finger protein 10 /FL=gb:D87451.1
			gb:NM_014868.1

207802_at_HG-U133A	SGP28	specific granule protein (28 kDa)	gb:NM_006061.1 /DEF=Homo sapiens specific granule protein (28 kDa); cysteine-rich secretory protein-3 (SGP28), mRNA. /FEA=mRNA /GEN=SGP28 /PROD=specific granule protein (28 kDa); cysteine-richsecretory protein-3 /DB_XREF=gi:5174674 /UG=Hs.54431 specific granule protein (28 kDa); cysteine-rich secretory protein-3 /FL=gb:NM_006061.1
207809_s_at_HG-U133A	ATP6IP1	ATPase, H ⁺ transporting, lysosomal interacting protein 1	gb:NM_001183.1 /DEF=Homo sapiens ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump), subunit 1 (ATP6S1), mRNA. /FEA=mRNA /GEN=ATP6S1 /PROD=ATPase, H ⁺ transporting, lysosomal subunit 1 /DB_XREF=gi:4557340 /UG=Hs.6551 ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump), subunit 1 /FL=gb:NM_001183.1
207819_s_at_HG-U133A	ABCB4	ATP-binding cassette, sub-family B (MDR/TAP), member 4	gb:NM_00443.2 /DEF=Homo sapiens ATP-binding cassette, sub-family B (MDRTAP), member 4 (ABCB4), transcript variant A, mRNA. /FEA=mRNA /GEN=ABCB4 /PROD=ATP-binding cassette, subfamily B, member 4;isoform A /DB_XREF=gi:9961253 /UG=Hs.73812 ATP-binding cassette, sub-family B (MDRTAP), member 4 /FL=gb:NM_00443.2
207871_s_at_HG-U133A	ST77	suppression of tumorigenicity 7	gb:NM_018412.2 /DEF=Homo sapiens suppression of tumorigenicity 7 (ST7), transcript variant a, mRNA. /FEA=mRNA /GEN=ST7 /PROD=suppression of tumorigenicity 7, isoform a /DB_XREF=gi:11761623 /UG=Hs.5814 suppression of tumorigenicity 7 /FL=gb:NM_018412.2 gb:AF234882.1
207957_s_at_HG-U133A	PRKCB1	protein kinase C, beta 1	gb:NM_002738.1 /DEF=Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA. /FEA=mRNA /GEN=PRKCB1 /PROD=protein kinase C, beta 1 /DB_XREF=gi:4506068 /UG=Hs.77202 protein kinase C, beta 1 /FL=gb:NM_002738.1
207971_s_at_HG-U133A	KIAA0582	KIAA0582 protein	gb:NM_015147.1 /DEF=Homo sapiens KIAA0582 protein (KIAA0582), mRNA. /FEA=mRNA /GEN=KIAA0582 /PROD=KIAA0582 protein /DB_XREF=gi:13124755 /UG=Hs.79507 KIAA0582 protein /FL=gb:BC002982.1 gb:NM_015147.1 gb:BC004873.1
207983_s_at_HG-	STAG2	stromal antigen 2	gb:NM_006603.1 /DEF=Homo sapiens stromal antigen 2 (STAG2), mRNA.

U133A		/FEA=mRNA /GEN=STAG2 /PROD=stromal antigen 2 /DB_XREF=gi:57300668
207996_s_at_HG-U133A	C18orf1	/UG=Hs.8217 stromal antigen 2 /FL=gb:NM_006603.1 gb:NM_004338.1 /DEF=Homo sapiens chromosome 18 open reading frame 1 (C18ORF1), mRNA. /FEA=mRNA /GEN=C18ORF1 /PROD=chromosome 18 open reading frame 1 /DB_XREF=gi:4757883 /UG=Hs.153498 chromosome 18 open reading frame 1 /FL=gb:AF009426.1 gb:NM_004338.1
208033_s_at_HG-U133A	ATBF1	chromosome 18 open reading frame 1 AT-binding transcription factor 1 /FL=gb:D10250.1 gb:NM_006385.1
208042_at_HG-U133A	HSU84971	AT-binding transcription factor 1 /FL=gb:HSU84971 /PROD=AT-binding transcription factor 1 /DB_XREF=gi:5901893 /UG=Hs.101842 AT-binding transcription factor 1 /FL=gb:HSU84971.1 gb:NM_013303.1
208091_s_at_HG-U133A	DKFZP564K0822	fetal hypothetical protein fetal hypothetical protein /FL=gb:NM_030796.1 /DEF=Homo sapiens hypothetical protein DKFZP564K0822 (DKFZP564K0822), mRNA. /FEA=mRNA /GEN=DKFZP564K0822 /PROD=hypothetical protein DKFZP564K0822 /DB_XREF=gi:13540577
208141_s_at_HG-U133A	MGC4293	hypothetical protein MGC4293 hypothetical protein MGC4293 /FL=gb:NM_030796.1
208146_s_at_HG-U133A	CPVL	hypothetical protein MGC4293 carboxypeptidase, vitellogenin-like carboxypeptidase, vitellogenin-like /FL=gb:NM_031311.1
208168_s_at_HG-U133A	CHIT1	chitinase 1 (chitotriosidase) chitinase 1 (chitotriosidase) /FL=gb:NM_003465.1 /DEF=Homo sapiens chitinase 1 (chitotriosidase) (CHIT1). mRNA. /FEA=mRNA /GEN=CHIT1 /PROD=chitotriosidase /DB_XREF=gi:4502808 /UG=Hs.91093 chitinase 1 (chitotriosidase)

			/FL=gb:U29615.1 gb:NM_003465.1
208190_s_at_HG-U133A	LISCH7	liver-specific bHLH-Zip transcription factor	gb:NM_015925.1 /DEF=Homo sapiens liver-specific bHLH-Zip transcription factor (LISCH7), mRNA. /FEA=mRNA /GEN=LISCH7 /PROD=LISCH protein factor /FL=gb:AF130386.1 gb:NM_015925.1
208195_at_HG-U133A	TTN	titin	gb:NM_003319.1 /DEF=Homo sapiens titin (TTN), mRNA. /FEA=mRNA /GEN=TTN /PROD=titin /DB_XREF=gi:4507720 /UG=Hs.172004 titin /FL=gb:NM_003319.1
208217_at_HG-U133A	GABRR2	gamma-aminobutyric acid (GABA) receptor, rho 2	gb:NM_002043.1 /DEF=Homo sapiens gamma-aminobutyric acid (GABA) receptor, rho 2 (GABRR2), mRNA. /FEA=mRNA /GEN=GABRR2 /PROD=gamma-aminobutyric acid (GABA) receptor, rho 2 precursor /DB_XREF=gi:4503870 /UG=Hs.9927 gamma-aminobutyric acid (GABA) receptor, rho 2 /FL=gb:M86868.1 gb:NM_002043.1
208229_at_HG-U133A	FGFR2	fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pleiffer syndrome, Jackson-Weiss syndrome)	gb:NM_02975.1 /DEF=Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pleiffer syndrome, Jackson-Weiss syndrome) (FGFR2), transcript variant 8, mRNA. /GEN=FGFR2 /PROD=fibroblast growth factor receptor 2, isoform 8 precursor /DB_XREF=gi:13186264 /UG=Hs.278581 fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pleiffer syndrome, Jackson-Weiss syndrome) /FL=gb:NM_022975.1
208248_x_at_HG-U133A	APLP2	amyloid beta (A4) precursor-like protein 2	gb:NM_001642.1 /DEF=Homo sapiens amyloid beta (A4) precursor-like protein 2 (APLP2), mRNA. /FEA=mRNA /GEN=APLP2 /PROD=amyloid beta (A4) precursor-like protein 2 /DB_XREF=gi:4502146 /UG=Hs.279518 amyloid beta (A4) precursor-like protein 2 /FL=gb:L09209.1 gb:NM_001642.1 gb:L27631.1 gb:AF168936.1
208268_at_HG-U133A	ADAM28	a disintegrin and metalloproteinase	gb:NM_021777.1 /DEF=Homo sapiens a disintegrin and metalloproteinase

		domain 28	domain 28 (ADAM28), transcript variant 3, mRNA. /FEA=mRNA /GEN=ADAM28 /PROD=a disintegrin and metalloproteinase domain 28, isoform 3 preprotein /DB_XREF=gi:11496993 /UG=Hs.174030 a disintegrin and metalloproteinase domain 28 /FL=gb:NM_021777.1 gb:AF137335.1
208302_at_HG-U133A	HB-1	minor histocompatibility antigen HB-1	gb:NM_021182.1 /DEF=Homo sapiens minor histocompatibility antigen HB-1 (HB-1), mRNA. /FEA=mRNA /GEN=HB-1 /PROD=minor histocompatibility antigen HB-1. /DB_XREF=gi:10863982 /UG=Hs.158320 minor histocompatibility antigen HB-1 /FL=gb:NM_021182.1 gb:AF103884.1
208306_x_at_HG-U133A	HLA-DRB4	major histocompatibility complex, class II, DR beta 4	gb:NM_021983.2 /DEF=Homo sapiens major histocompatibility complex, class II, DR beta 4 (HLA-DRB4), mRNA. /FEA=mRNA /GEN=HLA-DRB4 /PROD=major histocompatibility complex, class II, DRbeta 4 /DB_XREF=gi:11875206 /UG=Hs.299934 major histocompatibility complex, class II, DR beta 4 /FL=gb:NM_021983.2
208456_s_at_HG-U133A	RRAS2	related RAS viral (r-ras) oncogene homolog 2	gb:NM_012250.1 /DEF=Homo sapiens oncogene TC21 (TC21), mRNA. /FEA=CDS /GEN=TC21 /PROD=oncogene TC21 /DB_XREF=gi:6912697 /UG=Hs.206097 oncogene TC21 /FL=gb:NM31468.1 gb:NM_012250.1
208470_s_at_HG-U133A	HPR	haptoglobin-related protein	gb:NM_020995.1 /DEF=Homo sapiens haptoglobin-related protein (HPR), mRNA. /FEA=CDS /GEN=HPR /PROD=haptoglobin-related protein /DB_XREF=gi:10337588 /UG=Hs.328822 haptoglobin-related protein /FL=gb:NM_020995.1
208581_x_at_HG-U133A	MT1X	metallothionein 1X	gb:NM_005952.1 /DEF=Homo sapiens metallothionein 1X (MT1X), mRNA. /FEA=CDS /GEN=MT1X /PROD=metallothionein 1X /DB_XREF=gi:10835231 /UG=Hs.278462 metallothionein 1X /FL=gb:NM_005952.1
208611_s_at_HG-U133A	SPTAN1	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)	gb:U83867.1 /DEF=Human alpha II spectrin mRNA, complete cds. /FEA=mRNA /PROD=alpha II spectrin /DB_XREF=gi:1805279 /UG=Hs.77196 spectrin, alpha, non-erythrocytic 1 (alpha-fodrin) /FL=gb:J05243.1 gb:U83867.1 gb:NM_003127.1
208612_at_HG-U133A	GRP58	glucose regulated protein, 58kD	gb:D83485.1 /DEF=Homo sapiens mRNA for ER-60 protease, complete cds.

		/FEA=mRNA /PROD=ER-60 protease /DB_XREF=gi:1208426 /UG=Hs.289101 glucose regulated protein, 58kD /FL=gb:U42068.1 gb:D83485.1 gb:D16234.1 gb:NM_005313.1
208614_s_at_HG-U133A	FLNB	filamin B, beta (actin binding protein 278) gb:M62994.1 /DEF=Homo sapiens thyroid autoantigen (truncated actin-binding protein) mRNA, complete cds. /FEA=mRNA /PROD=thyroid autoantigen /DB_XREF=gi:349450 /UG=Hs.81008 filamin B, beta (actin-binding protein-278) /FL=gb:AF043045.1 gb:AF042166.1 gb:M62994.1 gb:NM_001457.1
208623_s_at_HG-U133A	VIL2	villin 2 (ezrin) gb:J05021.1 /DEF=Human cytovillin 2 (VIL2) mRNA, complete cds. /FEA=mRNA /GEN=VIL2 /DB_XREF=gi:340216 /UG=Hs.155191 villin 2 (ezrin) /FL=gb:J05021.1 gb:AL162086.1 gb:NM_003379.2
208629_s_at_HG-U133A	HADHA	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit gb:NM_000182.1 gb:D16480.1 gb:U04627.1 /DB_XREF=est:602513910F1 /CLONE=IMAGE:4645587 /UG=Hs.75860 Coenzyme A hydratase (trifunctional protein), alpha subunit /FL=gb:NM_000182.1 gb:BC001126.1 gb:BC003401.1 gb:NM_005617.1
208645_s_at_HG-U133A		ribosomal protein S14 /FL=gb:BC001126.1 gb:BC003401.1 gb:NM_005617.1 gb:AF116710.1 /DEF=Homo sapiens PRO2640 mRNA, complete cds. /FEA=mRNA /PROD=PRO2640 /DB_XREF=gi:7959918 /UG=Hs.244621 ribosomal protein S14 /FL=gb:BC001126.1 gb:BC003401.1 gb:NM_005617.1 gb:AF116710.1
208646_at_HG-U133A		gb:AF116710.1 /DEF=Homo sapiens PRO2640 mRNA, complete cds. /FEA=mRNA /PROD=PRO2640 /DB_XREF=gi:7959918 /UG=Hs.244621 ribosomal protein S14 /FL=gb:BC001126.1 gb:BC003401.1 gb:NM_005617.1 gb:AF116710.1 Consensus includes gb:BG327863 /FEA=EST /DB_XREF=gi:13134301 /DB_XREF=est:602426876F1 /CLONE=IMAGE:4564675 /UG=Hs.286124 CD24 antigen (small cell lung carcinoma cluster 4 antigen) /FL=gb:M58664.1
208650_s_at_HG-U133A	CD24	CD24 antigen (small cell lung carcinoma cluster 4 antigen) gb:L33930.1 gb:NM_013230.1
208651_x_at_HG-	CD24	CD24 antigen (small cell lung carcinoma gb:M58664.1 /DEF=Homo sapiens CD24 signal transducer mRNA, complete

U133A		cluster 4 antigen)	cds. /FEA=mRNA /PROD=signal transducer CD24 /DB_XREF=gi:180167 /UG=Hs.286124 CD24 antigen (small cell lung carcinoma cluster 4 antigen) /FL=gb:MG8664.1 gb:L33930.1 gb:NM_013230.1
208657_s_at_HG-U133A	MSF	MLL septin-like fusion	gb:AF142408.1 /DEF=Homo sapiens cell division control protein septin D1 mRNA, complete cds. /FEA=mRNA /PROD=cell division control protein septin D1 /DB_XREF=gi:11056010 /UG=Hs.181002 MLL septin-like fusion /FL=gb:AF142408.1 gb:AF142569.1
208664_s_at_HG-U133A	TTC3	tetratricopeptide repeat domain 3	Consensus includes gb:AU131711 /FEA=EST /DB_XREF=gi:10392065 /DB_XREF=est:AU131711 /CLONE=NT2RP3003092 /UG=Hs.118174 tetratricopeptide repeat domain 3 /FL=gb:D84294.1
208674_x_at_HG-U133A	DDOST	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	gb:BC002394.1 /DEF=Homo sapiens, dolichyl-diphosphooligosaccharide-protein glycosyltransferase, clone MGc.2191, mRNA, complete cds. /FEA=mRNA /PROD=dolichyl-diphosphooligosaccharide-protein glycosyltransferase /DB_XREF=gi:12803530 /UG=Hs.34789 dolichyl-diphosphooligosaccharide-protein glycosyltransferase /FL=gb:BC002394.1 gb:D29643.1 gb:NM_005216.1
208683_at_HG-U133A	CAPN2	calpain 2, (mII) large subunit	gb:M23254.1 /DEF=Human Ca2+-activated neutral protease large subunit (CANP) mRNA, complete cds. /FEA=mRNA /GEN=CANP /PROD=neutral protease large subunit /DB_XREF=gi:511636 /UG=Hs.76288 calpain 2, (mII) large subunit /FL=gb:NM_001748.3 gb:M23254.1 gb:AF261089.1
208689_s_at_HG-U133A	RPN2	ribophorin II	gb:BC003560.1 /DEF=Homo sapiens, ribophorin II, clone MGc:1817, mRNA, complete cds. /FEA=mRNA /PROD=ribophorin II /DB_XREF=gi:13097707 /UG=Hs.75722 ribophorin II /FL=gb:BC003560.1 gb:NM_002951.1
208697_s_at_HG-U133A	EIF3S6	eukaryotic translation initiation factor 3, subunit 6 (48kD)	gb:BC000734.1 /DEF=Homo sapiens, eukaryotic translation initiation factor 3, subunit 6 (48kD), clone MGc:2060, mRNA, complete cds. /FEA=mRNA /PROD=eukaryotic translation initiation factor 3, subunit 6 (48kD) /DB_XREF=gi:12653884 /UG=Hs.106673 eukaryotic translation initiation factor 3, subunit 6 (48kD) /FL=gb:BC000734.1 gb:U62962.1 gb:U54562.1 gb:U85947.1 gb:U94175.1 gb:NM_001568.1

208702_x_at_HG-U133A	APLP2	amyloid beta (A4) precursor-like protein 2	Consensus includes gb:AI525212 /FEA=EST /DB_XREF=gi:4439347 /DB_XREF=est:pt1.1-2.A08.r /UG=Hs.279518 amyloid beta (A4) precursor-like protein 2 /FL=gb:BC000373.1
208703_s_at_HG-U133A	APLP2	amyloid beta (A4) precursor-like protein 2	Consensus includes gb:BG427393 /FEA=EST /DB_XREF=gi:13333995 /DB_XREF=est:602499110F1 /CLONE=IMAGE:4612562 /UG=Hs.279518 amyloid beta (A4) precursor-like protein 2 /FL=gb:BC000373.1
208710_s_at_HG-U133A	AP3D1	adaptor-related protein complex 3, delta 1 subunit	Consensus includes gb:AI424923 /FEA=EST /DB_XREF=gi:4270841 /DB_XREF=est:tg19a07.x1 /CLONE=IMAGE:2109204 /UG=Hs.75056 adaptor-related protein complex 3, delta 1 subunit /FL=gb:AF002163.1
208741_at_HG-U133A	SAP18	sin3-associated polypeptide, 18kD	Consensus includes gb:AVW274856 /FEA=EST /DB_XREF=gi:6661886 /DB_XREF=est:xm61g03.x1 /CLONE=IMAGE:2688724 /UG=Hs.23964 sin3-associated polypeptide, 18kD /FL=gb:NM_005870.2 gb:U96915.1 gb:AF153608.1 gb:U78303.1
208754_s_at_HG-U133A	NAP1L1	nucleosome assembly protein 1-like 1	gb:AL162068.1 /DEF=Homo sapiens mRNA; cDNA DKFZp762G106 (from clone DKFZp762G106); complete cds. /FEA=mRNA /GEN=DKFZp762G106 /PROD=hypothetical protein /DB_XREF=gi:7328143 /UG=Hs.173662 nucleosome assembly protein 1-like 1 /FL=gb:BC002387.1 gb:AL162068.1
208819_at_HG-U133A	MEL		gb:BC002977.1 /DEF=Homo sapiens, mel transforming oncogene (derived from cell line NK14)- RAB8 homolog, clone MGC:2196, mRNA, complete cds. /FEA=mRNA /PROD=mel transforming oncogene (derived from cell line NK14)- RAB8 homolog /DB_XREF=gi:12804236 /UG=Hs.5947 mel transforming oncogene (derived from cell line NK14)- RAB8 homolog /FL=gb:BC002977.1 gb:NM_005370.2
208852_s_at_HG-U133A	CANX	calnexin	Consensus includes gb:AI761759 /FEA=EST /DB_XREF=gi:5177751 /DB_XREF=est:wg67n12.x1 /CLONE=IMAGE:2370215 /UG=Hs.155560 calnexin /FL=gb:NM_001746.1 gb:BC003552.1 gb:M98452.1 gb:L10284.1 gb:L18887.1
208858_s_at_HG-	KIAA0747	KIAA0747 protein	gb:BC004998.1 /DEF=Homo sapiens, Similar to membrane bound C2 domain

U133A			containing protein, clone MGC:4422, mRNA, complete cds. /FEA=mRNA /PROD=Similar to membrane bound C2 domain containing protein /DB_XREF=gi:13436457 /UG=Hs.8309 KIAA0747 protein /FL=gb:BC004998.1
208864_s_at_HG-U133A	TXN	thioredoxin	gb:AF313911.1 /DEF=Homo sapiens thioredoxin mRNA, complete cds. /FEA=mRNA /PROD=thioredoxin /DB_XREF=gi:11345419 /UG=Hs.76136 thioredoxin /FL=gb:AF313911.1 gb:BC003377.1 gb:NM_003329.1 gb:AF276919.1 gb:AY004872.1
208890_s_at_HG-U133A	PLXNB2	plexin B2	gb:BC004542.1 /DEF=Homo sapiens, clone MGCI:11315, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGCI:11315) /DB_XREF=gi:13528889 /UG=Hs.3989 plexin B2 /FL=gb:BC004542.1
208894_at_HG-U133A	HLA-DRA		gb:M60334.1 /DEF=Human MHC class II HLA-DR-alpha mRNA, complete cds. /FEA=mRNA /GEN=HLA-DRA /PROD=cell surface glycoprotein /DB_XREF=gi:188255 /UG=Hs.76807 major histocompatibility complex, class II, DR alpha /FL=gb:M60334.1 gb:NM_019111.1
208908_s_at_HG-U133A	CAST	calpastatin	gb:AF327443.1 /DEF=Homo sapiens calpastatin mRNA, complete cds. /FEA=mRNA /PROD=calpastatin /DB_XREF=gi:12056961 /UG=Hs.279607 calpastatin /FL=gb:AF327443.1 gb:U267724.2
208913_at_HG-U133A	GGA2		Consensus includes gb:AA868360 /FEA=EST /DB_XREF=gi:2964005 /DB_XREF=est:ak43g11.s1 /CLONE=IMAGE:1408772 /UG=Hs.155546 KIAA1080 protein; Golgi-associated, gamma-adaptin ear containing, ARF- binding protein 2 /FL=gb:AF233522.1 gb:AF165531.1 gb:NM_015044.1
208914_at_HG-U133A	GGA2		Consensus includes gb:BE646414 /FEA=EST /DB_XREF=gi:9970725 /DB_XREF=est:7e86d08.x1 /CLONE=IMAGE:3292047 /UG=Hs.155546 KIAA1080 protein; Golgi-associated, gamma-adaptin ear containing, ARF- binding protein 2 /FL=gb:AF190863.1 gb:AF233522.1 gb:AF165531.1 gb:NM_015044.1
208918_s_at_HG-	FLJ13052	NAD kinase	Consensus includes gb:AI334128 /FEA=EST /DB_XREF=gi:4070687

U133A			/DB_XREF=est:qq07e12.x1 /CLONE=IMAGE:1931854 /UG=Hs.220324
209003_at_HG-U133A	SLC25A11	solute carrier family 25 (mitochondrial carrier, oxoglutarate carrier), member 11	/DEF=Homo sapiens clone 24408 2-oxoglutarate carrier protein mRNA, complete cds. /FEA=mRNA /PROD=2-oxoglutarate carrier protein /DB_XREF=gi:3387910 /UG=Hs.184877 solute carrier family 25 (mitochondrial carrier, oxoglutarate carrier), member 11 /FL=gb:AF070548.1
209018_s_at_HG-U133A	PINK1	PTEN induced putative kinase 1	Consensus includes gb:BF432478 /FEA=EST /DB_XREF=gi:1144621 /DB_XREF=est:nacc5d04.x1 /CLONE=IMAGE:3406494 /UG=Hs.6163 Homo sapiens protein kinase BRPK mRNA, complete cds /FL=gb:AF316873.1
209019_s_at_HG-U133A	PINK1	PTEN induced putative kinase 1	gb:AF316873.1 /DEF=Homo sapiens protein kinase BRPK mRNA, complete cds. /FEA=mRNA /PROD=protein kinase BRPK /DB_XREF=gi:13492051 /UG=Hs.6163 Homo sapiens protein kinase BRPK mRNA, complete cds /FL=gb:AF316873.1
209023_s_at_HG-U133A	STAG2	stromal antigen 2	gb:BC001765.1 /DEF=Homo sapiens, Similar to stromal antigen 2, clone MGC:1282, mRNA, complete cds. /FEA=mRNA /PROD=Similar to stromal antigen 2 /DB_XREF=gi:12804678 /UG=Hs.8217 stromal antigen 2 /FL=gb:BC001765.1
209055_s_at_HG-U133A	CDC5L	CDC5 cell division cycle 5-like (S. pombe)	Consensus includes gb:AW268817 /FEA=EST /DB_XREF=gi:6655847 /DB_XREF=est:xv38c01.x1 /CLONE=IMAGE:2815392 /UG=Hs.155174 CDC5 (cell division cycle 5, S. pombe, homolog)-like /FL=gb:NM_001253.1 gb:U86753.1 gb:AB007892.1
209060_x_at_HG-U133A	NCOA3	nuclear receptor coactivator 3	Consensus includes gb:AI438999 /FEA=EST /DB_XREF=gi:4301251 /DB_XREF=est:tc84b12.x1 /CLONE=IMAGE:2072831 /UG=Hs.225977 nuclear receptor coactivator 3 /FL=gb:AF010227.1 gb:AF012108.1 gb:AF016031.1
209061_at_HG-U133A	NCOA3	nuclear receptor coactivator 3	Consensus includes gb:AI761748 /FEA=EST /DB_XREF=gi:5177504 /DB_XREF=est:wg67n01.x1 /CLONE=IMAGE:2370193 /UG=Hs.225977 nuclear receptor coactivator 3 /FL=gb:AF010227.1 gb:AF012108.1 gb:AF016031.1
209062_x_at_HG-	NCOA3	nuclear receptor coactivator 3	gb:AF010227.1 /DEF=Homo sapiens receptor-associated coactivator 3 (RAC3)

U133A			mRNA, complete cds. /FEA=mRNA /GEN=RAC3 /PROD=receptor-associated coactivator 3 /DB_XREF=gi:2318005 /UG=Hs.225977 nuclear receptor coactivator 3 /FL=gb:AF012108.1 gb:AF016031.1
209075_s_at_HG-U133A	NIFU	nitrogen fixation cluster-like	gb:AY009128.1 /DEF=Homo sapiens ISCU2 (ISCU) mRNA, complete cds, alternatively spliced. /FEA=mRNA /GEN=ISCU /PROD=ISCU2 /DB_XREF=gi:11545706 /UG=Hs.9908 nitrogen fixation cluster-like /FL=gb:AY009128.1
209085_x_at_HG-U133A	RFC1	replication factor C (activator 1) 1 (145kD)	gb:L14922.1 /DEF=Homo sapiens DNA-binding protein (PO-GA) mRNA, complete cds. /FEA=mRNA /PROD=DNA-binding protein /DB_XREF=gi:307337 /UG=Hs.166563 replication factor C (activator 1) 1 (145kD) /FL=gb:AF040250.1 gb:L14922.1
209101_at_HG-U133A	CTGF	connective tissue growth factor	gb:M92934.1 /DEF=Human connective tissue growth factor, complete cds. /FEA=mRNA /PROD=connective tissue growth factor /DB_XREF=gi:180923 /UG=Hs.75511 connective tissue growth factor /FL=gb:M92934.1
209135_at_HG-U133A	ASPH	aspartate beta-hydroxylase	gb:NW_001901.1 /DEF=Homo sapiens aspartyl beta-hydroxylase 2.8 kb transcript mRNA, complete cds; alternatively spliced. /FEA=mRNA /PROD=aspartyl beta-hydroxylase 2.8 kb transcript /DB_XREF=gi:11878115 /UG=Hs.283664 aspartate beta-hydroxylase /FL=gb:AF289489.1
209160_at_HG-U133A	AKR1C3		gb:AB018580.1 /DEF=Homo sapiens mRNA for hluPGFS, complete cds. /FEA=mRNA /GEN=hluPGFS /PROD=hluPGFS /DB_XREF=gi:5624210 /UG=Hs.78183 aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II) /FL=gb:AF149416.2 gb:NM_003739.2
209167_at_HG-U133A	GRM6B		gb:D17793.1 gb:AB018580.1
209168_at_HG-U133A	GRM6B		Consensus includes gb:AI419030 /FEA=EST /DB_XREF=gi:4264961 /DB_XREF=est:ff53bd1.x1 /CLONE=IMAGE:2102953 /UG=Hs.5422 glycoprotein M6B /FL=gb:AF016004.1
			Consensus includes gb:AW148844 /FEA=EST /DB_XREF=gi:6196740

			/DB_XREF=est:xf0506.x1 /CLONE=IMAGE:2617162 /UG=Hs.5422 glycoprotein M6B /FL=gb:AF016004.1
209169_at_HG-U133A	GPM6B	glycoprotein M6B	Consensus includes gb:N63576 /FEA=EST /DB_XREF=gi:1211405 /DB_XREF=est:yy6307.s1 /CLONE=IMAGE:278245 /UG=Hs.5422 glycoprotein M6B /FL=gb:AF016004.1
209170_s_at_HG-U133A	GPM6B	glycoprotein M6B	gb:AF016004.1 /DEF=Homo sapiens m6b1 mRNA, complete cds. /FEA=mRNA /GEN=m6b1 /DB_XREF=gi:3387766 /UG=Hs.5422 glycoprotein M6B /FL=gb:AF016004.1
209178_at_HG-U133A	DDX38	DEAD/H (Asp-Glu-Ala-Asp)/Hs box polypeptide 38	gb:AF038391.1 /DEF=Homo sapiens pre-mRNA splicing factor (PRP16) mRNA, complete cds. /FEA=mRNA /GEN=PRP16 /PROD=pre-mRNA splicing factor /DB_XREF=gi:3123905 /UG=Hs.78054 pre-mRNA splicing factor similar to S. cerevisiae Prp16 /FL=gb:BC004235.1 gb:D86977.1 gb:AF038391.1
209186_at_HG-U133A	ATP2A2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	gb:NM_014003.1
209188_x_at_HG-U133A	DR1	down-regulator of transcription 1, TBP-binding (negative cofactor 2)	gb:M23114.1 /DEF=Homo sapiens calcium-ATPase (HK1) mRNA, complete cds. /FEA=mRNA /GEN=HK1 /DB_XREF=gi:184100 /UG=Hs.1526 ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 /FL=gb:M23114.1
209190_s_at_HG-U133A	DIAPH1	diaphanous homolog 1 (Drosophila)	gb:BC002809.1 /DEF=Homo sapiens, down-regulator of transcription 1, TBP-binding (negative cofactor 2), clone MGC:4292, mRNA, complete cds. /FEA=mRNA /PROD=down-regulator of transcription 1, TBP-binding(negative cofactor 2) /DB_XREF=gi:12803924 /UG=Hs.16697 down-regulator of transcription 1, TBP-binding (negative cofactor 2) /FL=gb:BC002809.1
209197_at_HG-U133A	KIAA0080	KIAA0080 protein	gb:AF051782.1 /DEF=Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds. /FEA=mRNA /GEN=HDIA1 /PROD=diaphanous 1 /DB_XREF=gi:2947237 /UG=Hs.26584 diaphanous (Drosophila, Homolog) 1 /FL=gb:AF051782.1

			Consensus includes gb:AL389886 /DEF=Human DNA sequence from clone RP1-237C24 on chromosome 20 Contains the 3 end of the SLC23A1 gene encoding solute carrier family 23 member 1 (nucleobase transporters), ESTs, STSs and GSSs /FEA=mRNA /DB_XREF=gi:10086152 /UG=Hs.82042 solute carrier family 23 (nucleobase transporters), member 1 /FL=gb:AF058319.1 gb:NM_005116.1 gb:AF164142.1
209236_at_HG-U133A			gb:AF037261.1 /DEF=Homo sapiens SH3-containing adaptor molecule-1 mRNA, complete cds. /FEA=mRNA /PROD=SH3-containing adaptor molecule-1 /DB_XREF=gi:3004947 /UG=Hs.33787 vinexin beta (SH3-containing adaptor molecule-1) /FL=gb:AF037261.1
209253_at_HG-U133A	SCAM-1	vinemixin beta (SH3-containing adaptor molecule-1)	gb:AF020043.1 /DEF=Homo sapiens chromosome-associated polypeptide (HCAP) mRNA, complete cds. /FEA=mRNA /GEN=HCAP /PROD=chromosome-associated polypeptide /DB_XREF=gi:3089367 /UG=Hs.24485 chondroitin sulfate proteoglycan 6 (bamacan) /FL=gb:AF020043.1 gb:NM_005445.1 gb:AF067163.1
209259_s_at_HG-U133A	CSPG6	chondroitin sulfate proteoglycan 6 (bamacan)	gb:AB040120.1 /DEF=Homo sapiens mRNA for BCG induced integral membrane protein BIGMo-103, complete cds. /FEA=mRNA /GEN=BIGMo-103 /PROD=BCG induced integral membrane protein BIGMo-103 /DB_XREF=gi:12657580 /UG=Hs.284205 up-regulated by BCG-CWS /FL=gb:AB040120.1
209267_s_at_HG-U133A	LOC64116	up-regulated by BCG-CWS	Consensus includes gb:AI139569 /FEA=EST /DB_XREF=gi:3645541 /DB_XREF=estqc57a12.x1 /CLONE=IMAGE:1713694 /UG=Hs.153026 SWAP-70 protein /FL=gb:BC000616.1 gb:AF210818.1
209306_s_at_HG-U133A	SWAP70	SWAP-70 protein	Consensus includes gb:AB014540.1 /DEF=Homo sapiens mRNA for KIAA0640 protein, partial cds. /FEA=mRNA /GEN=KIAA0640 /PROD=KIAA0640 protein /DB_XREF=gi:3327093 /UG=Hs.153026 SWAP-70 protein /FL=gb:BC000616.1 gb:AF210818.1
209307_at_HG-U133A	SWAP70	SWAP-70 protein	gb:U65585.1 /DEF=Homo sapiens MHC class II antigen (HLA-DRB1) mRNA, major histocompatibility complex, class II
209312_x_at_HG-	HLA-DRB1		

U133A	II, DR beta 1	HLA-DRB1*PBL allele, complete cds. /FEA=mRNA /GEN=HLA-DRB1 /PROD=MHC class II antigen /DB_XREF=gi:5478215 /UG=Hs.180255 major histocompatibility complex, class II, DR beta 1 /FL=gb:M33600.1
209321_s_at_HG-U133A	ADCY3	gb:NM_002124.1 /DEF=Homo sapiens type III adenylyl cyclase (AC-III) mRNA, complete cds. /FEA=mRNA /GEN=AC-III /PROD=type III adenylyl cyclase /DB_XREF=gi:4104225 /UG=Hs.8402 adenylyl cyclase 3 /FL=gb:NM_004036.2 gb:AF03361.1
209344_at_HG-U133A	TPM4	gb:BC002827.1 /DEF=Homo sapiens, tropomyosin 4, clone MGC:3641, mRNA, complete cds. /FEA=mRNA /PROD=tropomyosin 4 /DB_XREF=gi:12803558 /UG=Hs.250641 tropomyosin 4 /FL=gb:BC002827.1
209354_at_HG-U133A	TNFRSF14	gb:NM_003290.1 /DEF=Homo sapiens, tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator), clone MGC:3753, mRNA, complete cds. /FEA=mRNA /PROD=tumor necrosis factor receptor superfamily,member 14 (herpesvirus entry mediator) /DB_XREF=gi:12803894 /UG=Hs.279899 tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator) /FL=gb:BC027934.1 gb:U70321.1 gb:U81232.1
209365_s_at_HG-U133A	ECM1	gb:NM_003820.1 gb:AF153978.1 /DEF=Human extracellular matrix protein 1 (ECM1) mRNA, complete cds. /FEA=mRNA /GEN=ECM1 /PROD=extracellular matrix protein 1 /DB_XREF=gi:1488323 /UG=Hs.81071 extracellular matrix protein 1 /FL=gb:NM_004425.2 gb:U65932.1 gb:U68186.1
209369_at_HG-U133A	ANXA3	gb:M63310.1 /DEF=Human 1,2-cyclic-inositol-phosphate phosphodiesterase (ANX3) mRNA, complete cds. /FEA=mRNA /GEN=ANX3 /PROD=1,2-cyclic-inositol-phosphate phosphodiesterase /DB_XREF=gi:178696 /UG=Hs.1378
209374_s_at_HG-	IgHM	annexin A3 /FL=gb:BC000871.1 gb:M63310.1 gb:M20560.1 gb:NM_005139.1 gb:BC001872.1 /DEF=Homo sapiens, clone MGC:1228, mRNA, complete cds.

U133A			/FEA=mRNA /PROD=Unknown (protein for MGC:1228) /DB_XREF=gi:12804852 /UG=Hs.302063 immunoglobulin heavy constant mu /FL=gb:BC002963.1 gb:BC001872.1
209380_s_at_HG-U133A	ABCC5	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	gb:AF146074.1 /DEF=Homo sapiens ABC protein mRNA, complete cds. /FEA=mRNA /PROD=ABC protein /DB_XREF=gi:5006890 /UG=Hs.108660 ATP-binding cassette, sub-family C (CFTR/MRP), member 5 /FL=gb:AF104942.1 gb:AB019002.1 gb:AF146074.1 gb:NM_005688.1 gb:U83661.2
209389_at_HG-U133A	HLC8	holocarboxylase synthetase (biotin-[propionyl-Coenzyme A-carboxylase (ATP-hydrolysing) ligase])	gb:D87328.1 /DEF=Homo sapiens mRNA for HCS, complete cds. /FEA=mRNA /PROD=HCS /DB_XREF=gi:1813423 /UG=Hs.79375 holocarboxylase synthetase (biotin-propionyl-Coenzyme A-carboxylase (ATP-hydrolysing) ligase) /FL=gb:D87328.1
209412_at_HG-U133A	TMEM1	transmembrane protein 1	gb:U61500.1 /DEF=Human GT334 protein (GT334) gene mRNA, complete cds. /FEA=mRNA /GEN=GT334 /PROD=GT334 protein /DB_XREF=gi:1778032 /UG=Hs.94479 transmembrane protein 1 /FL=gb:U61500.1
209428_s_at_HG-U133A	ZFPL1	zinc finger protein-like 1	Consensus includes gb:BG420865 /FEA=EST /DB_XREF=gi:13327371 /DB_XREF=est:602452067F1 /CLONE=IMAGE:4590353 /UG=Hs.155165 zinc finger protein-like 1 /FL=gb:AF001891.1 gb:NM_008782.1 gb:AF03291.1
209490_s_at_HG-U133A	PPT2	palmitoyl-protein thioesterase 2	gb:AF020543.1 /DEF=Homo sapiens palmitoyl-protein thioesterase-2 (PPT2) mRNA, complete cds. /FEA=mRNA /GEN=PPT2 /PROD=palmitoyl-protein thioesterase-2 /DB_XREF=gi:2501960 /UG=Hs.81737 palmitoyl-protein thioesterase 2 /FL=gb:BC001355.1 gb:AF020543.1
209499_x_at_HG-U133A	TNFSF13	tumor necrosis factor (ligand) superfamily, member 13	Consensus includes gb:BF448647 /FEA=EST /DB_XREF=gi:11514815 /DB_XREF=est:7n90g02.x1 /CLONE=IMAGE:3572138 /UG=Hs.54673 tumor necrosis factor (ligand) superfamily, member 13 /FL=gb:AF114012.1
209500_x_at_HG-U133A	TNFSF13	tumor necrosis factor (ligand) superfamily, member 13	gb:AF114012.1 /DEF=Homo sapiens tumor necrosis factor-related death ligand-1beta mRNA, complete cds. /FEA=mRNA /PROD=tumor necrosis

		factor-related deathligand-1beta /DB_XREF=gi:7328555 /UG=Hs_54673 tumor necrosis factor (ligand) superfamily, member 13 /FL=gb:AF114012.1
209522_s_at_HG-U133A	CRAT	clone MGC:1564, mRNA, complete cds. /FEA=mRNA /PROD=Similar to carnitine acetyltransferase /DB_XREF=gi:13111704 /UG=Hs_12068 carnitine acetyltransferase /FL=gb:BC000723.1
209523_at_HG-U133A		Consensus includes gb:AK001618.1 /DEF=Homo sapiens cDNA FLJ10756 fs, clone NT2RP3004572, highly similar to Homo sapiens cofactor of initiator function mRNA. /FEA=mRNA /DB_XREF=gi:7022983 /UG=Hs_122752 TATA box binding protein (TBP)-associated factor, RNA polymerase II, B, 150kD /FL=gb:AF026445.1 gb:AF040701.1 gb:AF057694.1 gb:NM_003184.1
209558_s_at_HG-U133A	HIP12	gb:AB013384.1 /DEF=Homo sapiens mRNA for HIP1R, complete cds. /FEA=mRNA /GEN=HIP1R /PROD=HIP1R /DB_XREF=gi:3721835 /UG=Hs_96731 huntingtin interacting protein-1-related /FL=gb:AB013384.1
209561_at_HG-U133A	THBS3	gb:L38989.1 /DEF=Homo sapiens thrombospondin 3 (THBS3) mRNA, complete cds. /FEA=mRNA /GEN=THBS3 /PROD=thrombospondin 3 /DB_XREF=gi:886298 /UG=Hs_169875 thrombospondin 3 /FL=gb:NM_007112.1
209604_s_at_HG-U133A	GATA3	gb:L38989.1 /DEF=Homo sapiens thrombospondin 3 /FL=gb:BC003070.1 /DEF=Homo sapiens, GATA-binding protein 3, clone MGC:2346, mRNA, complete cds. /FEA=mRNA /PROD=GATA-binding protein 3 /DB_XREF=gi:13111765 /UG=Hs_169946 GATA-binding protein 3 /FL=gb:BC003070.1 gb:M69106.1 gb:NM_002051.1
209616_s_at_HG-U133A	CES1	gb:S73751.1 /DEF=Homo sapiens acyl coenzyme A:cholesterol acyltransferase mRNA, complete cds. /FEA=mRNA /PROD=acyl coenzyme A:cholesterol acyltransferase /DB_XREF=gi:688112 /UG=Hs_76888 carboxylesterase 1 (monocyte/macrophage serine esterase 1) /FL=gb:M73499.1 gb:L07764.1 gb:AF17775.1 gb:S73751.1

209619_at_HG-U133A	CD74	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)	gb:K01144.1 /DEF=Human major histocompatibility class II antigen gamma chain mRNA, complete cds. /FEA=mRNA /PROD=class II antigen gamma chain /DB_XREF=gi:188469 /UG=Hs.84298 CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated) /FL=gb:NM_004355.1 gb:K01144.1
209628_at_HG-U133A	P15-2	hypothetical protein P15-2	Consensus includes gb:AK023289.1 /DEF=Homo sapiens cDNA FLJ13227 fis, clone OVARC1000071, weakly similar to Homo sapiens NTF2-related export protein NXT1 (NXT1) mRNA. /FEA=mRNA /DB_XREF=gi:10435160 /UG=Hs.25010 hypothetical protein P15-2 /FL=gb:AF246127.1 gb:NM_018698.1 gb:AF201942.1
209670_at_HG-U133A	TRA	T cell receptor alpha locus	gb:M12959.1 /DEF=Human T-cell receptor active-alpha-chain mRNA from JM cell line, complete cds. /FEA=mRNA /GEN=TCRA /DB_XREF=gi:338734 /UG=Hs.74647 Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds /FL=gb:NM_12959.1 gb:M12423.1
209679_s_at_HG-U133A	LOC57228	hypothetical protein from clone 643	gb:BC003379.1 /DEF=Homo sapiens, hypothetical protein from clone 643, clone MGC:5115, mRNA, complete cds. /FEA=mRNA /PROD=hypothetical protein from clone 643 /DB_XREF=gi:13097236 /UG=Hs.206501 hypothetical protein from clone 643 /FL=gb:BC003379.1 gb:NM_020467.1
209682_at_HG-U133A	CBLB	Cas-Br-M (murine) ectropic retroviral transforming sequence b	gb:U26710.1 /DEF=Human cb1-b mRNA, complete cds. /FEA=mRNA /PROD=cb1-b /DB_XREF=gi:862406 /UG=Hs.3144 Cas-Br-M (murine) ectropic retroviral transforming sequence b /FL=gb:U26710.1
209685_s_at_HG-U133A	PRKCB1	protein kinase C, beta 1	gb:M13975.1 /DEF=Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds. /FEA=mRNA /GEN=PRKCB1 /PROD=protein kinase C beta-II type /DB_XREF=gi:189968 /UG=Hs.77202 protein kinase C, beta 1 /FL=gb:NM_13975.1
209686_at_HG-U133A	S100B	S100 calcium binding protein, beta (neural)	gb:BC001766.1 /DEF=Homo sapiens, S100 calcium-binding protein, beta (neural), clone MG.C.1323, mRNA, complete cds. /FEA=mRNA /PROD=S100 calcium-binding protein, beta (neural) /DB_XREF=gi:12804680 /UG=Hs.83384

		S100 calcium-binding protein, beta (neural) /FL=gb:BC001766.1 - gb:NM_006272.1
209714_s_at_HG-U133A	CDKN3	gb:AF213033.1 /DEF=Homo sapiens isolate BX-01 cyclin-dependent kinase associated protein phosphatase mRNA, complete cds. /FEA=mRNA /PROD=cyclin-dependent kinase associated proteinphosphatase /DB_XREF=gi:12734643 /UG=Hs.84113 cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase) /FL=gb:AF213033.1 gb:AF213034.1 gb:AF213035.1 gb:AF213036.1 gb:AF213037.1 gb:AF213038.1 gb:AF213039.1 gb:AF213040.1 gb:AF213041.1 gb:AF213042.1 gb:AF213044.1 gb:AF213046.1 gb:AF213047.1 gb:AF213048.1 gb:AF213049.1 gb:AF213050.1 gb:AF213051.1 gb:AF213052.1 gb:AF213053.1 gb:U02681.1 gb:L25876.1 gb:NM_005192.1 gb:L27711.1
209732_at_HG-U133A	CLECSF2	gb:BC005254.1 /DEF=Homo sapiens, Similar to C-type (calcium dependent carbohydrate-recognition domain) lectin, superfamily member 2 (activation-induced), clone MGc:12289, mRNA, complete cds. /FEA=mRNA /PROD=Similar to C-type (calcium dependent,carbohydrate-recognition domain) lectin, superfamilymember 2 (activation-induced) /DB_XREF=gi:13528920 /UG=Hs.85201 C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 2 (activation-induced) /FL=gb:BC005254.1 gb:AB015628.1 gb:NM_005127.1
209735_at_HG-U133A	ATP-binding cassette, sub-family G (WHITE), member 2 (ABCG2)	gb:AF098551.2 /DEF=Homo sapiens breast cancer resistance protein (BCRP) mRNA, complete cds. /FEA=mRNA /GEN=BCRP /PROD=breast cancer resistance protein /DB_XREF=gi:12414050 /UG=Hs.194720 ATP-binding cassette, sub-family G (WHITE), member 2 /FL=gb:AF098551.2 - gb:AB056867.1 gb:AF03796.1 gb:NM_004827.1
209754_s_at_HG-U133A		gb:AF113682.1 /DEF=Homo sapiens clone FLB3436 PRO0868 mRNA, complete cds. /FEA=mRNA /PROD=PRO0868 /DB_XREF=gi:6855608 /UG=Hs.11355 thymopentin /FL=gb:U09087.1 gb:AF113682.1

209761_s_at_HG-U133A	SP110	SP110 nuclear body protein	Consensus includes gb:AA869194 /FEA=EST /DB_XREF=gi:3144374 /DB_XREF=est:op51c02.s1 /CLONE=IMAGE:1580354 /UG=Hs.38125 interferon-induced protein 75, 52kD /FL=gb:AF280094.1
209765_at_HG-U133A	ADAM19	a disintegrin and metalloproteinase domain 19 (meltrin beta)	Consensus includes gb:Y13786.2 /DEF=Homo sapiens mRNA for meltrin-betaADAM 19 homologue. /FEA=mRNA /PROD=meltrin-betaADAM 19 homologue /DB_XREF=gi:12053590 /UG=Hs.278679 a disintegrin and metalloproteinase domain 19 (meltrin beta) /FL=gb:AF311317.1
209771_x_at_HG-U133A	CD24	CD24 antigen (small cell lung carcinoma cluster 4 antigen)	Consensus includes gb:AA761181 /FEA=EST /DB_XREF=gi:2810111 /DB_XREF=est:n209g03.s1 /CLONE=IMAGE:1287316 /UG=Hs.286124 CD24 antigen (small cell lung carcinoma cluster 4 antigen) /FL=gb:X69397.1
209772_s_at_HG-U133A	CD24	CD24 antigen (small cell lung carcinoma cluster 4 antigen)	gb:X69397.1 /DEF=H.sapiens CD24 gene, complete CDS. /FEA=mRNA /GEN=CD24 /PROD=cell surface antigen /DB_XREF=gi:396167 /UG=Hs.2886124 CD24 antigen (small cell lung carcinoma cluster 4 antigen) /FL=gb:X69397.1
209780_at_HG-U133A	DKFZP564F013	hypothetical protein DKFZp564F013	gb:AL136883.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434D166 (from clone DKFZp434D166); complete cds. /FEA=mRNA /GEN=DKFZp434D166 /PROD=hypothetical protein /DB_XREF=gi:12053266 /UG=Hs.128653
209806_at_HG-U133A	H2B/S	histone family member	hypothetical protein DKFZp564F013 /FL=gb:AL136883.1 gb:BC000893.1 /DEF=Homo sapiens, H2B histone family, member A, clone MGC:5132, mRNA, complete cds. /FEA=mRNA /PROD=H2B histone family, member A /DB_XREF=gi:12654150 /UG=Hs.247817 H2B histone family, member A /FL=gb:BC000893.1
209815_at_HG-U133A	PTCH	patched homolog (Drosophila)	Consensus includes gb:BG054916 /FEA=EST /DB_XREF=gi:12512119 /DB_XREF=est:n202b02.x1 /CLONE=IMAGE:3441723 /UG=Hs.159526
209822_s_at_HG-U133A	VLDLR	very low density lipoprotein receptor	patched (Drosophila) homolog /FL=gb:U43148.1 gb:L22431.1 /DEF=Human very low density lipoprotein receptor, complete cds. /FEA=mRNA /PROD=very low density lipoprotein receptor /DB_XREF=gi:437386 /UG=Hs.73729 very low density lipoprotein receptor

			/FL=gb:D16493.1 /DEF=Homo sapiens, Similar to uridine monophosphate kinase, clone MGC:10318, mRNA, complete cds. /FEA=mRNA /PROD=Similar to uridine monophosphate kinase /DB_XREF=gi:12804106 /UG=Hs.75939
209825_s_at_HG-U133A	UMPK	uridine monophosphate kinase	Consensus includes gb:NM_004513.1 /DEF=Homo sapiens interleukin 16 (lymphocyte chemoattractant factor) (IL-16), mRNA, /FEA=CDS /GEN=IL16 /PROD=interleukin 16 /DB_XREF=gi:4758595 /UG=Hs.82127 Interleukin 16 (lymphocyte chemoattractant factor) /L=gb:S81601.1 gb:U82972.1
209827_s_at_HG-U133A	IL16	interleukin 16 (lymphocyte chemoattractant factor)	gb:AF053412.1 gb:NM0391.1 gb:NM_004513.1 gb:AB004574.1 /DEF=Homo sapiens mRNA for deoxyribonuclease II, complete cds. /FEA=mRNA /GEN=DNASE2 /PROD=deoxyribonuclease II, /DB_XREF=gi:3184394 /UG=Hs.118243 deoxyribonuclease II, lysosomal /FL=gb:AF045937.1 gb:AF047016.1 gb:AB004574.1 gb:AF060222.1 gb:NM_001375.1
209831_x_at_HG-U133A	DNASE2	deoxyribonuclease II, lysosomal	gb:AF124491.1 /DEF=Homo sapiens ARF GTPase-activating protein GIT2 (KIAA0148), mRNA, complete cds. /FEA=mRNA /GEN=KIAA0148 /PROD=ARF GTPase-activating protein GIT2 /DB_XREF=gi:4691727 /UG=Hs.57734 G protein-coupled receptor kinase-interactor 2 /FL=gb:AF124491.1 gb:AF225416.1 /DEF=Homo sapiens AD024 mRNA, complete cds. /FEA=mRNA /PROD=AD024 /DB_XREF=gi:9563834 /UG=Hs.21137 AD024 protein /FL=gb:NM_020675.1 gb:AF225416.1
209876_at_HG-U133A	GIT2	G protein-coupled receptor kinase-interactor 2	Consensus includes gb:AI246769 /FEA=EST /DB_XREF=gi:3842166 /DB_XREF=est:qk4008.x1 /CLONE=IMAGE:1871463 /UG=Hs.127428 homeobox A9 /FL=gb:U82759.1
209891_at_HG-U133A	AD024	AD024 protein	gb:AF05776.1 /DEF=Homo sapiens caspase-like apoptosis regulatory protein 2 (clar), mRNA, alternatively spliced, complete cds. /FEA=mRNA /GEN=clarp 2 (clar) mRNA, alternatively spliced, complete cds. /FEA=mRNA /GEN=clarp 2 (clar) mRNA, alternatively spliced, complete cds. /DB_XREF=gi:2286146 /PROD=caspase-like apoptosis regulatory protein 2 /DB_XREF=gi:2286146
209905_at_HG-U133A	HOXA9	homeo box A9	
209939_x_at_HG-U133A	CFLAR	CASP8 and FADD-like apoptosis regulator	

		/UG=Hs.195175 CASP8 and FADD-like apoptosis regulator /FL=gb:AF005775.1
209961_s_at_HG-U133A	HGF	gb:M60718.1 /DEF=human hepatocyte growth factor mRNA, complete cds. /FEA=mRNA /GEN=HGF /PROD=hepatocyte growth factor /DB_XREF=gi:184031 /UG=Hs.809 hepatocyte growth factor (hepatopoietin A; scatter factor) /FL=gb:M60718.1 gb:M29145.1 gb:M73239.1 gb:NM73240.1
209975_at_HG-U133A	CYP2E	gb:AF182276.1 /DEF=Homo sapiens cytochrome P450-2E1 (CYP2E1) mRNA, complete cds. /FEA=mRNA /GEN=CYP2E1 /PROD=cytochrome P450-2E1 /DB_XREF=gi:6470140 /UG=Hs.75183 cytochrome P450, subfamily IIIE (ethanol-inducible) /FL=gb:NM_000773.2 gb:J02625.1 gb:AF182276.1
209982_at_HG-U133A	PFKFB2	gb:AB044805.1 /DEF=Homo sapiens mRNA for 6-phosphofructo-2-kinase heart isozyme, complete cds. /FEA=mRNA /PROD=6-phosphofructo-2-kinase heart isozyme /DB_XREF=gi:11933148 /UG=Hs.211585 6-phosphofructo-2- kinase/fructose-2,6-biphosphatase 2 /FL=gb:AB044805.1
209994_s_at_HG-U133A	ABCB1	gb:AF016535.1 /DEF=Homo sapiens P-glycoprotein (mdr1) mRNA, complete cds. /FEA=mRNA /GEN=mdr1 /PROD=P-glycoprotein /DB_XREF=gi:2353263 /UG=Hs.21330 ATP-binding cassette, sub-family B (MDRTAP), member 1 /FL=gb:NM14758.1 gb:AF016535.1 gb:NM_000927.2
210004_at_HG-U133A	OLR1	gb:AF035776.1 /DEF=Homo sapiens oxidized low-density lipoprotein receptor mRNA, complete cds. /FEA=mRNA /PROD=oxidized low-density lipoprotein receptor /DB_XREF=gi:3841299 /UG=Hs.77729 oxidised low density lipoprotein (lectin-like) receptor 1 /FL=gb:AB010710.1 gb:AF035776.1 gb:NM_002543.1
210024_s_at_HG-U133A	UBE2E3	gb:AB017644.1 /DEF=Homo sapiens mRNA for ubiquitin-conjugating enzyme E2, complete cds. /FEA=mRNA /GEN=UbcH9 /PROD=ubiquitin-conjugating enzyme E2 /DB_XREF=gi:4586929 /UG=Hs.4890 ubiquitin-conjugating enzyme E2E 3 (homologous to yeast UBC45) /FL=gb:BC003554.1 gb:AB017644.1 gb:AF085362.1 gb:NM_006357.1

210036_s_at_HG-U133A	KCNH2	potassium voltage-gated channel, subfamily H (eag-related), member 2	gb:AB044806.1 /DEF=Homo sapiens HERG mRNA for HERG-USO, alternatively spliced, complete cds. /FEA=mRNA /GEN=HERG /PROD=HERG-USO /DB_XREF=gi:11933151 /UG=Hs.188021 potassium voltage-gated channel, subfamily H (eag-related), member 2 /FL=gb:AB044806.1
210038_at_HG-U133A			Consensus includes gb:AL137145 /DEF=Human DNA sequence from clone RP11-563Q2 on chromosome 10 Contains ESTs, STSs, GSSs and a CPG island. Contains a novel pseudogene and the 3 part of the PRKCQ gene for protein kinase C theta. /FEA=mRNA /DB_XREF=gi:9581557 /UG=Hs.211593 protein kinase C, theta /FL=gb:L07032.1 gb:NM_006257.1 gb:L01087.1
210045_at_HG-U133A	IDH2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	Consensus includes gb:AU151428 /FEA=EST /DB_XREF=gi:11012949 /DB_XREF=est:AU151428 /CLONE=NT2RP2005206 /UG=Hs.5337 isocitrate dehydrogenase 2 (NADP+), mitochondrial /FL=gb:U52144.1
210052_s_at_HG-U133A	C20orf1	chromosome 20 open reading frame 1	gb:AF098158.1 /DEF=Homo sapiens restricted expressed proliferation associated protein 100 mRNA, complete cds. /FEA=mRNA /PROD=restricted expressed proliferation associatedprotein 100 /DB_XREF=gi:6073830 /UG=Hs.9329 chromosome 20 open reading frame 1 /FL=gb:NM_012112.1 gb:BC004136.1 gb:AB024704.1 gb:AF146731.1 gb:AF098158.1 gb:AB027467.1
210053_at_HG-U133A	TAF5	TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 100 kD	Consensus includes gb:AW138827 /FEA=EST /DB_XREF=gi:6143145 /DB_XREF=est:U1-H-B1-aep-g-08-0-Ui.s1 /CLONE=IMAGE:2720079 /UG=Hs.96103 TATA box binding protein (TBP)-associated factor, RNA polymerase II, D, 100kD /FL=gb:U80191.1 gb:NM_006951.1
210095_s_at_HG-U133A	IGFBP3	insulin-like growth factor binding protein 3	gb:M31159.1 /DEF=Human growth hormone-dependent insulin-like growth factor-binding protein mRNA, complete cds. /FEA=mRNA /GEN=IGFBP1 /DB_XREF=gi:183115 /UG=Hs.77326 insulin-like growth factor binding protein 3 /FL=gb:BC000013.1 gb:NM31159.1
210116_at_HG-U133A	SH2D1A	SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome)	gb:AF072930.1 /DEF=Homo sapiens clone 14 T cell signal transduction molecule SAP mRNA, complete cds. /FEA=mRNA /PROD=T cell signal

			transduction molecule SAP /DB_XREF=gi:3695068 /UG=Hs.151544 SH2 domain protein 1A, Duncans disease (lymphoproliferative syndrome) /FL=gb:AF072930.1 gb:AF073019.1 gb:AF100541.1 gb:NM_002351.1
210117_at_HG-U133A	SPAG1	sperm associated antigen 1	gb:AF311312.1 /DEF=Homo sapiens infertility-related sperm protein mRNA, complete cds. /FEA=mRNA /PROD=infinity-related sperm protein /DB_XREF=gi:10863767 /UG=Hs.153057 sperm associated antigen 1 /FL=gb:AF311312.1 gb:NM_003114.1
210128_s_at_HG-U133A	LTB4R	leukotriene b4 receptor (chemokine receptor-like 1)	gb:U41070.1 /DEF=Human P2 purinergic receptor mRNA, complete cds. /FEA=mRNA /PROD=P2 purinergic receptor /DB_XREF=gi:1469913 /UG=Hs.28408 leukotriene b4 receptor (chemokine receptor-like 1) /FL=gb:U41070.1 gb:D89079.1
210140_at_HG-U133A	CST7	cystatin F (leukoystatin)	gb:AF031824.1 /DEF=Homo sapiens leukocystatin mRNA, complete cds. /FEA=mRNA /PROD=leukoystatin /DB_XREF=gi:3252857 /UG=Hs.143212 cystatin F (leukoystatin) /FL=gb:AF031824.1 gb:AB015225.1 gb:NM_003650.1
210145_at_HG-U133A	PLA2G4A	phospholipase A2, group IVA (cytosolic, calcium-dependent)	gb:M68874.1 /DEF=Homo sapiens phosphatidylcholine 2-acylhydrolase (cPLA2) mRNA, complete cds. /FEA=mRNA /GEN=cPLA2 /PROD=phosphatidylcholine 2-acylhydrolase /DB_XREF=gi:190003 /UG=Hs.211587 phospholipase A2, group IVA (cytosolic, calcium-dependent) /FL=gb:M68874.1 gb:M72393.1
210151_s_at_HG-U133A	DYRK3	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	gb:AF186773.1 /DEF=Homo sapiens regulatory erythroid kinase long form (RED) mRNA, alternatively spliced product, complete cds. /FEA=mRNA /GEN=RED /PROD=regulatory erythroid kinase long form /DB_XREF=gi:1044144 /UG=Hs.38018 dual-specificity tyrosine-(Y)- phosphorylation regulated kinase 3 /FL=gb:AF186773.1 gb:NM_003582.1
210192_at_HG-U133A	ATP8A1	ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1	gb:AB013452.1 /DEF=Homo sapiens mRNA for ATPaseII, complete cds. /FEA=mRNA /PROD=ATPaseII /DB_XREF=gi:4704323 /UG=Hs.144931 ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1

			/FL=gb:AB013452.1
			gb:U19970.1 /DEF=Human antimicrobial LPS-binding protein CAP18 precursor mRNA, complete cds. /FEA=mRNA /PROD=CAP18 precursor /DB_XREF=gi:643476 /UG=Hs.51120 cathecidin antimicrobial peptide /FL=gb:NM_004345.1 gb:U19970.1
210244_at_HG-U133A	CAMP	cathelicidin antimicrobial peptide	gb:AF112221.1 /DEF=Homo sapiens rap2 interacting protein x mRNA, complete cds. /FEA=mRNA /PROD=rap2 interacting protein x /DB_XREF=gi:6563227 /UG=Hs.7972 KIAA0871 protein /FL=gb:AF112221.1
210251_s_at_HG-U133A	KIAA0871	KIAA0871 protein	gb:L35848.1 /DEF=Homo sapiens IgE receptor beta chain (HTm4) mRNA, complete cds. /FEA=mRNA /GEN=HTm4 /PROD=IgE receptor beta subunit /DB_XREF=gi:561638 /UG=Hs.99960 membrane-spanning 4-domains, subfamily A, member 3 (hematopoietic cell-specific) /FL=gb:NM_006138.1 gb:I35848.1
210254_at_HG-U133A			gb:M25532.1 /DEF=Human testis-specific protein (Tpx-1) mRNA, complete cds. /FEA=mRNA /GEN=GAPDL5 /DB_XREF=gi:339982 /UG=Hs.2042 testis specific protein 1 (probe H4-1 p3-1) /FL=gb:M25532.1 gb:NM_003296.1
210262_at_HG-U133A	TPX1		gb:AF33209.1 /DEF=Homo sapiens nuclear transcription factor NFX2 (NF-X2) mRNA, complete cds. /FEA=mRNA /GEN=NFX2 /PROD=nuclear transcription factor NFX2 /DB_XREF=gi:13242068 /UG=Hs.3187 nuclear transcription factor, X-box binding 1 /FL=gb:AF33209.1
210268_at_HG-U133A	NFX1	nuclear transcription factor, X-box binding 1	gb:AF261135.1 /DEF=Homo sapiens GPR18-iso mRNA, complete cds. /FEA=mRNA /PROD=GPR18-iso /DB_XREF=gi:120055919 /UG=Hs.88269 Homo sapiens clone IMAGE:1837189, mRNA sequence /FL=gb:AF261135.1
210279_at_HG-U133A	GPR18	G protein-coupled receptor 18	gb:AF098518.1 /DEF=Homo sapiens four and a half LIM domains 1 protein isoform B (FHL1).mRNA, complete cds. /FEA=mRNA /GEN=FHL1 /PROD=four and a half LIM domains 1 protein isoform B /DB_XREF=gi:3851649 /UG=Hs.239069 four and a half LIM domains 1 /FL=gb:AF063002.1
210298_x_at_HG-U133A	FHL1	four and a half LIM domains 1	

210299_s_at_HG-U133A	FHL1	four and a half LIM domains 1	gb:AF063002.1 /DEF=Homo sapiens LIM protein SLIMMER mRNA, complete cds. /FEA=mRNA /PROD=LIM protein SLIMMER /DB_XREF=gi:3859848 /UG=Hs.239069 four and a half LIM domains 1 /FL=gb:AF098518.1
210314_x_at_HG-U133A	TNFSF13	tumor necrosis factor (ligand) superfamily, member 13	gb:AF114013.1 /DEF=Homo sapiens tumor necrosis factor-related death ligand-1 gamma mRNA, complete cds. /FEA=mRNA /PROD=tumor necrosis factor-related death ligand-1 gamma /DB_XREF=gi:7328557 /UG=Hs.54673 tumor necrosis factor (ligand) superfamily, member 13 /FL=gb:AF136294.1
210334_x_at_HG-U133A	BIRC5	baculoviral IAP repeat-containing 5 (survivin)	gb:AB028869.1 /DEF=Homo sapiens mRNA for survivin-beta, complete cds. /FEA=mRNA /PROD=survivin-beta /DB_XREF=gi:7416052 /UG=Hs.1578
210356_x_at_HG-U133A	MS4A2	membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for beta polypeptide)	gb:BC002807.1 /DEF=Homo sapiens, membrane-spanning 4-domains, subfamily A, member 2, clone MGC:3969, mRNA, complete cds. /FEA=mRNA /PROD=membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for beta polypeptide) /FL=gb:NM_021950.1 gb:BC002807.1
210358_x_at_HG-U133A	MGC2306	hypothetical protein MGC2306	gb:BC002557.1 /DEF=Homo sapiens, Similar to GATA-binding protein 2, clone MGC:2306, mRNA, complete cds. /FEA=mRNA /PROD=Similar to GATA-binding protein 2 /DB_XREF=gi:12803920 /UG=Hs.89751 membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for beta polypeptide) /FL=gb:BC002557.1
210448_s_at_HG-U133A	P2RX5	purinergic receptor P2X, ligand-gated ion channel, 5	gb:U49396.1 /DEF=Human ionotropic ATP receptor P2X5b mRNA, complete cds. /FEA=mRNA /PROD=P2X5b /DB_XREF=gi:1552523 /UG=Hs.77807
210487_at_HG-U133A	DNTT	deoxynucleotidyltransferase, terminal	gb:M11722.1 /DEF=Human terminal transferase mRNA, complete cds. /FEA=mRNA /GEN=LA0024A /PROD=terminal transferase

		/DB_XREF=gi:339436 /UG=Hs.272537 deoxymucleotidyltransferase, terminal /FL=gb:M11722.1 gb:NM_004088.1
210519_s_at_HG-U133A		gb:BC000906.1 /DEF=Homo sapiens, clone MGCG:5333, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGCG:5333) /DB_XREF=gi:12654176 /UG=Hs.80706 diaphorase (NADH/NADPH) (cytochrome b-5 reductase) /FL=gb:BC000906.1
210563_x_at_HG-U133A	CFLAR	gb:U97075.1 /DEF=Homo sapiens FLICE-like inhibitory protein short form mRNA, complete cds. /FEA=mRNA /PROD=FLICE-like inhibitory protein short form /DB_XREF=gi:2253680 /UG=Hs.195175 CASP8 and FADD-like apoptosis regulator /FL=gb:U97075.1
210609_s_at_HG-U133A	PIG3	gb:BC000474.1 /DEF=Homo sapiens, quinone oxidoreductase homolog, clone MGCG:8642, mRNA, complete cds. /FEA=mRNA /PROD=quinone oxidoreductase homolog /DB_XREF=gi:12653408 /UG=Hs.50649 quinone oxidoreductase homolog /FL=gb:BC000474.1
210613_s_at_HG-U133A	SYNGR1	gb:BC000731.1 /DEF=Homo sapiens, synaptogyrin 1, clone MGCG:1939, mRNA, complete cds. /FEA=mRNA /PROD=synaptogyrin 1 /DB_XREF=gi:12653878 /UG=Hs.6139 synaptogyrin 1 /FL=gb:BC000731.1
210616_s_at_HG-U133A	KIAA0905	gb:AB020712.1 /DEF=Homo sapiens mRNA for KIAA0905 protein, complete cds. /FEA=mRNA /GEN=KIAA0905 /PROD=KIAA0905 protein /DB_XREF=gi:4240298 /UG=Hs.70266 yeast Sec31p homolog /FL=gb:AB020712.1
210658_s_at_HG-U133A	GGA2	gb:BC000284.1 /DEF=Homo sapiens, KIAA1080 protein, Golgi-associated, gamma-adaptin ear containing, ARF-binding protein 2, clone MGCG:1002, mRNA, complete cds. /FEA=mRNA /PROD=KIAA1080 protein; Golgi- associated,gamma-adaptin ear containing, ARF-binding protein 2. /DB_XREF=gi:12653040 /UG=Hs.155546 KIAA1080 protein; Golgi-associated, golgi associated, gamma adaptin ear containing, ARF binding protein 2
210664_s_at_HG-	TFPI	gb:AF021834.1 /DEF=Homo sapiens tissue factor pathway inhibitor beta tissue factor pathway inhibitor

U133A	(lipoprotein-associated coagulation inhibitor)	(TFPIbeta) mRNA, complete cds. /FEA=mRNA /GEN=TFPIbeta /PROD=tissue factor pathway inhibitor beta /DB_XREF=gi:4103170 /UG=Hs.170279 tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor) /FL=gb:AF021834.1
210715_s_at_HG-U133A	SPINT2	serine protease inhibitor, Kunitz type, 2 discoidin domain receptor family, member 1 hepatocyte growth factor (hepatoletin A; scatter factor) HGF
210749_x_at_HG-U133A	DDR1	gb:L11315.1 /DEF=Homo sapiens receptor tyrosine kinase mRNA, complete cds. /FEA=mRNA /PROD=receptor tyrosine kinase /DB_XREF=gi:403386 /UG=Hs.75562 discoidin domain receptor family, member 1 /FL=gb:L11315.1
210755_at_HG-U133A	LY117	gb:U46010.1 /DEF=Human HGF agonistantagonist mRNA, complete cds. /FEA=mRNA /PROD=HGF agonistantagonist /DB_XREF=gi:1378041 /UG=Hs.809 hepatocyte growth factor (hepatoletin A; scatter factor) /FL=gb:U46010.1
210763_x_at_HG-U133A	LOC51635	gb:AF031137.1 /DEF=Homo sapiens 1C7 precursor, mRNA, alternatively spliced, complete cds. /FEA=mRNA /PROD=IC7 precursor /DB_XREF=gi:26223874 /UG=Hs.88411 lymphocyte antigen 117 /FL=gb:AF031137.1
210788_s_at_HG-U133A	CGI-86 protein	gb:AF126782.1 /DEF=Homo sapiens retinal short-chain dehydrogenasereductase retSDR4 mRNA, complete cds. /FEA=mRNA /PROD=retinal short-chain dehydrogenasereductase retSDR4 /DB_XREF=gi:6318547 /UG=Hs.109201 CGI-86 protein /FL=gb:AF126782.1
210789_x_at_HG-U133A	CEACAM3	gb:L00692.1 /DEF=Human carcinoembryonic antigen (CGM1) mRNA, complete cds. /FEA=mRNA /GEN=CGM1 /PROD=carcinoembryonic antigen /DB_XREF=gi:180226 /UG=Hs.11 carcinoembryonic antigen-related cell adhesion molecule 3 /FL=gb:L00692.1
210794_s_at_HG-		Consensus includes gb:AF119863.1 /DEF=Homo sapiens PRO2160 mRNA

U133A			complete cds. /FEA=mRNA /PROD=PRO2160 /DB_XREF=gi:7770162 /UG=Hs.112844 maternally expressed 3 /FL=gb:AF119863.1
210807_s_at_HG-U133A	SLC16A7	solute carrier family 16 (monocarboxylic acid transporters), member 7	gb:AF049608.1 /DEF=Homo sapiens monocarboxylate transporter 2 (MCT2) mRNA, complete cds. /FEA=mRNA /GEN=MCT2 /PROD=monocarboxylate transporter 2 /DB_XREF=gi:3834394 /UG=Hs.132183 solute carrier family 16 (monocarboxylic acid transporters), member 7 /FL=gb:AF049608.1
210817_s_at_HG-U133A	NDP52	nuclear domain 10 protein	gb:BC004130.1 /DEF=Homo sapiens, nuclear domain 10 protein, clone MGCI:1399, mRNA, complete cds. /FEA=mRNA /PROD=nuclear domain 10 protein /DB_XREF=gi:13278698 /UG=Hs.154230 nuclear domain 10 protein /FL=gb:BC004130.1
210896_s_at_HG-U133A	ASPH	aspartate beta-hydroxylase	gb:AF306765.1 /DEF=Homo sapiens junctate mRNA, complete cds. /FEA=mRNA /PROD=junctate /DB_XREF=gi:11991236 /UG=Hs.283664 aspartate beta-hydroxylase /FL=gb:AF306765.1
210916_s_at_HG-U133A		Homo sapiens CD44 isoform RC (CD44) mRNA, complete cds	gb:AF098641.1 /DEF=Homo sapiens CD44 isoform RC (CD44) mRNA, complete cds. /FEA=mRNA /GEN=CD44 /PROD=CD44 isoform RC /DB_XREF=gi:3832517 /UG=Hs.306278 Homo sapiens CD44 isoform RC (CD44) mRNA, complete cds /FL=gb:AF098641.1
210933_s_at_HG-U133A	MGC4655	hypothetical protein MGC4655	gb:BC004908.1 /DEF=Homo sapiens, clone MGC:4655, mRNA, complete cds /FL=gb:BC004908.1
210934_at_HG-U133A	BLK	B lymphoid tyrosine kinase	gb:BC004473.1 /DEF=Homo sapiens, clone MGC:10442, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:10442) /DB_XREF=gi:13325324 /UG=Hs.326772 Homo sapiens, clone MGC:10442, mRNA, complete cds /FL=gb:BC004473.1
210948_s_at_HG-U133A	LEF1	lymphoid enhancer-binding factor 1	gb:AF294627.1 /DEF=Homo sapiens lymphoid enhancer factor 1 isoform (LEF1) mRNA, complete cds. /FEA=mRNA /GEN=LEF1 /PROD=lymphoid enhancer factor 1 isoform /DB_XREF=gi:11024343 /UG=Hs.44865 lymphoid

			enhancer binding factor-1 /FL=gb:AF294627.1 gb:M63889.1 /DEF=Human heparin-binding growth factor receptor (HBGF-R-alpha-a3) mRNA, complete cds. /FEA=mRNA /GEN=HBGF-R /PROD=heparin-binding growth factor receptor /DB_XREF=gi:183882 /UG=Hs.748 fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome) /FL=gb:M63889.1
210973_s_at_HG-U133A	FGFR1		gb:M60333.1 /DEF=Human MHC class II HLA-DRA mRNA, complete cds. /FEA=mRNA /GEN=HLA-DRA /PROD=MHC cell surface glycoprotein /DB_XREF=gi:188268 /UG=Hs.76807 major histocompatibility complex, class II, DR alpha /FL=gb:M60333.1
210982_s_at_HG-U133A	HLA-DRA		gb:M77227.1 /DEF=H.sapiens competitive HGF antagonist mRNA, complete cds. /FEA=mRNA /PROD=competitive HGF antagonist /DB_XREF=gi:184029 cds. /FEA=mRNA /PROD=competitive HGF antagonist /DB_XREF=gi:184029 /UG=Hs.809 hepatocyte growth factor (hepatopoietin A; scatter factor) /FL=gb:M77227.1 gb:L02931.1
210997_at_HG-U133A	HGF		gb:M77227.1 /DEF=H.sapiens competitive HGF antagonist mRNA, complete cds. /FEA=mRNA /PROD=competitive HGF antagonist /DB_XREF=gi:184029 cds. /FEA=mRNA /GEN=hsp70 /PROD=heat shock protein 70 /UG=Hs.809 hepatocyte growth factor (hepatopoietin A; scatter factor) /FL=gb:M77227.1 gb:L02931.1
210998_s_at_HG-U133A	HGF		gb:L12723.1 /DEF=Human heat shock protein 70 (hsp70) mRNA, complete cds. /FEA=mRNA /GEN=hsp70 /PROD=heat shock protein 70 /DB_XREF=gi:292159 /UG=Hs.90093 heat shock 70kD protein 4 /FL=gb:L12723.1
211015_s_at_HG-U133A	HSPA4		gb:BC006259.1 /DEF=Homo sapiens, clone MG:11333, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MG:11333) /DB_XREF=gi:13623312 /FL=gb:BC006259.1
211031_s_at_HG-U133A	CYLN2		gb:BC003111.1 /DEF=Homo sapiens, Similar to pre-B-cell leukemia transcription factor 2, clone MG:2174, mRNA, complete cds. /FEA=mRNA /PROD=Similar to pre-B-cell leukemia transcriptionfactor 2
211097_s_at_HG-U133A	PBX2		

			/DB_XREF=gi:13111886 /UG=Hs.93728 pre-B-cell leukemia transcription factor 2 /FL=gb:BC003111.1
211101_x_at_HG-U133A	LILRA2	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2	gb:U82276.1 /DEF=Human immunoglobulin-like transcript 1a mRNA, complete cds. /FEA=mRNA /PROD=immunoglobulin-like transcript 1a /DB_XREF=gi:1907318 /UG=Hs.94498 leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2 /FL=gb:UB2276.1
211105_s_at_HG-U133A	NFATC1	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1	gb:U80918.1 /DEF=Homo sapiens transcription factor (NF-ATCc) mRNA, complete cds. /FEA=mRNA /GEN=NF-ATCc /PROD=transcription factor /DB_XREF=gi:4098860 /UG=Hs.96149 nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1 /FL=gb:U80918.1
211126_s_at_HG-U133A	CSRP2	cysteine and glycine-rich protein 2	gb:U46006.1 /DEF=Homo sapiens smooth muscle LIM protein (h-SmLIM) mRNA, complete cds. /FEA=mRNA /GEN=h-SmLIM /PROD=smooth muscle LIM protein /DB_XREF=gi:1314358 /UG=Hs.10526 cysteine and glycine-rich protein 2 /FL=gb:U46006.1
211138_s_at_HG-U133A	KMO	kynurenine 3-monoxygenase (kynurenine 3-hydroxylase)	gb:BC005297.1 /DEF=Homo sapiens Similar to kynurenine 3-monoxygenase (kynurenine 3-hydroxylase), clone MGC:12362, mRNA, complete cds. /FEA=mRNA /PROD=Similar to kynurenine 3-monoxygenase(kynurenine 3-hydroxylase) /DB_XREF=gi:13529016 /UG=Hs.107318 kynurenine 3-monoxygenase (kynurenine 3-hydroxylase) /FL=gb:BC005297.1
211275_s_at_HG-U133A	GYG	glycogenin	gb:AF087942.1 /DEF=Homo sapiens glycogenin-1L mRNA, complete cds. /FEA=mRNA /PROD=Glycogenin-1L /DB_XREF=gi:5814084 /UG=Hs.174071 glycogenin /FL=gb:AF087942.1
211297_s_at_HG-U133A	CDK7	cyclin-dependent kinase 7 (MO15 homolog, Xenopus laevis, cdk-activating kinase)	gb:L20320.1 /DEF=Human protein serine/threonine kinase stk1 mRNA, complete cds. /FEA=mRNA /PROD=protein serine/threonine kinase /DB_XREF=gi:348242 /UG=Hs.184298 cyclin-dependent kinase 7. (homolog of Xenopus MO15 cdk-activating kinase) /FL=gb:L20320.1
211341_at_HG-U133A	POU4F1	POU domain, class 4, transcription factor 1	gb:L20433.1 /DEF=Human octamer binding transcription factor 1 (OTF1) mRNA, complete cds. /FEA=mRNA /GEN=OTF1 /PROD=octamer binding

			transcription factor 1 /DB_XREF=gi:418015 /UG=Hs.211588 POU domain, class 4, transcription factor 1 /FL=gb:U20433.1
			gb:AB001328.1 /DEF=Homo sapiens mRNA for pH-sensing regulatory factor of peptide transporter, complete cds. /FEA=mRNA /GEN=hPEPT1-RF /PROD=pH-sensing regulatory factor of peptidetransporter /DB_XREF=gi:2506042 /UG=Hs.2217 solute carrier family 15 (oligopeptide transporter), member 1 /FL=gb:AB001328.1
211349_at_HG-U133A	SLC15A1		gb:U80737.1 /DEF=Homo sapiens CAGH16 mRNA, complete cds. /FEA=mRNA /GEN=CAGH16 /PROD=CAGH16 /DB_XREF=gi:2565049 /UG=Hs.225977 nuclear receptor coactivator 3 /FL=gb:U80737.1
211352_s_at_HG-U133A	NCOA3	nuclear receptor coactivator 3	gb:BC004371.1 /DEF=Homo sapiens, clone MGC:10449, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:10449) /DB_XREF=gi:13325115 /UG=Hs.279518 amyloid beta (A4) precursor-like protein 2 /FL=gb:BC004371.1
211404_s_at_HG-U133A	A1LP2	amyloid beta (A4) precursor-like protein 2	gb:AF333388.1 /DEF=Homo sapiens metallothionein 1H-like protein mRNA, complete cds. /FEA=mRNA /PROD=metallothionein 1H-like protein /DB_XREF=gi:13310411 /UG=Hs.326774 Homo sapiens metallothionein 1H-like protein mRNA, complete cds /FL=gb:AF333388.1
211456_x_at_HG-U133A		Homo sapiens metallothionein 1H-like protein mRNA, complete cds	gb:BC004948.1 /DEF=Homo sapiens, clone MGC:10846, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:10846) /DB_XREF=gi:13436313 /UG=Hs.41072 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6 /FL=gb:BC004948.1
211474_s_at_HG-U133A		Homo sapiens, clone MGC:10846 IMAGE:3616550, mRNA, complete cds	gb:AF114011.1 /DEF=Homo sapiens tumor necrosis factor-related death ligand-1alpha mRNA, complete cds. /FEA=mRNA /PROD=tumor necrosis factor-related deathligand-1alpha /DB_XREF=gi:7328553 /UG=Hs.54673 tumor necrosis factor (ligand) superfamily, member 13 /FL=gb:AF046888.1
211495_x_at_HG-U133A	TNFSF13	tumor necrosis factor (ligand) superfamily, member 13	gb:NM_003808.1 /FL=gb:AF114011.1
211502_s_at_HG-	PFTK1	PFTAIRe protein kinase 1	gb:AF119833.1 /DEF=Homo sapiens serine/threonine protein kinase PFTAIRe-

U133A		1 mRNA, complete cds. /FEA=mRNA /PROD=serine/threonine protein kinase 1 /FL=gb:AF119833.1
211540_s_at_HG-U133A	RB1	retinoblastoma 1 (including osteosarcoma) gb:M19701.1 /DEF=Human mutated retinoblastoma susceptibility (RB) mRNA, complete cds. /FEA=mRNA /GEN=RB1 /DB_XREF=gi:190967 /UG=Hs.75770
211574_s_at_HG-U133A	MCP	membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen) gb:D84105.1 /DEF=Human CD46 mRNA, complete cds. /FEA=mRNA /PROD=CD46 /DB_XREF=gi:1256700 /UG=Hs.83532 membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen) /FL=gb:M19701.1
211584_s_at_HG-U133A	NPAT	nuclear protein, ataxia-telangiectasia locus gb:U58852.1 /DEF=Human NPAT mRNA, complete cds. /FEA=mRNA /GEN=NPAT /DB_XREF=gi:1381666 /UG=Hs.89385 nuclear protein, ataxiatelangiectasia locus /FL=gb:U58852.1
211657_at_HG-U133A		gb:M18728.1 /DEF=Human nonspecific crossreacting antigen mRNA, complete cds. /FEA=mRNA /GEN=NCA; NCA /PROD=non-specific cross reacting antigen /DB_XREF=gi:189084 /FL=gb:M18728.1
211665_s_at_HG-U133A	PLAU	plasminogen activator, urokinase gb:120686.1 /DEF=Homo sapiens guanine nucleotide releasing factor (SOS2) mRNA, complete cds. /FEA=mRNA /GEN=SOS2 /PROD=guanine nucleotide releasing factor /DB_XREF=gi:1220367 /FL=gb:L20686.1
211668_s_at_HG-U133A		gb:K03226.1 /DEF=Human preprourokinase mRNA, complete cds. /FEA=mRNA /GEN=PLAU /DB_XREF=gi:340155 /FL=gb:K03226.1
211709_s_at_HG-U133A	SCGF	stem cell growth factor; lymphocyte secreted C-type lectin gb:BC005810.1 /DEF=Homo sapiens, stem cell growth factor; lymphocyte secreted C-type lectin, clone MGC:10378, mRNA, complete cds. /FEA=mRNA /PROD=stem cell growth factor; lymphocyte secretedC-type lectin /DB_XREF=gi:13543291 /FL=gb:BC005810.1
211743_s_at_HG-U133A	PRG2	proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major basic protein), clone MGC:14537, mRNA, complete cds. /FEA=mRNA /PROD=proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major basic protein), clone MGC:14537, mRNA, complete cds. /FEA=mRNA /PROD=proteoglycan 2,

			bone marrow (natural killer cellactivator, eosinophil granule major basic protein) /DB_XREF=gi:13543541 /FL=gb:BC005929.1
211748_x_at_HG-U133A	PTGDS	prostaglandin D2 synthase (21kD, brain)	gb:BC005939.1 /DEF=Homo sapiens, prostaglandin D2 synthase (21kD, brain), clone MGC:14559, mRNA, complete cds. /FEA=mRNA /PROD=prostaglandin D2 synthase (21kD, brain) /DB_XREF=gi:13543567 /FL=gb:BC005939.1
211771_s_at_HG-U133A	POU2F2	POU domain, class 2, transcription factor 2	gb:BC006101.1 /DEF=Homo sapiens, Similar to POU domain, class 2, transcription factor 2, clone MGC:12814, mRNA, complete cds. /FEA=mRNA /PROD=Similar to POU domain, class 2, transcriptionfactor 2 /DB_XREF=gi:13543912 /FL=gb:BC006101.1
211787_s_at_HG-U133A	EIF4A1	eukaryotic translation initiation factor 4A, isoform 1	gb:BC006210.1 /DEF=Homo sapiens, Similar to eukaryotic translation initiation factor 4A, isoform 1, clone MGC:8484, mRNA, complete cds. /FEA=mRNA /PROD=Similar to eukaryotic translation initiationfactor 4A, isoform 1 /DB_XREF=gi:13623224 /FL=gb:BC006210.1
211796_s_at_HG-U133A	TRB	T cell receptor beta locus	gb:AF043179.1 /DEF=Homo sapiens T cell receptor beta chain (TCRBV13S1-TCRBJ2S1) mRNA, complete cds. /FEA=CDS /GEN=TCRBV13S1-TCRBJ2S1 /PROD=T cell receptor beta chain /DB_XREF=gi:3002924 /UG=Hs.303157 T cell receptor beta locus /FL=gb:AF043179.1
211800_s_at_HG-U133A	USP4	ubiquitin specific protease 4 (proto-oncogene)	gb:AF017306.1 /DEF=Homo sapiens deubiquitinating enzyme UpES (UNP)mRNA, complete cds. /FEA=CDS /GEN=UNP /PROD=UpES /DB_XREF=gi:2656142 /UG=Hs.77500 ubiquilin specific protease 4 (proto-oncogene) /FL=gb:AF017306.1
211819_s_at_HG-U133A	SH3D5	SH3-domain protein 5 (ponsin)	gb:AF136381.1 /DEF=Homo sapiens c-Cbl-associated protein SH3P12 (SH3P12) mRNA, complete cds. /FEA=CDS /GEN=SH3P12 /PROD=c-Cbl-associated protein SH3P12 /DB_XREF=gi:6651088 /UG=Hs.108924 SH3-domain protein 5 (ponsin) /FL=gb:AF136381.1
211824_x_at_HG-U133A	DEFCAP	death effector filament-forming Ced-4-like apoptosis protein	gb:AF229062.1 /DEF=Homo sapiens NAC-delta splice variant (NAC) mRNA, complete cds, alternatively spliced. /FEA=CDS /GEN=NAC /PROD=NAC-delta

			splice variant /DB_XREF=gi:12656110 /UG=Hs.104305 death effector filament-forming Ced-4-like apoptosis protein /FL=gb:AF2299062.1
211852_s_at_HG-U133A	ATRN	attractin	gb:AF106861.1 /DEF=Homo sapiens attractin-2 (ATRN) mRNA, complete cds. /FEA=CDS /GEN=ATRN /PROD=attractin-2 /DB_XREF=gi:4093195 /UG=Hs.194019 attractin /FL=gb:AF106861.1
211883_x_at_HG-U133A	CEACAM1	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	gb:MF76742.1 /DEF=Homo sapiens alternatively spliced biliary glycoprotein (BGPa) mRNA, complete cds. /FEA=CDS /GEN=BGPa /PROD=biliary glycoprotein /DB_XREF=gi:179480 /UG=Hs.50964 carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) /FL=gb:MF76742.1
211889_x_at_HG-U133A	CEACAM1	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	gb:D12502.1 /DEF=Human mRNA for biliary glycoprotein, complete cds. /FEA=CDS /GEN=BGP /PROD=biliary glycoprotein /DB_XREF=gi:219494 /UG=Hs.50964 carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) /FL=gb:D12502.1
211918_x_at_HG-U133A	PLAC3	placenta-specific 3	gb:AF311940.1 /DEF=Homo sapiens pregnancy-associated plasma preproprotein-A2 mRNA, complete cds. /FEA=CDS /PROD=pregnancy-associated plasma preproprotein-A2 /DB_XREF=gi:13569344 /FL=gb:AF311940.1
211934_x_at_HG-U133A	G2AN	alpha glucosidase II alpha subunit	Consensus includes gb:W87689 /FEA=EST /DB_XREF=gi:1401814 /DB_XREF=est:zh68c04.s1 /CLONE=IMAGE:417222 /UG=Hs.76847 KIAA0088 protein /FL=gb:NM_014610.1
211950_at_HG-U133A	RBAF600	retinoblastoma-associated factor 600	Consensus includes gb:AB007931.1 /DEF=Homo sapiens mRNA for KIAA0462 protein, partial cds. /FEA=mRNA /GEN=KIAA0462 /PROD=KIAA0462 protein /DB_XREF=gi:3413885 /UG=Hs.297641 KIAA0462 protein
211953_s_at_HG-U133A	KPNB3	karyopherin (importin) beta 3	Consensus includes gb:AU148466 /FEA=EST /DB_XREF=gi:11009987 /DB_XREF=est:AU148466 /CLONE=NT2RM4000332 /UG=Hs.113503 karyopherin (importin) beta 3 /FL=gb:U72761.1 gb:NM_002271.1
211984_at_HG-U133A		Human calmodulin-1 (CALM1) mRNA,	Consensus includes gb:AI653730 /FEA=EST /DB_XREF=gi:4737709

		3'UTR, partial sequence	/DB_XREF=est:wb36f12.x1 /CLONE=IMAGE:2307791 /UG=Hs.279009 matrix Gla protein
211990_at_HG-U133A	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	Consensus includes gb:M27487.1 /DEF=Homo sapiens MHC class II DPw3- alpha-1 chain mRNA, complete cds. /FEA=CDS /GEN=HLA-DPA1 /PROD=MHC class II DP3-alpha /DB_XREF=gi:703088 /UG=Hs.914 Human mRNA for SB classII histocompatibility antigen alpha-chain /FL=gb:M27487.1
211991_s_at_HG-U133A	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	Consensus includes gb:M27487.1 /DEF=Homo sapiens MHC class II DPw3- alpha-1 chain mRNA, complete cds. /FEA=CDS /GEN=HLA-DPA1 /PROD=MHC class II DP3-alpha /DB_XREF=gi:703088 /UG=Hs.914 Human mRNA for SB classII histocompatibility antigen alpha-chain /FL=gb:M27487.1
212012_at_HG-U133A	D2S448	Melanoma associated gene	Consensus includes gb:BF342851 /FEA=EST /DB_XREF=gi:11289878 /DB_XREF=est:602015135F1 /CLONE=IMAGE:4150664 /UG=Hs.118893
212013_at_HG-U133A	D2S448	Melanoma associated gene	Melanoma associated gene Consensus includes gb:D86983.1 /DEF=Human mRNA for KIAA0230 gene, partial cds. /FEA=mRNA /GEN=KIAA0230 /DB_XREF=gi:1504039 /UG=Hs.118893 Melanoma associated gene
212020_s_at_HG-U133A	MKI67	antigen identified by monoclonal antibody Ki-67	Consensus includes gb:AU152107 /FEA=EST /DB_XREF=gi:11013628 /DB_XREF=est:AU152107 /CLONE=NT2RP3000209 /UG=Hs.80976 antigen identified by monoclonal antibody Ki-67
212022_s_at_HG-U133A	MKI67	antigen identified by monoclonal antibody Ki-67	Consensus includes gb:BF001086 /FEA=EST /DB_XREF=gi:10702081 /DB_XREF=est:7693e04.x1 /CLONE=IMAGE:3314046 /UG=Hs.80976 antigen identified by monoclonal antibody Ki-67
212032_s_at_HG-U133A	PTOV1	prostate tumor over expressed gene 1	Consensus includes gb:AL046054 /FEA=EST /DB_XREF=gi:5936153 /DB_XREF=est:DKFZp434D2072_r1 /CLONE=DKFZp434D2072 /UG=Hs.19555 prostate tumor over expressed gene 1
212058_at_HG-U133A	KIAA0332	KIAA0332 protein	Consensus includes gb:AI184562 /FEA=EST /DB_XREF=gi:3735200 /DB_XREF=est:Lqd60b05.x1 /CLONE=IMAGE:1733841 /UG=Hs.7976 KIAAC0332 protein

212074_at_HG-U133A	KIAA0810	KIAA0810 protein	Consensus includes gb:BE972774 /FEA=EST /DB_XREF=gi:10586110 /DB_XREF=est:601652004F1 /CLONE=IMAGE:3935281 /UG=Hs.7531
212107_s_at_HG-U133A	DDX9	DEAD1H (Asp-Glu-Ala-Asp/His) box polypeptide 9 (RNA helicase A, nuclear DNA helicase I; leukophysisin)	Consensus includes gb:BE561014 /FEA=EST /DB_XREF=gi:9804734 /DB_XREF=est:601344618F1 /CLONE=IMAGE:3677500 /UG=Hs.74578 DEAD1H (Asp-Glu-Ala-Asp/His) box polypeptide 9 (RNA helicase A, nuclear DNA helicase I; leukophysisin)
212133_at_HG-U133A	MGC5466	hypothetical protein MGC5466	Consensus includes gb:A681536 /FEA=EST /DB_XREF=gi:4891718 /DB_XREF=est:tx47e03.x1 /CLONE=IMAGE:2272732 /UG=Hs.83724
212146_at_HG-U133A	KIAA0842	KIAA0842 protein	hypothetical protein MGCG5466
212150_at_HG-U133A	KIAA0143	KIAA0143 protein	Consensus includes gb:AB020649.1 /DEF=Homo sapiens mRNA for KIAA0842 protein, partial cds. /FEA=mRNA /GEN=KIAA0842 /PROD=KIAA0842 protein /DB_XREF=gi:4240172 /UG=Hs.74569 KIAA0842 protein
212171_x_at_HG-U133A	VEGF	vascular endothelial growth factor	Consensus includes gb:AA805651 /FEA=EST /DB_XREF=gi:2874401 /DB_XREF=est:nz41a04.s1 /CLONE=IMAGE:1290318 /UG=Hs.84087 KIAA0143 protein
212185_x_at_HG-U133A	MT2A	metallothionein 2A	Consensus includes gb:H95344 /FEA=EST /DB_XREF=gi:1102977 /DB_XREF=est:yu21b08.s1 /CLONE=IMAGE:234423 /UG=Hs.73793 vascular endothelial growth factor /FL=gb:AF214570.1
212187_x_at_HG-U133A	PTGDS	prostaglandin D2 synthase (21kD, brain)	Consensus includes gb:NM_005953.1 /DEF=Homo sapiens metallothionein 2A (MT2A), mRNA. /FEA=CDS /GEN=MT2A /PROD=metallothionein 2A /DB_XREF=gi:5174763 /UG=Hs.118786 metallothionein 2A /FL=gb:NM_005953.1
			Consensus includes gb:NM_000954.1 /DEF=Homo sapiens prostaglandin D2 synthase (21kD, brain) (PTGDS), mRNA. /FEA=CDS /GEN=PTGDS /PROD=prostaglandin D2 synthase (21kD, brain) /DB_XREF=gi:4506250 /UG=Hs.8272 prostaglandin D2 synthase (21kD, brain) /FL=gb:AY026356.1

			gb:NM_000954.1
212168_at_HG-U133A	LOC115207	hypothetical protein BC013784	Consensus includes gb:AA551075 /FEA=EST /DB_XREF=gi:2321327 /DB_XREF=est:rk74h06 s1 /CLONE=IMAGE:1019291 /UG=Hs:109438 Homo sapiens clone 24775 mRNA sequence
212207_at_HG-U133A	KIAA1025	KIAA1025 protein	Consensus includes gb:BG426689 /FEA=EST /DB_XREF=gi:13333195 /DB_XREF=est:602493234F1 /CLONE=IMAGE:4607168 /UG=Hs:4084 KIAA1025 protein
212222_at_HG-U133A	KIAA0077	KIAA0077 protein	Consensus includes gb:AU143855 /FEA=EST /DB_XREF=gi:11005376 /DB_XREF=est:AU143855 /CLONE=HEMBA1000210 /UG=Hs:112396 KIAA0077 protein
212229_s_at_HG-U133A			Consensus includes gb:AK001699.1 /DEF=Homo sapiens cDNA FLJ10837 fis, clone NT2RP4001260, highly similar to Homo sapiens mRNA for KIAA0875 protein. /FEA=mRNA /DB_XREF=gi:7023121 /UG=Hs:184227 F-box only protein 21 /FL=gb:AF174601.1
212231_at_HG-U133A	FBXO21	F-box only protein 21	Consensus includes gb:AB020682.1 /DEF=Homo sapiens mRNA for KIAA0875 protein, partial cds. /FEA=mRNA /GEN=KIAA0875 /PROD=KIAA0875 protein /DB_XREF=gi:4240238 /UG=Hs:184227 F-box only protein 21 /FL=gb:AF174601.1
212232_at_HG-U133A	KIAA1014	KIAA1014 protein	Consensus includes gb:AB023231.1 /DEF=Homo sapiens mRNA for KIAA1014 protein, partial cds. /FEA=mRNA /GEN=KIAA1014 /PROD=KIAA1014 protein /DB_XREF=gi:4589677 /UG=Hs:6834 KIAA1014 protein
212236_x_at_HG-U133A			Consensus includes gb:Z19574 /DEF=H.sapiens gene for cytokeratin 17 /FEA=mRNA /DB_XREF=gi:30378 /UG=Hs:2785 keratin 17
212250_at_HG-U133A			Consensus includes gb:AV700332 /FEA=EST /DB_XREF=gi:10302303 /DB_XREF=est:AV700332 /CLONE=GKCDIF11 /UG=Hs:243891 Homo sapiens cDNA FLJ20738 fis, clone HEP08257
212251_at_HG-U133A			Consensus includes gb:AI972475 /FEA=EST /DB_XREF=gi:5769391

		DKFZp564C1563 (from clone DKFZp564C1563)	/DB_XREF=est:wr40b09.x1 /CLONE=IMAGE:2490137 /UG=Hs.243901 Homo sapiens cDNA FLJ20738 fis, clone HEP08237
212259_s_at_HG-U133A	HPIP	hematopoietic PBX-interacting protein	Consensus includes gb:BF344265 /FEA=EST /DB_XREF=gi:11291478 /DB_XREF=est:602017327F1 /CLONE=IMAGE:4152943 /UG=Hs.8068
212268_at_HG-U133A	SERPINB1	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1	Consensus includes gb:NM_030666.1 /DEF=Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1 (SERPINB1), mRNA. /FEA=CDS /GEN=SERPINB1 /PROD=serine (or cysteine) proteinase inhibitor, cladeB (ovalbumin), member 1 /DB_XREF=gi:13489086 /UG=Hs.183583 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1 /FI=gb:NM_030666.1
212271_at_HG-U133A	MAPK1	mitogen-activated protein kinase 1	Consensus includes gb:AA195999 /FEA=EST /DB_XREF=gi:1791623 /DB_XREF=est:zp9906.s1 /CLONE=IMAGE:629355 /UG=Hs.324473 mitogen-activated protein kinase 1
212281_s_at_HG-U133A	MAC30	hypothetical protein	Consensus includes gb:BF038366 /FEA=EST /DB_XREF=gi:10744142 /DB_XREF=est:601459338F1 /CLONE=IMAGE:3862808 /UG=Hs.199695 hypothetical protein
212285_s_at_HG-U133A	AGRN	agrin	Consensus includes gb:AW008051 /FEA=EST /DB_XREF=gi:5856829 /DB_XREF=est:ww48h10.x1 /CLONE=IMAGE:2532835 /UG=Hs.273330 Homo sapiens, clone IMAGE:3506210, mRNA, partial cds
212287_at_HG-U133A	JJAZ1	joined to JAZF1	Consensus includes gb:BF382924 /FEA=EST /DB_XREF=gi:11364313 /DB_XREF=est:601816985F1 /CLONE=IMAGE:4050909 /UG=Hs.197803 KIAA0160 protein
212293_at_HG-U133A	KIAA0630	KIAA0630 protein	Consensus includes gb:BG11260 /FEA=EST /DB_XREF=gi:12604766 /DB_XREF=est:602281701F1 /CLONE=IMAGE:4369057 /UG=Hs.12239 KIAA0630 protein
212309_at_HG-U133A	CLASP2	CLIP-associating protein 2	Consensus includes gb:AV725315 /FEA=EST /DB_XREF=gi:10830580 /DB_XREF=est:AV725315 /CLONE=HTCCAG11 /UG=Hs.108614 KIAA0627

			protein; Drosophila multiple asters (Mast)-like homolog 2
212311_at_HG-U133A	KIAA0746	KIAA0746 protein	Consensus includes gb:AA522514 /FEA=EST /DB_XREF=gi:2263226 /DB_XREF=est:ni38e01.s1 /CLONE=IMAGE979104 /UG=Hs.4950 KIAA0746 protein
212313_at_HG-U133A		Homo sapiens cDNA FLJ11714 fis, clone HEMBA1005219, weakly similar to NUCLEAR PROTEIN SNF7	Consensus includes gb:BC004344.1 /DEF=Homo sapiens, clone IMAGE:3633354, mRNA, partial cds. /FEA=mRNA /PROD=Unknown (protein for IMAGE:3633354) /DB_XREF=gi:13279286 /UG=Hs.5019 Homo sapiens, clone IMAGE:3633354, mRNA, partial cds
212314_at_HG-U133A	KIAA0746	KIAA0746 protein	Consensus includes gb:AB018289.1 /DEF=Homo sapiens mRNA for KIAA0746 protein, partial cds. /FEA=mRNA /GEN=KIAA0746 /PROD=KIAA0746 protein /DB_XREF=gi:3882212 /UG=Hs.4950 KIAA0746 protein
212345_s_at_HG-U133A	DKFZP586F2423	hypothetical protein DKFZp586F2423	Consensus includes gb:BE675139 /FEA=EST /DB_XREF=gi:10035680 /DB_XREF=est:7f03b12.x1 /CLONE=IMAGE:3293567 /UG=Hs.13659 hypothetical protein DKFZp586F2423
212346_s_at_HG-U133A			Consensus includes gb:AK026392.1 /DEF=Homo sapiens cDNA, FJ227739 fis, clone HUV00686. /FEA=mRNA /DB_XREF=gi:10439242 /UG=Hs.102402 Mad4 homolog
212349_at_HG-U133A	POFUT1	protein O-fucosyltransferase 1	Consensus includes gb:AL045513 /FEA=EST /DB_XREF=gi:5439349 /DB_XREF=est:DKFZp434j015_1 /CLONE=DKFZp434j015 /UG=Hs.178292 KIAA0180 protein
212357_at_HG-U133A	KIAA0280	KIAA0280 protein	Consensus includes gb:AI096888 /FEA=EST /DB_XREF=gi:3446470 /DB_XREF=est:qb58108.x1 /CLONE=IMAGE:1704327 /UG=Hs.75400 KIAA0280 protein
212365_at_HG-U133A	MYO1B	myosin IB	Consensus includes gb:BF215996 /FEA=EST /DB_XREF=gi:11109582 /DB_XREF=est:601881549F1 /CLONE=IMAGE:4093740 /UG=Hs.121576 Homo sapiens cDNA FJ20153 fis, clone COLO8656, highly similar to AJ001381 Homo sapiens incomplete cDNA for a mutated allele

212382_at_HG-U133A	Homo sapiens cDNA FLJ11918 fis, clone HEMBB1000272	Consensus includes gb:BF433429 /FEA=EST /DB_XREF=gi:11445592 /DB_XREF=est:7q53a12.x1 /CLONE=IMAGE:3702046 /UG=Hs.289068 Homo sapiens cDNA FLJ11918 fis, clone HEMBB1000272
212385_at_HG-U133A	Homo sapiens cDNA FLJ11918 fis, clone HEMBB1000272	Consensus includes gb:AU118026 /CLONE=HEMBB10002729 /UG=Hs.289068 Homo sapiens cDNA FLJ11918 fis, clone HEMBB1000272
212386_at_HG-U133A	Homo sapiens cDNA FLJ11918 fis, clone HEMBB1000272	Consensus includes gb:BF592782 /FEA=EST /DB_XREF=gi:11685106 /DB_XREF=est:7j94d06.x1 /CLONE=IMAGE:3442594 /UG=Hs.289068 Homo sapiens cDNA FLJ11918 fis, clone HEMBB1000272
212387_at_HG-U133A	Homo sapiens cDNA FLJ11918 fis, clone HEMBB1000272	Consensus includes gb:BG495771 /FEA=EST /DB_XREF=gi:13457287 /DB_XREF=est:602540396f1 /CLONE=IMAGE:4671599 /UG=Hs.289068 Homo sapiens cDNA FLJ11918 fis, clone HEMBB1000272
212397_at_HG-U133A	RDX	Consensus includes gb:AL137751.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434l0812 (from clone DKFZp434l0812); partial cds. /FEA=mRNA (GEN=DKFZp434l0812 /PROD=hypothetical protein /DB_XREF=gi:6808387 /UG=Hs.263671 Homo sapiens mRNA; cDNA DKFZp434l0812 (from clone DKFZp434l0812); partial cds
212400_at_HG-U133A		Consensus includes gb:AL043266 /FEA=EST /DB_XREF=gi:5935844 /DB_XREF=est:DKFZp434l1423_s1 /CLONE=DKFZp434l1423 /UG=Hs.111334 ferritin, light polypeptide
212417_at_HG-U133A	SCAMP1	Consensus includes gb:BF058944 /FEA=EST /DB_XREF=gi:10812840 /DB_XREF=est:7k36cd5.x1 /CLONE=IMAGE:3477489 /UG=Hs.31218 secretory carrier membrane protein 1
212449_s_at_HG-U133A	LYPLA1	Consensus includes gb:BG288007 /FEA=EST /DB_XREF=gi:13042412 /DB_XREF=est:602387785f1 /CLONE=IMAGE:4516701 /UG=Hs.12540 lysophospholipase 1
212463_at_HG-U133A		Consensus includes gb:BE379006 /FEA=EST /DB_XREF=gi:9324371 /DB_XREF=est:601236272f1 /CLONE=IMAGE:3608680 /UG=Hs.99766 Homo sapiens mRNA; cDNA DKFZp564j0323 (from clone

		DKFZp564J0323)	sapiens mRNA; cDNA DKFZp564J0323 (from clone DKFZp564J0323)
			Consensus includes gb:AB019494.1 /DEF=Homo sapiens IDN3 mRNA, partial cds. /FEA=mRNA /GEN=IDN3 /DB_XREF=gi:4760548 /UG=Hs.225/67 IDN3 protein
212469_at_HG-U133A	IDN3	IDN3 protein	Consensus includes gb:AK022815.1 /DEF=Homo sapiens cDNA FLJ12753 fs, clone NT2RP2001226. /FEA=mRNA /DB_XREF=gi:10434432 /UG=Hs.75277
212479_s_at_HG-U133A	FLJ13910	hypothetical protein FLJ13910	Consensus includes gb:AB002374.1 /DEF=Human mRNA for KIAA0376 gene, partial cds. /FEA=mRNA /GEN=KIAA0376 /DB_XREF=gi:2280484
212480_at_HG-U133A	KIAA0376	KIAA0376 protein	Consensus includes gb:AI214061 /FEA=EST /DB_XREF=gi:377762 /UG=Hs.4791 KIAA0376 protein
212481_s_at_HG-U133A	TPM4	tropomyosin 4	Consensus includes gb:BF974389 /FEA=EST /DB_XREF=gi:12341604 /DB_XREF=est:602244063F1 /CLONE=IMAGE:4335182 /UG=Hs.18686 Mouse Mammary Tumor Virus Receptor homolog
212484_at_HG-U133A	MTVR	Mouse Mammary Tumor Virus Receptor homolog	Consensus includes gb:BF968134 /FEA=EST /DB_XREF=gi:12353349 /DB_XREF=est:602269121F1 /CLONE=IMAGE:4357349 /UG=Hs.250723 FK506 binding protein 12-rapamycin associated protein 1
212509_s_at_HG-U133A		ESTs, Weakly similar to N-WASP [H.sapiens]	Consensus includes gb:NM_005564.1 /DEF=Homo sapiens lipocalin 2 (oncogene 24p3) (LCN2), mRNA. /FEA=CDS /GEN=LCN2 /PROD=lipocalin 2 (oncogene 24p3) /DB_XREF=gi:5031852 /UG=Hs.204238 lipocalin 2 (oncogene 24p3) /FL=gb:NM_005564.1
212531_at_HG-U133A	LCN2	lipocalin 2 (oncogene 24p3)	Consensus includes gb:AA142929 /FEA=EST /DB_XREF=gi:1712307 Homo sapiens cDNA FLJ32156 fs, clone PLACE6000137
212535_at_HG-U133A			Consensus includes gb:AL576253 /FEA=EST /DB_XREF=gi:12398214 /DB_XREF=est:AL576253 /CLONE=CS0D073YM22 (3 prime) /UG=Hs.8021 KIAA1058 protein
212538_at_HG-U133A	KIAA1058	KIAA1058 protein	

212549_at_HG-U133A	Homo sapiens mRNA; cDNA DKFZp588N1323 (from clone DKFZp588N1323)	Consensus includes gb:BE645861 /FEA=EST /DB_XREF=gi:3970172 /DB_XREF=est:7e77d05.x1 /CLONE=IMAGE:3288489 /UG=Hs.24064 Homo sapiens mRNA; cDNA DKFZp588N1323 (from clone DKFZp588N1323)
212569_at_HG-U133A	KIAA0650	Consensus includes gb:AV699744 /FEA=EST /DB_XREF=gi:10301715 /DB_XREF=est:AV699744 /CLONE=GKCEDF05 /UG=Hs.8118 KIAA0650 protein
212577_at_HG-U133A	KIAA0650	Consensus includes gb:AA868754 /FEA=EST /DB_XREF=gi:2964199 /DB_XREF=est:ak52e09.s1 /CLONE=IMAGE:1409868 /UG=Hs.8118 KIAA0650 protein
212579_at_HG-U133A	KIAA0650	Consensus includes gb:AB014550.1 /DEF=Homo sapiens mRNA for KIAA0650 protein, partial cds. /FEA=mRNA /GEN=KIAA0650 /PROD=KIAA0650 protein /DB_XREF=gi:327113 /UG=Hs.8118 KIAA0650 protein
212586_at_HG-U133A	ARTS-1	Consensus includes gb:AA195244 /FEA=EST /DB_XREF=gi:1784944 /DB_XREF=est:zr3b02.s1 /CLONE=IMAGE:665451 /UG=Hs.247043 type 1 tumor necrosis factor receptor shedding aminopeptidase regulator
212587_s_at_HG-U133A	PTPRC	Consensus includes gb:AI809341 /FEA=EST /DB_XREF=gi:5395907 /DB_XREF=est:we96c09.x1 /CLONE=IMAGE:2348944 /UG=Hs.170121 protein tyrosine phosphatase, receptor type, C
212589_at_HG-U133A	RRAS2	Consensus includes gb:AI753792 /FEA=EST /DB_XREF=gi:5132144 /DB_XREF=est:cr16f06.x2 /CLONE=HBMSMC_cr16f06 /UG=Hs.206097 oncogene TC21
212590_at_HG-U133A		Consensus includes gb:AI431643 /FEA=EST /DB_XREF=gi:4304619 /DB_XREF=est:tg74ff2.x1 /CLONE=IMAGE:2114543 /UG=Hs.206097 oncogene TC21
212592_at_HG-U133A		Consensus includes gb:AV733266 /FEA=EST /DB_XREF=gi:10850811 /DB_XREF=est:AV733266 /CLONE=cdaAG04 /UG=Hs.76325 step II splicing factor SLU7

		KIAA0399 protein	Consensus includes gb:AB007859.2 /DEF=Homo sapiens mRNA for KIAA0399 protein, partial cds. /FEA=mRNA /GEN=KIAA0399 /PROD=KIAA0399 protein /DB_XREF=gi:6634028 /UG=Hs.100955 KIAA0399 protein
212601_at_HG-U133A	KIAA0399	Homo sapiens mRNA; cDNA DKFZp586N012 (from clone DKFZp586N012)	Consensus includes gb:BG285011 /FEA=EST /DB_XREF=gi:13036541 /DB_XREF=est:602409278F1 /CLONE=IMAGE:4538275 /UG=Hs.12702 Homo sapiens mRNA; cDNA DKFZp586N012 (from clone DKFZp586N012)
212614_at_HG-U133A			Consensus includes gb:AI633689 /FEA=EST /DB_XREF=gi:4685019 /DB_XREF=est:th71d03.x1 /CLONE=IMAGE:2124101 /UG=Hs.69171 protein kinase C-like 2
212629_s_at_HG-U133A	PRKCL2	lipoma HMGIC fusion partner-like 2	Consensus includes gb:N66633 /FEA=EST /DB_XREF=gi:1218758 /DB_XREF=est:yy70102.s1 /CLONE=IMAGE:278907 /UG=Hs.79299 lipoma HMGIC fusion partner-like 2
212658_at_HG-U133A	LHFPL2		Consensus includes gb:AI735639 /FEA=EST /DB_XREF=gi:5057163 /DB_XREF=est:at18h12.x1 /CLONE=IMAGE:2355527 /UG=Hs.9729 KIAA0239 protein
212660_at_HG-U133A	KIAA0239	KIAA0239 protein	Consensus includes gb:AL575922 /FEA=EST /DB_XREF=gi:12937561 /DB_XREF=est:AL575922 /CLONE=CS001067YN03 (3 prime) /UG=Hs.111779 secreted protein, acidic, cysteine-rich (osteonectin)
212667_at_HG-U133A	SPARC		Consensus includes gb:AB032983.1 /DEF=Homo sapiens mRNA for KIAA1157 protein, partial cds. /FEA=mRNA /GEN=KIAA1157 /PROD=KIAA1157 protein /DB_XREF=gi:65330128 /UG=Hs.21894 KIAA1157 protein
212686_at_HG-U133A	KIAA1157	KIAA1157 protein	Consensus includes gb:AB011178.1 /DEF=Homo sapiens mRNA for KIAA0606 protein, partial cds. /FEA=mRNA /GEN=KIAA0606 /PROD=KIAA0606 protein /DB_XREF=gi:3043735 /UG=Hs.38176 KIAA0606 protein; SCN Circadian Oscillatory Protein (SCOP)
212719_at_HG-U133A	SCOP		Consensus includes gb:AI798908 /FEA=EST /DB_XREF=gi:5364380
212733_at_HG-U133A	KIAA0226	KIAA0226 gene product	

			/DB_XREF=est:we94b11.x1 /CLONE=IMAGE:2348733 /UG=Hs.141296 KIAA0226 gene product
			Consensus includes gb:BF448041 /FEA=EST /DB_XREF=gi:11513102 /DB_XREF=est:7q97f09.x1 /CLONE=IMAGE:3706504 /UG=Hs.141296
		KIAA0226	KIAA0226 gene product
			Consensus includes gb:AB020630.1 /DEF=Homo sapiens mRNA for KIAA0823 protein, partial cds. /FEA=mRNA /GEN=KIAA0823 /PROD=KIAA0823 protein /DB_XREF=gi:4240131 /UG=Hs.45719 KIAA0823 protein
212735_at_HG-U133A	KIAA0226		Consensus includes gb:AL583340 /FEA=EST /DB_XREF=gi:12952206 /DB_XREF=est:AL583340 /CLONE=CS0DL012YA08 (3 prime) /UG=Hs.37656
212750_at_HG-U133A	PPP1R16B		KIAA0602 protein
212778_at_HG-U133A	KIAA0602		Consensus includes gb:AI538172 /FEA=EST /DB_XREF=gi:4452307 /DB_XREF=est:ii7508.x1 /CLONE=IMAGE:2137863 /UG=Hs.91065 hypothetical protein DKFZp761B2423
212783_at_HG-U133A	DKFZp761B2423		Consensus includes gb:AI700633 /FEA=EST /DB_XREF=gi:4988533 /DB_XREF=est:we38g03.x1 /CLONE=IMAGE:2343412 /UG=Hs.288232 Homo sapiens cDNA: FLJ22642 fis, clone HS106970
212812_at_HG-U133A			Consensus includes gb:AA149644 /FEA=EST /DB_XREF=gi:1720445 /DB_XREF=est:z139d08.s1 /CLONE=IMAGE:504303 /UG=Hs.55016 hypothetical protein FLJ21935
212813_at_HG-U133A	FLJ14529		Consensus includes gb:X17115.1 /DEF=Human mRNA for IgM heavy chain complete sequence. /FEA=mRNA /DB_XREF=gi:33450 /UG=Hs.302063 immunoglobulin heavy constant mu
212827_at_HG-U133A	IGHM		Consensus includes gb:AA191573 /FEA=EST /DB_XREF=gi:1780272 /DB_XREF=est:zp81b09.s1 /CLONE=IMAGE:626585 /UG=Hs.61289 synaptotagmin 2
212828_at_HG-U133A	SYNJ2		Consensus includes gb:AB023227.1 /DEF=Homo sapiens mRNA for KIAA1010 protein
212838_at_HG-U133A	KIAA1010		

		KIAA1010 protein, partial cds. /FEA=mRNA /GEN=KIAA1010 /PROD=KIAA1010 protein /DB_XREF=gi:4589669 /UG=Hs.23860 KIAA1010 protein
		Consensus includes gb:AL080168.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434C171 (from clone DKFZp434C171); partial cds. /FEA=mRNA /GEN=DKFZp434C171 /PROD=hypothetical protein /DB_XREF=gi:5262637 /UG=Hs.209100 DKFZP434C171 protein
212886_at_HG-U133A	DKFZP434C171	DKFZP434C171 protein
212895_s_at_HG-U133A	ABR	active BCR-related gene
212914_at_HG-U133A	PKP4	plakophilin 4
212953_x_at_HG-U133A	CALR	calreticulin
212956_at_HG-U133A	KIAA0882	KIAA0882 protein
212960_at_HG-U133A	KIAA0882	KIAA0882 protein
212967_x_at_HG-U133A	NAP1L1	nucleosome assembly protein 1-like 1
212970_at_HG-U133A		Homo sapiens mRNA; cDNA DKFZp434E033 (from clone DKFZp434E033)
212973_at_HG-U133A	RPIA	ribose 5'-phosphate isomerase A (ribose

		5'-phosphate epimerase)	/DB_XREF=est:wd85g04.x1 /CLONE=IMAGE:2338422 /UG=Hs.79886 ribose 5'-phosphate isomerase A (ribose 5'-phosphate epimerase)
		KIAA0870	Consensus includes gb:AB020677.2 /DEF=Homo sapiens mRNA for KIAA0870 protein, partial cds. /FEA=mRNA /GEN=KIAA0870 /PROD=KIAA0870 protein /DB_XREF=gi:6635136 /UG=Hs.18166 KIAA0870 protein
212975_at_HG-U133A	KIAA0870	KIAA0870 protein	Consensus includes gb:BF115739 /FEA=EST /DB_XREF=gi:10985215 /DB_XREF=est:7n64b08.x1 /CLONE=IMAGE:3569246 /UG=Hs.15740 Homo sapiens mRNA; cDNA DKFZp434E033 (from clone DKFZp434E033)
212985_at_HG-U133A		Homo sapiens mRNA for Hmob33	Consensus includes gb:AI377497 /FEA=EST /DB_XREF=gi:4187350 /DB_XREF=est:tc37c06.x1 /CLONE=IMAGE:2066794 /UG=Hs.153716 Homo sapiens mRNA for Hmob33 protein, 3 untranslated region
212989_at_HG-U133A		Homo sapiens mRNA for Hmob33 protein, 3' untranslated region	Consensus includes gb:AI583173 /FEA=EST /DB_XREF=gi:4569070 /DB_XREF=est:tg64e04.x1 /CLONE=IMAGE:2213598 /UG=Hs.73931 major histocompatibility complex, class II, DQ beta 1
212998_x_at_HG-U133A	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	Consensus includes gb:W26593 /FEA=EST /DB_XREF=gi:1307454 /DB_XREF=est:33g5 /UG=Hs.145279 SET translocation (myeloid leukemia-associated)
213048_s_at_HG-U133A	SET	SET translocation (myeloid leukemia-associated)	Consensus includes gb:BG436400 /FEA=EST /DB_XREF=gi:13342906 /DB_XREF=est:602509062F1 /CLONE=IMAGE:4619679 /UG=Hs.167031 DKKZP566D133 protein
213049_at_HG-U133A	DKFZp566D133	DKFZp566D133 protein	Consensus includes gb:AB002319.1 /DEF=Human mRNA for KIAA0321 gene, partial cds. /FEA=mRNA /GEN=KIAA0321 /DB_XREF=gi:2224582 /UG=Hs.8663 KIAA0321 protein
213073_at_HG-U133A	KIAA0321	KIAA0321 protein	Consensus includes gb:AL523144 /FEA=EST /DB_XREF=gi:12786637 /DB_XREF=est:AL523144 /CLONE=CS0DC001YO14 (3 prime) /UG=Hs.206770 zinc finger protein 297 /FL=gb:NM_005453.2
213081_at_HG-U133A	ZNF297	zinc finger protein 297	Consensus includes gb:ZT8330 /FEA=EST /DB_XREF=gi:1495103 interleukin 27
213101_s_at_HG-	IL27	interleukin 27	

U133A			/DB_XREF=estHSZ78330 /CLONE=2.49 (CEPH) /UG=Hs.10927 hypothetical protein EUROIMAGE1875335
213142_x_at_HG-U133A	LOC54103	hypothetical protein	Consensus includes gb:AV700415 /FEA=EST /DB_XREF=gi:10302386 /DB_XREF=est:AV700415 /CLONE=GKCDGA04 /UG=Hs.12969 hypothetical protein
213147_at_HG-U133A	HOXA10	homeo box A10	Consensus includes gb:AI375919 /FEA=EST /DB_XREF=gi:4175909 /DB_XREF=est:tc14d04.x1 /CLONE=IMAGE:2063815 /UG=Hs.110637 homeobox A10 /FL=gb:NM_018951.1
213150_at_HG-U133A	HOXA10	homeo box A10	Consensus includes gb:BF792917 /FEA=EST /DB_XREF=gi:12097902 /DB_XREF=est:602253224F1 /CLONE=IMAGE:4345588 /UG=Hs.110637 homeo box A10 /FL=gb:NM_018951.1
213159_at_HG-U133A	KIAA0805	KIAA0805 protein	Consensus includes gb:AB018348.1 /DEF=Homo sapiens mRNA for KIAA0805 protein, partial cds. /FEA=mRNA /GEN=KIAA0805 /PROD=KIAA0805 protein /DB_XREF=gi:3882330 /UG=Hs.55947 KIAA0805 protein
213238_at_HG-U133A	ATP10D	ATPase, Class V, type 10D	Consensus includes gb:AU145127 /FEA=EST /DB_XREF=gi:4371373 /DB_XREF=est:tm3406.x1 /CLONE=IMAGE:2160035 /UG=Hs.173540 ATPase, Class V, type 10D
213249_at_HG-U133A	FBXL7	F-box and leucine-rich repeat protein 7	Consensus includes gb:AU145127 /FEA=EST /DB_XREF=gi:11006648 /DB_XREF=est:AU145127 /CLONE=HEMBA1003978 /UG=Hs.76798 f-box and leucine-rich repeat protein 7 /FL=gb:AF199356.1 gb:NM_012304.1
213288_at_HG-U133A		Homo sapiens clone 23620 mRNA sequence	Consensus includes gb:AI761250 /FEA=EST /DB_XREF=gi:5176917 /DB_XREF=est:w16801.x1 /CLONE=IMAGE:2398489 /UG=Hs.90797 Homo sapiens clone 23620 mRNA sequence
213295_at_HG-U133A		Homo sapiens mRNA; cDNA DKFZp586D1122 (from clone DKFZp586D1122)	Consensus includes gb:AA556096 /FEA=EST /DB_XREF=gi:2325635 /DB_XREF=est:n140e01.s1 /CLONE=IMAGE:994968 /UG=Hs.26295 Homo sapiens mRNA; cDNA DKFZp586D1122 (from clone DKFZp586D1122)
213309_at_HG-U133A	PLCL2	phospholipase C-like 2	Consensus includes gb:AL117515.1 /DEF=Homo sapiens mRNA; cDNA

		DKFZp434L0735 (from clone DKFZp434L0735); partial cds. /FEA=mRNA /GEN=DKFZp434L0735 /PROD=hypothetical protein /DB_XREF=gi:5912029 /UG=Hs.54886 phospholipase C, epsilon 2
		Consensus includes gb:AI922519 /FEA=EST /DB_XREF=gi:5658483 /DB_XREF=est:wm89a07.x1 /CLONE=IMAGE:2443092 /UG=Hs.55099 rab6
213313_at_HG-U133A	GAPCENA	rab6 GTPase activating protein (GAP and centrosome-associated)
213353_at_HG-U133A	ABCAS5	ATP-binding cassette, sub-family A (ABC1), member 5
213370_s_at_HG-U133A	DKFZP434L243	DKFZP434L243 protein
213447_at_HG-U133A	IPW	imprinted in Prader-Willi syndrome
213452_at_HG-U133A	ZNF184	zinc finger protein 184 (Kruppel-like)
213453_X_at_HG-U133A	GAPD	glyceraldehyde-3-phosphate dehydrogenase
213474_at_HG-U133A		ESTs
213504_at_HG-U133A	MOV34-34KD	COP9 subunit 6 (MOV34 homolog, 34 kD)
213511_s_at_HG-U133A		Homo sapiens, clone MGC:17492 IMAGE:3453013, mRNA, complete cds

		myotubularin related protein 1	
213514_s_at_HG-U133A	DIAPH1	diaphanous homolog 1 (Drosophila)	Consensus includes gb:AU158818 /FEA=EST /DB_XREF=gi:11020339 /DB_XREF=est:AU158818 /CLONE=THYRO10000147 /UG=Hs.26584
213539_at_HG-U133A	CD3D	CD3D antigen, delta polypeptide (TTT3 complex)	Consensus includes gb:NM_000732.1 /DEF=Homo sapiens CD3D antigen, diaphanous (Drosophila, homolog) 1 delta polypeptide (TTT3 complex) (CD3D), mRNA. /FEA=CDS /GEN=CD3D /PROD=CD3D antigen, delta polypeptide (TTT3 complex) /DB_XREF=gi:4502668 /UG=Hs.95327 CD3D antigen, delta polypeptide (TTT3 complex) /FL=gb:NM_000732.1
213572_s_at_HG-U133A	SERPINB1	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1	Consensus includes gb:AI554300 /FEA=EST /DB_XREF=gi:44866663 /DB_XREF=est:tc05007.x1 /CLONE=MAGE-2207940 /UG=Hs.183583 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1
213582_at_HG-U133A	ATP11A	ATPase, Class VI, type 11A	Consensus includes gb:BF439472 /FEA=EST /DB_XREF=gi:11451989 /DB_XREF=est:nab65ad05.x1 /CLONE=IMAGE:3272361 /UG=Hs.29189 ATPase, Class VI, type 11A
213600_at_HG-U133A	KIAA0545	KIAA0545 protein	Consensus includes gb:AA426633 /FEA=EST /DB_XREF=gi:2107236 /DB_XREF=est:zv47a01.s1 /CLONE=IMAGE:756744 /UG=Hs.129943 KIAA0545 protein
213622_at_HG-U133A	COL9A2	collagen, type IX, alpha 2	Consensus includes gb:AI733465 /FEA=EST /DB_XREF=gi:5054578 /DB_XREF=est:od93g07.x5 /CLONE=IMAGE:1593948 /UG=Hs.37165 collagen, type IX, alpha 2 /FL=gb:NM_001852.1
213624_at_HG-U133A	ASM3A	acid sphingomyelinase-like phosphodiesterase	Consensus includes gb:AA873600 /FEA=EST /DB_XREF=gi:2969722 /DB_XREF=est:ob12a02.s1 /CLONE=IMAGE:1323434 /UG=Hs.37165 acid sphingomyelinase-like phosphodiesterase
213639_s_at_HG-U133A	KIAA0557	KIAA0557 protein	Consensus includes gb:AI871396 /FEA=EST /DB_XREF=gi:5545445 /DB_XREF=est:w18107.x1 /CLONE=IMAGE:2431333 /UG=Hs.101414 KIAA0557 protein
213674_x_at_HG-	IGHG3	immunoglobulin heavy constant gamma	Consensus includes gb:AI858004 /FEA=EST /DB_XREF=gi:5511620

U133A		3 (G3m marker)	/DB_XREF=est:wf69b09.x1 /CLONE=IMAGE:2408057 /UG=Hs.284277 Homo sapiens immunoglobulin mu chain antibody MO30 (IgM) mRNA, complete cds
213689_x_at_HG-U133A	RPL5	ribosomal protein L5	Consensus includes gb:AL137958 /FEA=EST /DB_XREF=gi:6854638 /DB_XREF=est:DKFZp761C1715_r1 /CLONE=DKFZp761C1715 /UG=Hs.180946 ribosomal protein L5
213716_s_at_HG-U133A	SECTM1	secreted and transmembrane 1	Consensus includes gb:BF939575 /FEA=EST /DB_XREF=gi:12357086 /DB_XREF=est:nac79g07.x1 /CLONE=IMAGE:3440820 /UG=Hs.326612 Homo sapiens secreted and transmembrane 1 (SECTM1), mRNA
213725_x_at_HG-U133A	DKFZp586F071	Homo sapiens mRNA; cDNA DKFZp586F071 (from clone DKFZp586F071)	Consensus includes gb:AI693140 /FEA=EST /DB_XREF=gi:4970480 /DB_XREF=est:wd68a05.x1 /CLONE=IMAGE:2336720 /UG=Hs.22907. Homo sapiens mRNA; cDNA DKFZp586F071 (from clone DKFZp586F071)
213737_x_at_HG-U133A	ESTs		Consensus includes gb:AI620911 /FEA=EST /DB_XREF=gi:4630037 /DB_XREF=est:tu05d12.x1 /CLONE=IMAGE:2250167 /UG=Hs.205125 ESTs
213772_s_at_HG-U133A	GGA2	golgi associated, gamma adaptin ear containing, ARF binding protein 2	Consensus includes gb:BF196572 /FEA=EST /DB_XREF=gi:11084646 /DB_XREF=est:7m98a04.x1 /CLONE=IMAGE:3563023 /UG=Hs.155546 KIAA1080 protein; Golgi-associated, gamma-adaptin ear containing, ARF-binding protein 2
213779_x_at_HG-U133A	CAP		Consensus includes gb:AL031186 /DEF=Human DNA sequence from clone CTA-984G1 on chromosome 22q12.1-12.2 Contains the 5 part of the EWSR1 gene for Ewing sarcoma breakpoint region 1 protein, a novel gene and the 3 part of a novel gene with Collagen triple helix repeats. Contains ESTs... /FEA=mRNA_1 /DB_XREF=gi:4581429 /UG=Hs.289106 Human DNA sequence from clone CTA-984G1 on chromosome 22q12.1-12.2 Contains the 5 part of the EWSR1 gene for Ewing sarcoma breakpoint region 1 protein, a novel gene and the 3 part of a novel gene with Collagen triple helix repeats. Contains ESTs, GSSs a
213798_s_at_HG-			Consensus includes gb:AA806142 /FEA=EST /DB_XREF=gi:2874892

U133A		/DB_XREF=est:oe29d06.s1 /CLONE=IMAGE:1409963 /UG=Hs.104125 adenylyl cyclase-associated protein
213810_s_at_HG-U133A	FLJ10342	hypothetical protein FLJ10342
213844_at_HG-U133A	HOXA5	homeo box A5
213846_at_HG-U133A	COX7C	cytochrome c oxidase subunit VIic
213850_s_at_HG-U133A	SFRS2IP	splicing factor, arginine/serine-rich 2, interacting protein
213854_at_HG-U133A	SYNGR1	synaptogyrin 1
213857_s_at_HG-U133A	CD47	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)
213891_s_at_HG-U133A		Homo sapiens cDNA FLJ11918 fis, clone HEMBB1000272
213894_at_HG-U133A	KIAA0960	KIAA0960 protein
213895_at_HG-U133A	EMP1	epithelial membrane protein 1

			membrane protein 1
213902_at_HG-U133A	ASAH	N-acylsphingosine amidohydrolase (acid ceramidase)	Consensus includes gb:AI379338 /FEA=EST /DB_XREF=gi:4189191 /DB_XREF=est:ic73df5.x1 /CLONE=IMAGE:2070296 /UG=Hs.75811 N-
213922_at_HG-U133A	KIAA0847	KIAA0847 protein	Consensus includes gb:AW294686 /FEA=EST /DB_XREF=gi:6701322 /DB_XREF=est:U1-H-BW0-all-H-04-O-Ui.s1 /CLONE=IMAGE:2729719 /UG=Hs.125636 KIAA0847 protein
213927_at_HG-U133A		ESTs	Consensus includes gb:AV753204 /FEA=EST /DB_XREF=gi:10911052 /DB_XREF=est:AV753204 /CLONE=NPDBDB08 /UG=Hs.170267 ESTs /DB_XREF=est:DKFZp547K034_r1 /CLONE=DKFZp547K034 /UG=Hs.56186
213942_at_HG-U133A	EGFL3	EGF-like-domain, multiple 3	Consensus includes gb:BG236220 /FEA=EST /DB_XREF=gi:12750151 /DB_XREF=est:nat25h11.x1 /CLONE=IMAGE:4142085 /UG=Hs.323067 Homo sapiens mRNA; cDNA DKFZp434J194 (from clone DKFZp434J194)
213944_x_at_HG-U133A			Consensus includes gb:AW589975 /FEA=EST /DB_XREF=gi:7277100 /DB_XREF=est:hg28b08.x1 /CLONE=IMAGE:2946903 /UG=Hs.20985 sin3-associated polypeptide, 30kD
213963_s_at_HG-U133A	SAP30		Consensus includes gb:BF984434 /FEA=EST /DB_XREF=gi:4399313 /CLONE=IMAGE:4399313 /UG=Hs.239737 C-terminal binding protein 1
213979_s_at_HG-U133A	CTBP1		Consensus includes gb:AI744627 /FEA=EST /DB_XREF=gi:5113004 /DB_XREF=est:wg04g05.x1 /CLONE=IMAGE:2364152 /UG=Hs.82280 regulator of G-protein signalling 10
214000_s_at_HG-U133A	RGS10	regulator of G-protein signalling 10	Consensus includes gb:AA039439 /FEA=EST /DB_XREF=gi:1515780 /DB_XREF=est:zk39a11.s1 /CLONE=IMAGE:485180 /UG=Hs.151706 KIAA0134 gene product
214017_s_at_HG-U133A	DDX34	DEAD/H (Asp-Glu-Ala-Asp)/His box polypeptide 34	Consensus includes gb:BE501352 /FEA=EST /DB_XREF=gi:9703760 hypothetical protein FLJ14393
214030_at_HG-U133A	FLJ14393		

		/DB_XREF=est:7a41e05.x1 /CLONE=IMAGE:32221312 /UG=Hs.23294 ESTs. Weakly similar to T15138 hypothetical protein T28F2.4 - Caenorhabditis elegans C.elegans
214051_at_HG-U133A	TMSNB	thymosin, beta, identified in neuroblastoma cells /DB_XREF=est:602085745f1 /CLONE=IMAGE:4249834 /UG=Hs.56145 thymosin, beta, identified in neuroblastoma cells
214109_at_HG-U133A	LRBA	vesicle trafficking, beach and anchor containing /DB_XREF=est:tu12d08.x1 /CLONE=IMAGE:2250831 /UG=Hs.62354 cell division cycle 4-like
214116_at_HG-U133A	BTD	biotinidase /DB_XREF=est:wi95g11.x1 /CLONE=IMAGE:2401124 /UG=Hs.78385.
214144_at_HG-U133A	POLR2D	polymerase (RNA) II (DNA directed) polypeptide D /DB_XREF=est:nab80a7.x1 /CLONE=IMAGE:32273900 /UG=Hs.194638 polymerase (RNA) II (DNA directed) polypeptide D
214203_s_at_HG-U133A	PIGB	phosphatidylinositol glycan, class B /DB_XREF=est:AU144243 /CLONE=HEMBA1001328 /UG=Hs.247118 phosphatidylinositol glycan, class B
214228_x_at_HG-U133A	PRODH	proline dehydrogenase (oxidase) 1 /DB_XREF=est:78g06.s1 /CLONE=IMAGE:383098 /UG=Hs.274550 proline oxidase homolog
214238_at_HG-U133A		Hom sapiens clone DT1P1B6 mRNA, CAG repeat region /DB_XREF=est:gb15f11.x1 /CLONE=IMAGE:1696365 /UG=Hs.18081 Homo sapiens clone DT1P1B6 mRNA, CAG repeat region
214310_s_at_HG-	ZFPL1	zinc finger protein-like 1 /DB_XREF=est:gi:5234393 Consensus includes gb:AI767884 /FEA=EST /DB_XREF=gi:5234393

U133A			/DB_XREF=est:wi98g11.x1 /CLONE=IMAGE:2401412 /UG=Hs.155165 zinc finger protein-like 1
214315_x_at_HG-U133A	CALR	calreticulin	Consensus includes gb:AI348935 /FEA=EST /DB_XREF=gi:4086141 /DB_XREF=est:tb60a01.x1 /CLONE=IMAGE:2058696 /UG=Hs.16488 calreticulin
214316_x_at_HG-U133A	CALR	calreticulin	Consensus includes gb:AI378706 /FEA=EST /DB_XREF=gi:4188559 /DB_XREF=est:ib91109.x1 /CLONE=IMAGE:2061737 /UG=Hs.16488 calreticulin
214317_x_at_HG-U133A	RPS9	ribosomal protein S9	Consensus includes gb:BE348997 /FEA=EST /DB_XREF=gi:9260850 /DB_XREF=est:ht47e11.x1 /CLONE=IMAGE:3149900 /UG=Hs.180920 ribosomal protein S9
214321_at_HG-U133A	NOV	nephroblastoma overexpressed gene	Consensus includes gb:BF440025 /FEA=EST /DB_XREF=gi:11452542 /DB_XREF=est:nac52c12.x1 /CLONE=IMAGE:3406079 /UG=Hs.235935 nephroblastoma overexpressed gene
214394_x_at_HG-U133A	FLJ20897	hypothetical protein FLJ20897	Consensus includes gb:AI613383 /FEA=EST /DB_XREF=gi:4622550 /DB_XREF=est:tb80e08.x1 /CLONE=IMAGE:2247110 /UG=Hs.223241 eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)
214395_x_at_HG-U133A	FLJ20897	hypothetical protein FLJ20897	Consensus includes gb:AI335509 /FEA=EST /DB_XREF=gi:4072436 /DB_XREF=est:tb66h02.x1 /CLONE=IMAGE:2059347 /UG=Hs.223241 eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)
214430_at_HG-U133A	GLA	galactosidase, alpha	Consensus includes gb:NM_000169.1 /DEF=Homo sapiens galactosidase, alpha (GLA), mRNA, /FEA=CDS /GEN=GLA /PROD=galactosidase, alpha /DB_XREF=gi:4504008 /UG=Hs.69089 galactosidase, alpha /FL=gb:BC002689.1 gb:NM_000169.1
214439_x_at_HG-U133A	BIN1	bridging integrator 1	Consensus includes gb:AF043899.1 /DEF=Homo sapiens amphiphysin IIC1 mRNA, complete cds, /FEA=CDS /PROD=amphiphysin IIC1 /DB_XREF=gi:3064256 /UG=Hs.193163 bridging integrator 1 /FL=gb:AF043899.1

214450_at_HG-U133A	CTSW	cathepsin W (lymphopain)	Consensus includes gb:NM_001335.1 /DEF=Homo sapiens cathepsin W (lymphopain) (CTSW), mRNA, /FEA=CDS /GEN=CTSW /PROD=cathepsin W (lymphopain) /FL=gb:AF013611.1 gb:NM_001335.1
214452_at_HG-U133A	BCAT1	branched chain aminotransferase 1, cytosolic	Consensus includes gb:NM_005504.1 /DEF=Homo sapiens branched chain aminotransferase 1, cytosolic (BCAT1), mRNA, /FEA=CDS /GEN=BCAT1 /PROD=branched chain aminotransferase 1, cytosolic /DB_XREF=gi:5031606 /UG=Hs.157205 branched chain aminotransferase 1, cytosolic /FL=gb:U21551.1 gb:NM_005504.1
214475_x_at_HG-U133A	CAPN3	calpain 3, (p94)	Consensus includes gb:AF127764.1 /DEF=Homo sapiens calpain 3 (CAPN3) mRNA, alternatively spliced, complete cds. /FEA=CDS /GEN=CAPN3 /PROD=calpain 3 /DB_XREF=gi:4704751 /UG=Hs.40300 calpain 3, (p94) /FL=gb:AF127764.1
214500_at_HG-U133A	H2AFY	H2A histone family, member Y	Consensus includes gb:AF044286.1 /DEF=Homo sapiens histone macroH2A1.1 mRNA, complete cds. /FEA=CDS /PROD=histone macroH2A1.1 /DB_XREF=gi:3493530 /UG=Hs.75258 H2A histone family, member Y /FL=gb:AF044286.1
214501_s_at_HG-U133A	H2AFY	H2A histone family, member Y	Consensus includes gb:AF044286.1 /DEF=Homo sapiens histone macroH2A1.1 mRNA, complete cds. /FEA=CDS /PROD=histone macroH2A1.1 /DB_XREF=gi:3493530 /UG=Hs.75258 H2A histone family, member Y /FL=gb:AF044286.1
214505_s_at_HG-U133A	FHL1	four and a half LIM domains 1	Consensus includes gb:AF220153.1 /DEF=Homo sapiens four and a half LIM domains 1 protein isoform C (FHL1) mRNA, complete cds, alternatively spliced. /FEA=CDS /GEN=FHL1 /PROD=four and a half LIM domains 1 protein isoform C /DB_XREF=gi:6942192 /UG=Hs.239059 four and a half LIM domains 1 /FL=gb:AF220153.1
214523_at_HG-U133A	CEBPE	CCAAT/enhancer binding protein (C/EBP), epsilon	Consensus includes gb:NM_001805.1 /DEF=Homo sapiens CCAAT/enhancer binding protein (C/EBP), epsilon (CEBPE), mRNA, /FEA=CDS /GEN=CEBPE

			/PROD=CCAATenhancer binding protein (CEBP), epsilon /DB_XREF=gi:4502766 /UG=Hs.158323 CCAATenhancer binding protein (CEBP), epsilon /FL=gb:NM_001805.1
214558_at_HG-U133A	GPR12	G protein-coupled receptor 12	Consensus includes gb:NM_005288.1 /DEF=Homo sapiens G protein-coupled receptor 12 (GPR12), mRNA. /FEA=CDS /GEN=GPR12 /PROD=G protein-coupled receptor 12 /DB_XREF=gi:4885294 /UG=Hs.123034 G protein-coupled receptor 12 /FL=gb:NM_005288.1
214575_s_at_HG-U133A	AZU1	azurocidin 1 (cationic antimicrobial protein 37)	Consensus includes gb:NM_001700.1 /DEF=Homo sapiens azurocidin 1 (cationic antimicrobial protein 37) (AZU1), mRNA. /FEA=CDS /GEN=AZU1 /PROD=azurocidin 1 (cationic antimicrobial protein37) /DB_XREF=gi:11342669 /UG=Hs.72885 azurocidin 1 (cationic antimicrobial protein 37) /FL=gb:NM_001700.1
214615_at_HG-U133A	P2Y10	putative purinergic receptor	Consensus includes gb:NM_014499.1 /DEF=Homo sapiens putative purinergic receptor (P2Y10), mRNA. /FEA=CDS /GEN=P2Y10 /PROD=putative purinergic receptor /DB_XREF=gi:10092632 /UG=Hs.296433 putative purinergic receptor /FL=gb:NM_014499.1
214651_s_at_HG-U133A	HOXA9	homeo box A9	Consensus includes gb:U41813.1 /DEF=Human class I homeoprotein (HOXA9) mRNA, partial cds. /FEA=mRNA /GEN=HOXA9 /PROD=HOXA9 /DB_XREF=gi:1184168 /UG=Hs.127428 homeo box A9 /FL=gb:NM_002142.1
214686_at_HG-U133A	ZNF266	zinc finger protein 266	Consensus includes gb:AA868898 /FEA=EST /DB_XREF=gi:2964343 /DB_XREF=estak55b08.s1 /CLONE=IMAGE:1409847 /UG=Hs.118281 zinc finger protein 266
214693_x_at_HG-U133A	DJ328E19.C1.1	hypothetical protein DJ328E19.C1.1	Consensus includes gb:BE732345 /FEA=EST /DB_XREF=gi:10146337 /DB_XREF=est:601566954F1 /CLONE=IMAGE:3841692 /UG=Hs.41569 phosphatidic acid phosphatase type 2A
214700_x_at_HG-U133A			Consensus includes gb:AK000323.1 /DEF=Homo sapiens cDNA FLJ20316 fis, clone HEP07903, highly similar to U79263 Human clone 23760 mRNA. /FEA=mRNA /DB_XREF=gi:7020332 /UG=Hs.225841 DKFZP434D193 protein

214761_at_HG-U133A	OAZ	OLF-1/EBF associated zinc finger gene	Consensus includes gb:AW149417 /FEA=EST /DB_XREF=gi:6197313 /DB_XREF=est:x36107.x1 /CLONE=IMAGE:2620189 /UG=Hs.137168 OLF-1EBF associated zinc finger gene
214786_at_HG-U133A	MAP3K1	mitogen-activated protein kinase kinase 1	Consensus includes gb:AA361361 /FEA=EST /DB_XREF=gi:2013679 /DB_XREF=est:EST70631 /UG=Hs.298727 mitogen-activated protein kinase kinase 1
214789_x_at_HG-U133A	SRP46	Splicing factor, arginine/serine-rich, 46kD	Consensus includes gb:AA524274 /FEA=EST /DB_XREF=gi:2265202 /DB_XREF=est:estrg34d08.s1 /CLONE=IMAGE:936687 /UG=Hs.155160 Splicing factor, arginineserine-rich, 46kD
214849_at_HG-U133A	APLP2	-	Consensus includes gb:AW500220 /FEA=EST /DB_XREF=gi:7112628 /DB_XREF=est:U1-HF-BNO-akd-c-02-0-U1.r1 /CLONE=IMAGE:3076610 /UG=Hs.332496 Human DNA sequence from clone 108K11 on chromosome 6p21 Contains SRP20 (SR protein family member), Ndr protein kinase gene similar to yeast suppressor protein SRP40, EST and GSS
214875_x_at_HG-U133A	-	amyloid beta (A4) precursor-like protein 2	Consensus includes gb:AW001847 /FEA=EST /DB_XREF=gi:5848763 /DB_XREF=est:w181a04.x1 /CLONE=IMAGE:2513838 /UG=Hs.279518 amyloid beta (A4) precursor-like protein 2
214894_x_at_HG-U133A	MACF1	microtubule-actin crosslinking factor 1	Consensus includes gb:AK023285.1 /DEF=Homo sapiens cDNA FLJ13223 fis, clone OVARC1000001, highly similar to Homo sapiens mRNA for actin binding protein ABP620. /FEA=mRNA /DB_XREF=gi:10435154 /UG=Hs.108258 actin binding protein; macrophin (microfilament and actin filament cross-linker protein)
214911_s_at_HG-U133A	-	-	Consensus includes gb:S78771.1 /DEF=NAT=CpG island-associated gene human, mRNA, 1741 nt. /FEA=mRNA /DB_XREF=gi:244232 /UG=Hs.75243 bromodomain-containing 2
214924_s_at_HG-U133A	-	-	Consensus includes gb:AK000754.1 /DEF=Homo sapiens cDNA FLJ20747 fis, clone HEP05884, highly similar to J03068 Human DNF1552. /FEA=mRNA /DB_XREF=gi:7021038 /UG=Hs.6705 KIAA1042 protein

		Consensus includes gb:AL050136.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586L141 (from clone DKFZp586L141). /FEA=mRNA /DB_XREF=gi:4884346 /UG=Hs.140945 Homo sapiens mRNA; cDNA DKFZp586L141 (from clone DKFZp586L141)
214949_at_HG-U133A		Consensus includes gb:AL139064 /DEF=Homo sapiens interleukin 9 receptor precursor (IL9R) gene, complete cds /FEA=mRNA /DB_XREF=gi:6329992 /UG=Hs.1702 interleukin 9 receptor
214950_at_HG-U133A		Consensus includes gb:AL161952.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434M0813 (from clone DKFZp434M0813); partial cds. /FEA=mRNA /GEN=DKFZp434M0813 /PROD=hypothetical protein /DB_XREF=gi:7328002 /UG=Hs.170171 glutamate-ammonia ligase (glutamine synthase)
215001_s_at_HG-U133A	GLUL	Consensus includes gb:Z22296.1 /DEF=H.sapiens mRNA for M130 antigen cytoplasmic variant 1. /FEA=mRNA /PROD=M130 antigen cytoplasmic variant 1 /DB_XREF=gi:312143 /UG=Hs.74076 CD163 antigen
215049_x_at_HG-U133A	CD163	Consensus includes gb:AL109730.1 /DEF=Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 68600. /FEA=mRNA /DB_XREF=gi:5689835 /UG=Hs.306331 Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 68600
215087_at_HG-U133A		Consensus includes gb:AL022724 /DEF=Human DNA sequence from clone 413H6 on chromosome 6p22.3-24.3. Contains a hamster Androgen-dependent Expressed Protein like protein gene, ESTs and GSSs /FEA=mRNA /DB_XREF=gi:4468306 /UG=Hs.97411 Human DNA sequence from clone 413H6 on chromosome 6p22.3-24.3. Contains a hamster Androgen-dependent Expressed Protein like protein gene, ESTs and GSSs
215100_at_HG-U133A		Consensus includes gb:AL613045 /FEA=EST /DB_XREF=gi:4622212 /DB_XREF=estly68g03.x1 /CLONE=IMAGE:2284276 /UG=Hs.169081 ests variant gene 6 (TEL oncogene)
215115_x_at_HG-U133A	NTRK3	Consensus includes gb:AC004381 /DEF=Homo sapiens Chromosome 16 BAC
215215_s_at_HG-		

U133A			clone C1T987SK-44M2 /FEA=CDS_1 /DB_XREF=gi:29882169 /UG=Hs.307353 Homo sapiens Chromosome 16 BAC clone C1T987SK-44M2
215227_x_at_HG-U133A	ACP1	acid phosphatase 1, soluble	Consensus includes gb:BG035989 /FEA=EST /DB_XREF=gi:12430674 /DB_XREF=est:602326204F1 /CLONE=IMAGE:4414128 /UG=Hs.75393 acid phosphatase 1, soluble
215346_at_HG-U133A	TNFRSF5	tumor necrosis factor receptor superfamily, member 5	Consensus includes gb:BF664114 /FEA=EST /DB_XREF=gi:11938009 /DB_XREF=est:602145911F1 /CLONE=IMAGE:4309610 /UG=Hs.25648 tumor necrosis factor receptor superfamily, member 5
215379_x_at_HG-U133A	IGL3	immunoglobulin lambda joining 3	Consensus includes gb:AV98647 /FEA=EST /DB_XREF=gi:10300618 /DB_XREF=est:AV698647 /CLONE=GKCB1C12 /UG=Hs.289110 immunoglobulin -lambda joining 3
215450_at_HG-U133A	SNRPE	small nuclear ribonucleoprotein polypeptide E	Consensus includes gb:W87901 /FEA=EST /DB_XREF=gi:1401985 /DB_XREF=est:zh66104.r1 /CLONE=IMAGE:417055 /UG=Hs.1066 small nuclear ribonucleoprotein polypeptide E
215537_x_at_HG-U133A			Consensus includes gb:AJ012008 /DEF=Homo sapiens genes encoding RNCC protein, DDAH protein, Ly6-C protein, Ly6-D protein and immunoglobulin receptor /FEA=mRNA_4 /DB_XREF=gi:5304874 /UG=Hs.247362 dimethylarginine dimethylaminohydrolase 2
215622_x_at_HG-U133A	HSPC226	hypothetical protein HSPC226	Consensus includes gb:AL137671.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434L1850 (from clone DKFZp434L1850); partial cds. /FEA=mRNA /GEN=DKFZp434L1850 /PROD=hypothetical protein /DB_XREF=gi:6807837 /UG=Hs.30127 hypothetical protein
215785_s_at_HG-U133A	CYFIP2	cytoplasmic FMR1 interacting protein 2	Consensus includes gb:AL161998.1 /DEF=Homo sapiens mRNA; cDNA DKFZp761H087 (from clone DKFZp761H087); partial cds. /FEA=mRNA /GEN=DKFZp761H087 /PROD=hypothetical protein /DB_XREF=gi:7328000 /UG=Hs.258503 p53 inducible protein
215855_s_at_HG-U133A			Consensus includes gb:AK027741.1 /DEF=Homo sapiens cDNA FLJ11679 fis, clone HEMBA1004807. /FEA=mRNA /DB_XREF=gi:10432986 /UG=Hs.287439

		Homo sapiens cDNA FLJ11679 fis, clone HEMBA1004807
215925_s_at_HG-U133A		Consensus includes gb:AF283777.2 /DEF=Homo sapiens clone TCBAP07/02 mRNA sequence. /FEA=mRNA /DB_XREF=gi:10281735 /UG=Hs.116481 CD72 antigen
216015_s_at_HG-U133A		Consensus includes gb:AK027194.1 /DEF=Homo sapiens cDNA: FLJ23541 fis; clone LNG08276, highly similar to AF054176 Homo sapiens angiotensinvasopressin receptor AIIAVP mRNA. /FEA=mRNA /DB_XREF=gi:10440263 /UG=Hs.159483 chromosome 1 open reading frame 7
216032_s_at_HG-U133A		Consensus includes gb:AF091085.1 /DEF=Homo sapiens clone 638 unknown mRNA, complete sequence. /FEA=mRNA /PROD=unknown /DB_XREF=gi:3860007 /UG=Hs.169992 hypothetical 43.2 Kd protein
216044_x_at_HG-U133A		Consensus includes gb:AK027146.1 /DEF=Homo sapiens cDNA: FLJ23493 fis, clone LNG01831, highly similar to HSU66589 Human ribosomal L5 pseudogene mRNA. /FEA=mRNA /DB_XREF=gi:10440199 /UG=Hs.180946 ribosomal protein L5
216095_x_at_HG-U133A		Consensus includes gb:AF057354.1 /DEF=Homo sapiens myotubularin-related protein 1a mRNA, partial cds. /FEA=mRNA /PROD=myotubularin-related protein 1a /DB_XREF=gi:5138901 /UG=Hs.23200 myotubularin related protein 1
216218_s_at_HG-U133A		Consensus includes gb:AK023546.1 /DEF=Homo sapiens cDNA FLJ13484 fis, clone PLACE100388, weakly similar to 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11). /FEA=mRNA /DB_XREF=gi:10435512 /UG=Hs.54886 phospholipase C, epsilon 2
216304_x_at_HG-U133A		Consensus includes gb:AJ295618 /DEF=Homo sapiens FTSH gene for putative ATPases, exons 1 and 2 and join CDS /FEA=mRNA /DB_XREF=gi:9506352 /UG=Hs.206521 YME1 (S.cerevisiae)-like 1

216320_x_at_HG-U133A			Consensus includes gb:U37055 /DEF=Human hepatocyte growth factor-like protein gene, complete cds /FEA=mRNA /DB_XREF=gi:1311660 /UG=Hs.278657 macrophage stimulating 1 (hepatocyte growth factor-like)
216356_x_at_HG-U133A	BA1AP3	BA1-associated protein 3	Consensus includes gb:AB018277.1 /DEF=Homo sapiens mRNA for KIAA0734 protein, partial cds. /FEA=mRNA /GEN=KIAA0734 /PROD=KIAA0734 protein /DB_XREF=gi:38821188 /UG=Hs.101516 BA1-associated protein 3
216363_at_HG-U133A			Consensus includes gb:St3614.1 /DEF=Homo sapiens transgenic-JHD mouse 2357 immunoglobulin heavy chain variable region (IgG VH251) mRNA, partial cds. /FEA=mRNA /GEN=IgG VH251 /DB_XREF=gi:6863334 /UG=Hs.283878 Homo sapiens transgenic-JHD mouse 2357 immunoglobulin heavy chain variable region (IgG VH251) mRNA, partial cds
216379_x_at_HG-U133A			Consensus includes gb:AK00168.1 /DEF=Homo sapiens cDNA FLJ20161 fis, clone COL09252, highly similar to L33930 Homo sapiens CD24 signal transducer mRNA. /FEA=mRNA /DB_XREF=gi:7020079 /UG=Hs.332045 Homo sapiens cDNA FLJ20161 fis, clone COL09252, highly similar to L33930 Homo sapiens CD24 signal transducer mRNA
216399_s_at_HG-U133A			Consensus includes gb:AK025663.1 /DEF=Homo sapiens cDNA: FLJ22010 fis, clone HEP07134. /FEA=mRNA /DB_XREF=gi:10438253 /UG=Hs.285848 KIAA1454 protein
216449_x_at_HG-U133A			Consensus includes gb:AK025862.1 /DEF=Homo sapiens cDNA: FLJ22209 fis, clone HRC01496. /FEA=mRNA /DB_XREF=gi:10438505 /UG=Hs.288528 Homo sapiens cDNA: FLJ22209 fis, clone HRC01496
216450_x_at_HG-U133A			Consensus includes gb:AK025862.1 /DEF=Homo sapiens cDNA: FLJ22209 fis, clone HRC01496. /FEA=mRNA /DB_XREF=gi:10438505 /UG=Hs.288528 Homo sapiens cDNA: FLJ22209 fis, clone HRC01496
216609_at_HG-U133A			Consensus includes gb:AF065241.1 /DEF=Homo sapiens thioredoxin delta 3 (TXN delta 3) mRNA, partial cds. /FEA=mRNA /GEN=TXN delta 3

			/PROD=thioredoxin delta 3 /DB_XREF=gi:3153858 /UG=Hs.306243 Homo sapiens thioredoxin delta 3 (TXN delta 3) mRNA, partial cds
216640_s_at_HG-U133A			Consensus includes gb:AK026926.1 /DEF=Homo sapiens cDNA: FLJ23273 fis, clone HEP02611, highly similar to HSU79278 Human protein disulfide isomerase-related protein P5 mRNA. /FEA=mRNA /DB_XREF=gi:10439898
216652_s_at_HG-U133A			/UG=Hs.182429 protein disulfide isomerase-related protein DKFZp434H0872 (from clone DKFZp434H0872). /FEA=mRNA /DB_XREF=gi:6807841 /UG=Hs.306454 Homo sapiens mRNA; cDNA DKFZp434H0872 (from clone DKFZp434H0872)
216680_s_at_HG-U133A	EphB4	EphB4	Consensus includes gb:BC004264.1 /DEF=Homo sapiens, Similar to EphB4, clone IMAGE:3611312, mRNA, partial cds. /FEA=mRNA /PROD=Similar to EphB4 /DB_XREF=gi:13279061 /UG=Hs.155227 EphB4
216698_x_at_HG-U133A			Consensus includes gb:AF065654 /DEF=Homo sapiens OR7E12P pseudogene, complete sequence /FEA=CDS /DB_XREF=gi:38331591 /UG=Hs.120017 olfactory receptor, family 7, subfamily E, member 12 pseudogene
216833_x_at_HG-U133A			Consensus includes gb:U05255.1 /DEF=Human glycoporphin Hep2 mRNA, partial cds. /FEA=mRNA /PROD=glycoporphin Hep2 /DB_XREF=gi:454085 /UG=Hs.307185 Human glycoporphin Hep2 mRNA, partial cds
216860_s_at_HG-U133A	GDF11		Consensus includes gb:AF028333.1 /DEF=Homo sapiens growth differentiation factor-11 (GDF11) mRNA, partial cds. /FEA=mRNA /GEN=GDF11 /PROD=growth differentiation factor-11 /DB_XREF=gi:6649913 /UG=Hs.34941 growth differentiation factor 11
217047_s_at_HG-U133A			Consensus includes gb:AK027138.1 /DEF=Homo sapiens cDNA: FLJ23485 fis, clone KIAA05211. /FEA=mRNA /DB_XREF=gi:10440190 /UG=Hs.177664 KIAA0914 gene product
217080_s_at_HG-	HOMER_2B		Consensus includes gb:Y19026.1 /DEF=Homo sapiens mRNA for Homer-2

U133A	2	protein, Homer-2B splicing form. /FEA=mRNA /GEN=Homer-2 /PROD=Homer-2 protein, Homer-2B splicing form /DB_XREF=gi:6996435 /UG=Hs.93564 Homer, neuronal immediate early gene, 2
217156_at_HG-U133A		Consensus includes gb:U04628 /DEF=Human 78 kDa gastrin binding protein GBP gene, complete cds /FEA=CDS /DB_XREF=gi:606608 /UG=Hs.247943 Human 78 kDa gastrin binding protein GBP gene, complete cds
217179_x_at_HG-U133A		Consensus includes gb:X79782.1 /DEF=H.sapiens (T1.1) mRNA for Ig lambda light chain. /FEA=mRNA /PROD=immunoglobulin lambda light chain /DB_XREF=gi:506428 /UG=Hs.247949 H.sapiens (T1.1) mRNA for Ig lambda light chain
217185_s_at_HG-U133A		Consensus includes gb:Z95118 /DEF=Human DNA sequence from clone 354J5 on chromosome 6q21-22. Contains pseudogene similar to zinc finger protein (ZPR1), EST, STS, GSS /FEA=CDS /DB_XREF=gi:3821018 /UG=Hs.211509 zinc finger protein 259, pseudogene
217223_s_at_HG-U133A		Consensus includes gb:U07000 /DEF=Human breakpoint cluster region (BCR) gene, complete cds /FEA=CDS_4 /DB_XREF=gi:487344 /UG=Hs.234799 breakpoint cluster region
217225_x_at_HG-U133A	PM5	Consensus includes gb:AL512687.1 /DEF=Homo sapiens mRNA; cDNA DKFZp547A1913 (from clone DKFZp547A1913). /FEA=mRNA /GEN=DKFZp547A1913 /PROD=hypothetical protein /DB_XREF=gi:12224839 /UG=Hs.227823 pM5 protein
217375_at_HG-U133A		Consensus includes gb:Z93929 /DEF=Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism /FEA=CDS /DB_XREF=gi:3425887 /UG=Hs.247809 Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism

		Consensus includes gb:S81916.1 /DEF=phosphoglycerate kinase {alternatively spliced} human, phosphoglycerate kinase deficient patient with episodes of muscl, mRNA Partial Mutant, 307 nt. /FEA=mRNA /PROD=phosphoglycerate kinase /DB_XREF=gi:1470308 /UG=Hs.168313 Phosphoglycerate kinase {alternatively spliced} human, phosphoglycerate kinase deficient patient with episodes of muscl, mRNA Partial Mutant, 307 nt
217383_at_HG-U133A		Consensus includes gb:AK026525.1 /DEF=Homo sapiens cDNA: FLJ22872 /DB_XREF=gi:10439402 /UG=Hs.169476 glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA. /FEA=mRNA /DB_XREF=gi:10439402 /UG=Hs.169476 glyceraldehyde-3-phosphate dehydrogenase
217398_x_at_HG-U133A	MS4A2	membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for beta polypeptide)
217418_x_at_HG-U133A		membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for beta polypeptide)
217419_x_at_HG-U133A		Consensus includes gb:X12530.1 /DEF=Human mRNA for B lymphocyte antigen CD20 (B1, Bp35). /FEA=mRNA /DB_XREF=gi:29773 /UG=Hs.89751 clone HEMBA1002547, highly similar to Homo sapiens IgE, membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for beta polypeptide)
217478_s_at_HG-U133A	ABC1	Consensus includes gb:AK021586.1 /DEF=Homo sapiens cDNA FLJ11524 /DB_XREF=gi:10432794 /UG=Hs.273330 Homo sapiens, clone IMAGE:3506210, mRNA, partial cds
217504_at_HG-U133A	ABC46	Consensus includes gb:AA09357 /DEF=H.sapiens HLA-DMA gene /FEA=mRNA_1 /DB_XREF=gi:512468 /UG=Hs.77522 major histocompatibility complex, class II, DM alpha
217520_x_at_HG-U133A		Consensus includes gb:z85c01.s1 /CLONE=IMAGE:489600 /UG=Hs.15780 ATP-binding cassette, sub-family A (ABC1), member 6 /DB_XREF=est:602459468F1 /CLONE=IMAGE:4581928 /UG=Hs.154999 ESTs, Moderately similar to HERC2 H.sapiens [H.sapiens]

217521_at_HG-U133A		ESTs	Consensus includes gb:N54942 /FEA=EST /DB_XREF=gi:1196262 /DB_XREF=est;yy38bb08.s1 /CLONE=IMAGE:244983 /UG=Hs.276590 ESTs
217559_at_HG-U133A	RPL10L	ribosomal protein L10-like	Consensus includes gb:AI001784 /FEA=EST /DB_XREF=gi:3202255 /DB_XREF=est;ot41g06.s1 /CLONE=IMAGE:1619386 /UG=Hs.308332 ESTs, Highly similar to A42735 ribosomal protein L10, cytosolic H.sapiens
217716_s_at_HG-U133A	SEC61A1	protein transport protein SEC61 alpha subunit isoform 1	gb:NM_013336.1 /DEF=Homo sapiens sec61 homolog (HSEC61), mRNA /FEA=mRNA /GEN=HSEC61 /PROD=sec61 homolog /DB_XREF=gi:7019414 /UG=Hs.306079 sec61 homolog /FL=gb:BC002951.1 gb:AF346602.1
217768_at_HG-U133A	LOC51637	CGI-99 protein	gb:AF084458.1 gb:NM_013336.1 /DEF=Homo sapiens CGI-99 protein (LOC51637), mRNA /FEA=mRNA /GEN=LOC51637 /PROD=CGI-99 protein /DB_XREF=gi:7706321 /UG=Hs.110803 CGI-99 protein /FL=gb:BC001722.1 gb:AF151857.1
217816_s_at_HG-U133A	pcnp	PEST-containing nuclear protein	gb:NM_020357.1 /DEF=Homo sapiens PEST-containing nuclear protein (pcnp), mRNA /FEA=mRNA /GEN=pcnp /PROD=PEST-containing nuclear protein /DB_XREF=gi:99666826 /UG=Hs.283728 PEST-containing nuclear protein /FL=gb:AB037675.1 gb:NM_020357.1
217838_s_at_HG-U133A	RNB6	RNB6	gb:NM_016337.1 /DEF=Homo sapiens RNB6 (RNB6), mRNA /FEA=mRNA /GEN=RNB6 /PROD=RNB6 /DB_XREF=gi:7706686 /UG=Hs.241471 RNB6 /FL=gb:AF052504.1 gb:NM_016337.1
217916_s_at_HG-U133A	BM-009	hypothetical protein BM-009	gb:NM_016623.1 /DEF=Homo sapiens hypothetical protein (BM-009), mRNA /FEA=mRNA /GEN=BM-009 /PROD=hypothetical protein /DB_XREF=gi:7705303 /UG=Hs.92918 hypothetical protein /FL=gb:BC003599.1 gb:AF208851.1 gb:NM_016623.1
217920_at_HG-U133A		Homo sapiens, clone MGc:27474 IMAGE:4714032, mRNA, complete cds	Consensus includes gb:H97940 /FEA=EST /DB_XREF=gi:1118825 /DB_XREF=est;xy34d03.s1 /CLONE=IMAGE:260741 /UG=Hs.239114 mannosidase, alpha, class 1A, member 2 /FL=gb:AF027156.1 gb:NM_006699.1

217950_at_HG-U133A	NOSIP	eNOS interacting protein	gb:NM_015953.1 /DEF=Homo sapiens CGI-25 protein (LOC51070), mRNA /FEA=mRNA /GEN=LOC51070 /PROD=CGI-25 protein /FL=gb:AF132959.1 gb:NM_015953.1 /UG=Hs:7236 CGI-25 protein /FL=gb:AF132959.1 gb:NM_015953.1
217963_s_at_HG-U133A	HCS	cytochrome c	gb:NM_014380.1 /DEF=Homo sapiens p75NTR-associated cell death executor; ovarian granulosa cell protein (13kD) (DXS6984E), mRNA /FEA=mRNA /GEN=DXS6984E /PROD=p75NTR-associated cell death executor; ovarian granulosa cell protein (13kD) /DB_XREF=gi:7657043 /UG=Hs:17775 p75NTR-associated cell death executor; ovarian granulosa cell protein (13kD) /FL=gb:NM_014380.1 gb:AF187064.1
217966_s_at_HG-U133A	C1orf24	chromosome 1 open reading frame 24	gb:NM_022083.1 /DEF=Homo sapiens niban protein (NIBAN), mRNA /FEA=mRNA /GEN=NIBAN /PROD=niban protein /DB_XREF=gi:11545796 /UG=Hs:48778 niban protein /FL=gb:AB050477.1 gb:NM_022083.1 /UG=Hs:488391.1
217979_at_HG-U133A	NET-6	tetraspan NET-6 protein	gb:NM_014399.1 /DEF=Homo sapiens tetraspan NET-6 protein (NET-6), mRNA /FEA=mRNA /GEN=NET-6 /PROD=tetraspan NET-6 protein /DB_XREF=gi:7657372 /UG=Hs:284243 tetraspan NET-6 protein /FL=gb:AF120255.1 gb:AF100759.1 gb:NM_014399.1
217988_at_HG-U133A	HE110	enhancer of invasion 10	gb:NM_021178.1 /DEF=Homo sapiens enhancer of invasion 10 (HEI10), mRNA /FEA=mRNA /GEN=HEI10 /PROD=enhancer of invasion 10 /DB_XREF=gi:10863978 /UG=Hs:107003 enhancer of invasion 10 /FL=gb:NM_021178.1 gb:BC000369.1 gb:BC001218.1 gb:BC004435.1 /GB=AF216381.1
217989_at_HG-U133A	LOC51170	retinal short-chain dehydrogenase/reductase retSDR2	gb:NM_016245.1 /DEF=Homo sapiens retinal short-chain dehydrogenase/reductase retSDR2 (LOC51170), mRNA /FEA=mRNA /GEN=LOC51170 /PROD=retinal short-chain dehydrogenase/reductase retSDR2 /DB_XREF=gi:7705904 /UG=Hs:12150 retinal short-chain dehydrogenase/reductase retSDR2 /FL=gb:AF126780.1 gb:NM_016245.1 /GB=NM_017871.1 /DEF=Homo sapiens hypothetical protein FLJ20542
217984_x_at_HG-			

U133A			(FLJ20542), mRNA. /FEA=mRNA /GEN=FLJ20542 /PROD=hypothetical protein FLJ20542 /DB_XREF=gi:8923511 /UG=Hs.6449 hypothetical protein FLJ20542 /FL=gb:AL136813.1 gb:NM_017871.1
			gb:NM_016359.1 /DEF=Homo sapiens clone HQ0310 PRO0310p1 (LOC51203), mRNA. /FEA=mRNA /GEN=LOC51203 /PROD=clone HQ0310 PRO0310p1 /DB_XREF=gi:7705950 /UG=Hs.279905 clone HQ0310 PRO0310p1 /FL=gb:AF305711.1 gb:BC001308.1 gb:AF290812.1 gb:AF090915.1 gb:NM_016359.1
218039_at_HG-U133A	ANK1T	nucleolar protein ANK1T	gb:NM_018573.1 /DEF=Homo sapiens hypothetical protein PRO1068 (PRO1068), mRNA. /FEA=mRNA /GEN=PRO1068 /PROD=hypothetical protein PRO1068 /DB_XREF=gi:8924006 /UG=Hs.321158 hypothetical protein PRO1068 /FL=gb:AF116620.1 gb:NM_018573.1
218041_x_at_HG-U133A	PRO1068	hypothetical protein PRO1068	gb:NM_022908.1 /DEF=Homo sapiens hypothetical protein FLJ12442. (FLJ12442), mRNA. /FEA=mRNA /GEN=FLJ12442 /PROD=hypothetical protein FLJ12442 /DB_XREF=gi:12597652 /UG=Hs.84753 hypothetical protein FLJ12442 /FL=gb:NM_022908.1
218051_s_at_HG-U133A	FLJ12442	hypothetical protein FLJ12442	gb:NM_015511.1 /DEF=Homo sapiens DKFZP564N1363 protein (DKFZP564N1363), mRNA. /FEA=mRNA /GEN=DKFZP564N1363 /PROD=DKFZP564N1363 protein /DB_XREF=gi:7661627 /UG=Hs.11314 DKFZP564N1363 protein /FL=gb:BC001751.1 gb:AF132957.1 gb:AL117419.1
218089_at_HG-U133A	C20orf4	chromosome 20 open reading frame 4	gb:AF113672.1 gb:NM_015511.1 gb:NM_018117.8 /DEF=Homo sapiens WD40 repeat domain 11 protein (WDR11), mRNA. /FEA=mRNA /GEN=WDR11 /PROD=WD40 repeat domain 11 protein /DB_XREF=gi:13324687 /UG=Hs.16677 WD repeat domain 15 /FL=gb:AF320223.1 gb:NM_018117.8
218090_s_at_HG-U133A			gb:NM_018478.1 /DEF=Homo sapiens uncharacterized hypothalamus protein HSMNP1 (HSMNP1), mRNA. /FEA=mRNA /GEN=HSMNP1 /PROD=uncharacterized hypothalamus protein HSMNP1
218094_s_at_HG-U133A	C20orf35	chromosome 20 open reading frame 35	

			/DB_XREF=gi:8923782 /UG=Hs.1798666 undifferentiated hypothalamus protein HSMNP1 /FL=gb:BC001105.1 gb:AF220191.1 gb:NM_018478.1
218100_s_at_HG-U133A	ESRRBL1	estrogen-related receptor beta like 1	gb:NM_018010.1 /DEF=Homo sapiens hypothetical protein FLJ10147 (FLJ10147), mRNA. /FEA=mRNA /GEN=FLJ10147 /PROD=hypothetical protein FLJ10147 /DB_XREF=gi:8922255 /UG=Hs.170318 hypothetical protein FLJ10147 /FL=gb:AF139576.1 gb:AF245220.1 gb:NM_018010.1
218109_s_at_HG-U133A	FLJ14153	hypothetical protein FLJ14153	gb:NM_022736.1 /DEF=Homo sapiens hypothetical protein FLJ14153 (FLJ14153), mRNA. /FEA=mRNA /GEN=FLJ14153 /PROD=hypothetical protein FLJ14153 /DB_XREF=gi:12232392 /UG=Hs.7503 hypothetical protein FLJ14153 /FL=gb:NM_022736.1 gb:AB014732.1
218122_s_at_HG-U133A	SENP2	sentrin-specific protease	gb:NM_021627.1 /DEF=Homo sapiens sentrin-specific protease (SENP2), mRNA. /FEA=mRNA /GEN=SENP2 /PROD=sentrin-specific protease /DB_XREF=gi:11055993 /UG=Hs.3355 sentrin-specific protease /FL=gb:AF151697.2 gb:NM_021627.1
218144_s_at_HG-U133A	FLJ22056	hypothetical protein FLJ22056	gb:NM_02489.1 /DEF=Homo sapiens hypothetical protein FLJ22056 (FLJ22056), mRNA. /FEA=mRNA /GEN=FLJ22056 /PROD=hypothetical protein FLJ22056 /DB_XREF=gi:11968044 /UG=Hs.24956 hypothetical protein FLJ22056 /FL=gb:NM_022489.1
218151_x_at_HG-U133A	FLJ11856	hypothetical protein FLJ11856	gb:NM_024531.1 /DEF=Homo sapiens hypothetical protein FLJ11856 (FLJ11856), mRNA. /FEA=mRNA /GEN=FLJ11856 /PROD=hypothetical protein FLJ11856 /DB_XREF=gi:13375681 /UG=Hs.6459 hypothetical protein FLJ11856 /FL=gb:BC002917.1 gb:NM_024531.1
218168_s_at_HG-U133A	CABC1	chaperone, ABC1 activity of bc1 complex like (S. pombe)	gb:NM_020247.1 /DEF=Homo sapiens hypothetical protein, clone Telethon(Italy_B41)_Strait02270_FL142 (LOC56997), mRNA. /FEA=mRNA /GEN=LOC56997 /PROD=hypothetical protein, clone Telethon(Italy_B41)_Strait02270_FL142 /DB_XREF=gi:9910387 /UG=Hs.273186 hypothetical protein, clone Telethon(Italy_B41)_Strait02270_FL142 /FL=gb:BC005171.1 gb:NM_020247.1

218172_s_at_HG-U133A	PRO2577	hypothetical protein PRO2577	gb:NM_018630.1 /DEF=Homo sapiens hypothetical protein PRO2577 (PRO2577), mRNA, /FEA=mRNA /GEN=PRO2577 /PROD=hypothetical protein PRO2577 /DB_XREF=gi:8924181 /UG=Hs.241576 hypothetical protein PRO2577 /FL=gb:AF116708.1 gb:NM_018630.1
218191_s_at_HG-U133A	FLJ11240	hypothetical protein FLJ11240	gb:NM_018368.1 /DEF=Homo sapiens hypothetical protein FLJ11240 (FLJ11240), mRNA, /FEA=mRNA /GEN=FLJ11240 /PROD=hypothetical protein FLJ11240 /DB_XREF=gi:8922955 /UG=Hs.301308 hypothetical protein FLJ11240 /FL=gb:AF113224.1 gb:NM_018368.1
218223_s_at_HG-U133A	LOC51177	CK2 interacting protein 1; HQ0024c protein	gb:NM_016274.1 /DEF=Homo sapiens CK2 interacting protein 1; HQ0024c protein (LOC51177), mRNA, /FEA=mRNA /GEN=LOC51177 /PROD=CK2 interacting protein 1; HQ0024c protein /DB_XREF=gi:7705918 /UG=Hs.173380
218224_at_HG-U133A	PNMA1	paraneoplastic antigen MA1	gb:AF073836.1 gb:NM_016274.1 gb:AF168576.1
218237_s_at_HG-U133A	SLC38A1	solute carrier family 38, member 1	gb:NM_006029.2 /DEF=Homo sapiens paraneoplastic antigen MA1 (PNMA1), mRNA, /FEA=mRNA /GEN=PNMA1 /PROD=paraneoplastic antigen MA1 /DB_XREF=gi:11141858 /UG=Hs.194709 paraneoplastic antigen MA1 /FL=gb:AF037364.2 gb:NM_006029.2
218259_at_HG-U133A	KIAA1243	KIAA1243 protein	gb:NM_030674.1 /DEF=Homo sapiens amino acid transporter system A1 (ATA1), mRNA, /FEA=mRNA /GEN=ATA1 /PROD=amino acid transporter system A1 /DB_XREF=gi:13492978 /UG=Hs.18272 amino acid transporter system A1 /FL=gb:AF271070.1 gb:NM_030674.1
218319_at_HG-U133A	PELI1	pellino homolog 1 (Drosophila)	gb:NM_014048.1 /DEF=Homo sapiens KIAA1243 protein (KIAA1243), mRNA, /FEA=mRNA /GEN=KIAA1243 /PROD=NPD001 protein /DB_XREF=gi:7662513 /UG=Hs.151076 KIAA1243 protein /FL=gb:AF078853.1 gb:NM_014048.1
			gb:NM_020651.2 /DEF=Homo sapiens pellino (Drosophila) homolog 1 (PELI1), mRNA, /FEA=mRNA /GEN=PELI1 /PROD=pellino protein /DB_XREF=gi:111037062 /UG=Hs.7886 pellino (Drosophila) homolog 1 /FL=gb:AF302505.1 gb:AF300987.1 gb:NM_020651.2

			gb:NM_012406.2 /DEF=Homo sapiens PR domain containing 4 (PRDM4), mRNA. /FEA=mRNA /GEN=PRDM4 /PROD=PR domain containing 4 /DB_XREF=gi:9056315 /UG=Hs.21807 PR domain containing 4 /FL=gb:AF144757.2 gb:NM_012406.2
218329_at_HG-U133A	PRDM4	PR domain containing 4	gb:NM_017782.1 /DEF=Homo sapiens hypothetical protein FLJ20360 (FLJ20360), mRNA. /FEA=mRNA /GEN=FLJ20360 /PROD=hypothetical protein FLJ20360 /DB_XREF=gi:8923334 /UG=Hs.26434 hypothetical protein FLJ20360 /FL=gb:BC001759.1 gb:NM_017782.1
218331_s_at_HG-U133A	FLJ20360	hypothetical protein FLJ20360	gb:NM_004426.1 /DEF=Homo sapiens early development regulator 1 (homolog of polyhomeotic 1) (EDR1), mRNA. /FEA=mRNA /GEN=EDR1 /PROD=early development regulator 1 /DB_XREF=gi:11038623 /UG=Hs.305985 early development regulator 1 (homolog of polyhomeotic 1) /FL=gb:NM_004426.1
218338_at_HG-U133A	EDR1	early development regulator 1 (polyhomeotic 1 homolog)	gb:NM_024664.1 /DEF=Homo sapiens hypothetical protein FLJ11838 (FLJ11838), mRNA. /FEA=mRNA /GEN=FLJ11838 /PROD=hypothetical protein FLJ11838 /DB_XREF=gi:13375918 /UG=Hs.72531 hypothetical protein FLJ11838 /FL=gb:NM_024664.1
218341_at_HG-U133A	FLJ11838	hypothetical protein FLJ11838	gb:NM_017845.1 /DEF=Homo sapiens hypothetical protein FLJ20502 (FLJ20502), mRNA. /FEA=mRNA /GEN=FLJ20502 /PROD=hypothetical protein FLJ20502 /DB_XREF=gi:8923457 /UG=Hs.23956 hypothetical protein FLJ20502 /FL=gb:AF182421.1 gb:NM_017845.1
218351_at_HG-U133A	FLJ20502	hypothetical protein FLJ20502	gb:NM_016209.1 /DEF=Homo sapiens unknown (LOC51693), mRNA. /FEA=mRNA /GEN=LOC51693 /PROD=unknown /DB_XREF=gi:7706428 /UG=Hs.27445 unknown /FL=gb:AF089106.1 gb:NM_016209.1
218354_at_HG-U133A	LOC51693	unknown	gb:NM_012310.2 /DEF=Homo sapiens kinesin family member 4A (KIF4A), mRNA. /FEA=mRNA /GEN=KIF4A /PROD=kinesin family member 4A (KIF4A), /DB_XREF=gi:7305204 /UG=Hs.279766 kinesin family member 4A /FL=gb:AF179308.1 gb:AF071592.2 gb:NM_012310.2
218355_at_HG-U133A	KIF4A	kinesin family member 4A	

	RBM7	RNA binding motif protein 7	gb:NM_016090.1 /DEF=Homo sapiens RNA binding motif protein 7 (RBM7), mRNA. /FEA=mRNA /GEN=RBM7 /PROD=RNA binding motif protein 7 /DB_XREF=gi:9994184 /UG=Hs.5887 RNA binding motif protein 7 /FL=gb:AF156098.1 gb:NM_016090.1
218379_at_HG-U133A	CRHSP-24	calcium-regulated heat-stable protein (24kD)	gb:NM_014316.1 /DEF=Homo sapiens calcium-regulated heat-stable protein (24kD) (CRHSP-24), mRNA. /FEA=mRNA /GEN=CRHSP-24 /PROD=calcium-regulated heat-stable protein (24kD) /DB_XREF=gi:7656994 /UG=Hs.92198 calcium-regulated heat-stable protein (24kD) /FL=gb:BC001333.1
218384_at_HG-U133A	FLJ10829	dudulin 2	gb:NM_018234.1 /DEF=Homo sapiens hypothetical protein FLJ10829 (FLJ10829), mRNA. /FEA=mRNA /GEN=FLJ10829 /PROD=hypothetical protein FLJ10829 /DB_XREF=gi:8922696 /UG=Hs.57655 hypothetical protein FLJ10829 /FL=gb:NM_018234.1
218424_s_at_HG-U133A	FLJ10700	hypothetical protein FLJ10700	gb:NM_018182.1 /DEF=Homo sapiens hypothetical protein FLJ10700 (FLJ10700), mRNA. /FEA=mRNA /GEN=FLJ10700 /PROD=hypothetical protein FLJ10700 /DB_XREF=gi:8922595 /UG=Hs.295909 hypothetical protein FLJ10700 /FL=gb:NM_018182.1
218464_s_at_HG-U133A	CKTSF1B1	cysteine knot superfamily 1, BMP antagonist 1	gb:AF154054.1 /DEF=Homo sapiens DRM (DRM) mRNA, complete cds. /FEA=mRNA /GEN=DRM /PROD=DRM /DB_XREF=gi:10863087 /UG=Hs.40098 cysteine knot superfamily 1, BMP antagonist 1 /FL=gb:AF154054.1 gb:AF045800.1 gb:NM_013372.1
218468_s_at_HG-U133A	DC6	cysteine knot superfamily 1, BMP antagonist 1	gb:NM_013372.1 /DEF=Homo sapiens cysteine knot superfamily 1, BMP antagonist 1 (CKTSF1B1), mRNA. /FEA=mRNA /GEN=CKTSF1B1 /PROD=cysteine knot superfamily 1, BMP antagonist 1 /DB_XREF=gi:7019348 /UG=Hs.40098 cysteine knot superfamily 1, BMP antagonist 1 /FL=gb:AF154054.1 gb:AF045800.1 gb:NM_013372.1
218469_at_HG-U133A	CKTSF1B1	cysteine knot superfamily 1, BMP antagonist 1	gb:NM_020189.1 /DEF=Homo sapiens DC6 protein (DC6), mRNA.
218482_at_HG-U133A	DC6	DC6 protein	

		/FEA=mRNA /GEN=DC6 /PROD=DC6 protein /DB_XREF=gi:9910185 /UG=Hs.283740 DC6 protein /FL=gb:AF201940.1 gb:AF173296.1 gb:NM_020189.1
218499_at_HG-U133A	MST4	Mst3 and SOK1-related kinase gb:NM_017813.1 /DEF=Homo sapiens hypothetical protein FLJ20421 (FLJ20421), mRNA. /FEA=mRNA /GEN=FLJ20421 /PROD=hypothetical protein FLJ20421 /DB_XREF=gi:8923391 /UG=Hs.263727 hypothetical protein
218516_s_at_HG-U133A	FLJ20421	hypothetical protein FLJ20421 gb:NM_024900.1 /DEF=Homo sapiens hypothetical protein FLJ22479 (FLJ22479), mRNA. /FEA=mRNA /GEN=FLJ22479 /PROD=hypothetical protein FLJ22479 /DB_XREF=gi:13376356 /UG=Hs.238246 hypothetical protein
218517_at_HG-U133A	FLJ22479	hypothetical protein FLJ22479 gb:NM_025124.1 /DEF=Homo sapiens hypothetical protein FLJ21749 (FLJ21749), mRNA. /FEA=mRNA /GEN=FLJ21749 /PROD=hypothetical protein FLJ21749 /DB_XREF=gi:13376700 /UG=Hs.288761 hypothetical protein
218531_at_HG-U133A	FLJ21749	hypothetical protein FLJ21749 gb:NM_022750.1 /DEF=Homo sapiens hypothetical protein FLJ22693 (FLJ22693), mRNA. /FEA=mRNA /GEN=FLJ22693 /PROD=hypothetical protein FLJ22693 /DB_XREF=gi:12232412 /UG=Hs.12646 hypothetical protein
218543_s_at_HG-U133A	FLJ22693	hypothetical protein FLJ22693 gb:NM_016033.1 /DEF=Homo sapiens CGI-90 protein (LOC51115), mRNA. /FEA=mRNA /GEN=LOC51115 /PROD=CGI-90 protein /DB_XREF=gi:7705802 /UG=Hs.44222 CGI-90 protein /FL=gb:AF151848.1 gb:NM_016033.1
218549_s_at_HG-U133A	LOC51115	CGI-90 protein gb:NM_017768.1 /DEF=Homo sapiens hypothetical protein FLJ20331 (FLJ20331), mRNA. /FEA=mRNA /GEN=FLJ20331 /PROD=hypothetical protein
218577_at_HG-U133A	FLJ20331	hypothetical protein FLJ20331

			FLJ20331 /DB_XREF=gi:8923306 /UG=Hs.50848 hypothetical protein _ . FLJ20331 /FL=gb:BC003407.1 gb:NM_017768.1
218582_at_HG-U133A	FLJ20445	hypothetical protein FLJ20445	gb:NM_017824.1 /DEF=Homo sapiens hypothetical protein FLJ20445 (FLJ20445), mRNA. /FEA=mRNA /GEN=FLJ20445 /PROD=hypothetical protein FLJ20445 /DB_XREF=gi:8923414 /UG=Hs.10340 hypothetical protein FLJ20445 /FL=gb:NM_017824.1
218589_at_HG-U133A	P215	purinergic receptor (family A group 5)	gb:NM_005767.1 /DEF=Homo sapiens purinergic receptor (family A group 5) (P2Y5), mRNA. /FEA=mRNA /GEN=P2Y5 /PROD=purinergic receptor (family A group 5) /DB_XREF=gi:5031988 /UG=Hs.189999 purinergic receptor (family A group 5) /FL=gb:AF000546.1 gb:NM_005767.1
218614_at_HG-U133A	FLJ10652	hypothetical protein FLJ10652	gb:NM_018169.1 /DEF=Homo sapiens hypothetical protein FLJ10652 /PROD=hypothetical protein (FLJ10652), mRNA. /FEA=mRNA /GEN=FLJ10652 /PROD=hypothetical protein FLJ10652 /DB_XREF=gi:8922572 /UG=Hs.236844 hypothetical protein FLJ10652 /FL=gb:NM_018169.1
218642_s_at_HG-U133A	MGC2217	hypothetical protein MGC2217	gb:NM_024300.1 /DEF=Homo sapiens hypothetical protein MGC2217 (MGC2217), mRNA. /FEA=mRNA /GEN=MGC2217 /PROD=hypothetical protein MGC2217 /DB_XREF=gi:13236525 /UG=Hs.323164 hypothetical protein MGC2217 /FL=gb:BC002546.1 gb:NM_024300.1
218645_at_HG-U133A	ZNF277	zinc finger protein 277	gb:NM_021994.1 /DEF=Homo sapiens zinc finger protein 277 (ZNF277), mRNA. /FEA=mRNA /GEN=ZNF277 /PROD=zinc finger protein 277 /DB_XREF=gi:11496268 /UG=Hs.42636 zinc finger protein 277 /FL=gb:NM_021994.1 gb:AF209198.1
218662_s_at_HG-U133A	HCAP-G	chromosome condensation protein G	gb:NM_022346.1 /DEF=Homo sapiens chromosome condensation protein G (HCAP-G), mRNA. /FEA=mRNA /GEN=HCAP-G /PROD=chromosome condensation protein G /DB_XREF=gi:11641252 /UG=Hs.193602 chromosome condensation protein G /FL=gb:AF235023.1 gb:NM_022346.1 gb:AF331785.1
218663_at_HG-U133A	HCAP-G	chromosome condensation protein G	gb:BC000827.1 gb:AB013299.1 gb:NM_022346.1 /DEF=Homo sapiens chromosome condensation protein G

			(HCAP-G), mRNA. /FEA=mRNA /GEN=HCAP-G /PROD=chromosome condensation protein G /DB_XREF=gi:11641252 /UG=Hs.193602 chromosome condensation protein G /FL=gb:AF235023.1 gb:NM_022346.1 gb:AF331786.1 gb:BC000827.1 gb:AB013299.1
218692_at_HG-U133A	FLJ20366	hypothetical protein FLJ20366	gb:NM_017786.1 /DEF=Homo sapiens hypothetical protein FLJ20366 (FLJ20366), mRNA. /FEA=mRNA /GEN=FLJ20366 /PROD=hypothetical protein FLJ20366 /DB_XREF=gi:8923340 /UG=Hs.8358 hypothetical protein FLJ20366 /FL=gb:NM_017786.1
218718_at_HG-U133A	PDGFC	platelet derived growth factor C	gb:NM_016205.1 /DEF=Homo sapiens platelet derived growth factor C (PDGFC), mRNA. /FEA=mRNA /GEN=PDGFC /PROD=secretory growth factor-like protein fallotin /DB_XREF=gi:9994186 /UG=Hs.43080 platelet derived growth factor C /FL=gb:AF244813.1 gb:AB033831.1
218764_at_HG-U133A	MGC5363	hypothetical protein MGC5363	gb:NM_024064.1 /DEF=Homo sapiens hypothetical protein MGC5363 (MGC5363), mRNA. /FEA=mRNA /GEN=MGC5363 /PROD=hypothetical protein MGC5363 /DB_XREF=gi:13129041 /UG=Hs.1880 hypothetical protein MGC5363 /FL=gb:BC001000.2 gb:NM_024064.1
218836_at_HG-U133A	FLJ22638	hypothetical protein FLJ22638	gb:NM_024839.1 /DEF=Homo sapiens hypothetical protein FLJ22638 /PROD=hypothetical protein FLJ22638 /DB_XREF=gi:13376252 /UG=Hs.183232 hypothetical protein FLJ22638 /FL=gb:NM_024839.1
218913_s_at_HG-U133A	LOC51291	Gem-interacting protein	gb:NM_016573.1 /DEF=Homo sapiens Gem-interacting protein (LOC51291), mRNA. /FEA=mRNA /GEN=LOC51291 /PROD=Gem-interacting protein /DB_XREF=gi:7706106 /UG=Hs.49427 Gem-interacting protein /FL=gb:AF132541.1 gb:NM_016573.1
218916_at_HG-U133A	FLJ23436	hypothetical protein FLJ23436	gb:NM_024671.1 /DEF=Homo sapiens hypothetical protein FLJ23436 (FLJ23436), mRNA. /FEA=mRNA /GEN=FLJ23436 /PROD=hypothetical protein FLJ23436 /DB_XREF=gi:13375931 /UG=Hs.85658 hypothetical protein

			FLJ23436 /FL=gb:NM_024671.1
			gb:NM_024063.1 /DEF=Homo sapiens hypothetical protein MGC5347
			(MGC5347), mRNA, /FEA=mRNA /GEN=MGC5347 /PROD=hypothetical protein MGC5347 /DB_XREF=gi:13129039 /UG=Hs.5555 hypothetical protein MGC5347 /FL=gb:BC000981.2 gb:NM_024063.1
218933_at_HG-U133A	MGC5347	hypothetical protein MGC5347	gb:NM_024326.1 /DEF=Homo sapiens hypothetical protein MGC11279
			(MGC11279), mRNA, /FEA=mRNA /GEN=MGC11279 /PROD=hypothetical protein MGC11279 /DB_XREF=gi:13236572 /UG=Hs.10915 hypothetical protein MGC11279 /FL=gb:BC002912.1 gb:NM_024326.1
218938_at_HG-U133A	MGC11279	hypothetical protein MGC11279	gb:NM_024779.1 /DEF=Homo sapiens hypothetical protein FLJ22055
			(FLJ22055), mRNA, /FEA=mRNA /GEN=FLJ22055 /PROD=hypothetical protein FLJ22055 /DB_XREF=gi:13376135 /UG=Hs.144502 hypothetical protein FLJ22055 /FL=gb:NM_024779.1
218942_at_HG-U133A	FLJ22055	hypothetical protein FLJ22055	gb:NM_018013.1 /DEF=Homo sapiens hypothetical protein FLJ10159
			(FLJ10159), mRNA, /FEA=mRNA /GEN=FLJ10159 /PROD=hypothetical protein FLJ10159 /DB_XREF=gi:8922262 /UG=Hs.22505 hypothetical protein FLJ10159 /FL=gb:NM_018013.1
218974_at_HG-U133A	FLJ10159	hypothetical protein FLJ10159	gb:NM_022087.1 /DEF=Homo sapiens hypothetical protein FLJ21634
			(FLJ21634), mRNA, /FEA=mRNA /GEN=FLJ21634 /PROD=hypothetical protein FLJ21634 /DB_XREF=gi:11545800 /UG=Hs.97056 hypothetical protein FLJ21634 /FL=gb:NM_022087.1
219013_at_HG-U133A	FLJ21634	hypothetical protein FLJ21634	gb:NM_006901.1 /DEF=Homo sapiens myosin IXA (MYO9A), mRNA, /FEA=mRNA /GEN=MYO9A /PROD=myosin IXA /DB_XREF=gi:5902011
219027_s_at_HG-U133A	MYO9A	myosin IXA	/UG=Hs.23395 myosin IXA /FL=gb:AF117888.1 gb:NM_006901.1
219029_at_HG-U133A	FLJ21657	hypothetical protein FLJ21657	gb:NM_022483.1 /DEF=Homo sapiens hypothetical protein FLJ21657 (FLJ21657), mRNA, /FEA=mRNA /GEN=FLJ21657 /PROD=hypothetical protein FLJ21657 /DB_XREF=gi:11968834 /UG=Hs.26498 hypothetical protein FLJ21657 /FL=gb:NM_022483.1

219033_at_HG-U133A	FLJ21308	hypothetical protein FLJ21308	gb:NM_024615.1 /DEF=Homo sapiens hypothetical protein FLJ21308 (FLJ21308), mRNA. /FEA=mRNA /GEN=FLJ21308 /PROD=hypothetical protein FLJ21308 /DB_XREF=gi:13375631 /UG=Hs.29977 hypothetical protein
219036_at_HG-U133A	BITE	p10-binding protein	gb:NM_024491.1 /DEF=Homo sapiens p10-binding protein (BITE), mRNA. /FEA=mRNA /GEN=BITE /PROD=p10-binding protein /DB_XREF=gi:13346499 /UG=Hs.42315 p10-binding protein /FL=gb:AF202146.1 gb:NM_024491.1
219073_s_at_HG-U133A	OSBPL10	oxysterol binding protein-like 10	gb:NM_017784.1 /DEF=Homo sapiens hypothetical protein FLJ20363 (FLJ20363), mRNA. /FEA=mRNA /GEN=FLJ20363 /PROD=hypothetical protein FLJ20363 /DB_XREF=gi:89233366 /UG=Hs.321622 hypothetical protein
219076_s_at_HG-U133A	PXMP2	peroxisomal membrane protein 2 (22kD)	gb:NM_018663.1 /DEF=Homo sapiens 22kDa peroxisomal membrane protein like (LOC55895), mRNA. /FEA=mRNA /GEN=LOC55895 /PROD=22kDa peroxisomal membrane protein-like /DB_XREF=gi:8923891 /UG=Hs.49912 22kDa peroxisomal membrane protein-like /FL=gb:AF250136.1
219079_at_HG-U133A	b5&b5R	flavohemoprotein b5+b5R	gb:NM_016230.1 /DEF=Homo sapiens flavohemoprotein b5+b5R (LOC51167), mRNA. /FEA=mRNA /GEN=LOC51167 /PROD=flavohemoprotein b5+b5R /DB_XREF=gi:7705898 /UG=Hs.5741 flavohemoprotein b5+b5R /FL=gb:AF169803.1 gb:NM_016230.1
219084_at_HG-U133A	NSD1	nuclear receptor binding SET domain protein 1	gb:NM_022455.1 /DEF=Homo sapiens hypothetical protein FLJ22263 similar to nuclear receptor-binding SET-domain protein 1 (FLJ22263), mRNA. /FEA=mRNA /GEN=FLJ22263 /PROD=hypothetical protein FLJ22263 similar to nuclear receptor-binding SET-domain protein 1 /DB_XREF=gi:11967992 /UG=Hs.99010 hypothetical protein FLJ22263 similar to nuclear receptor-binding SET-domain protein 1 /FL=gb:NM_022455.1
219090_at_HG-U133A	SLC24A3	solute carrier family 24 (sodium/potassium/calcium exchanger),	gb:NM_020689.2 /DEF=Homo sapiens sodium calcium exchanger (NCX3), mRNA. /FEA=mRNA /GEN=NCX3 /PROD=sodium calcium exchanger

		member-3	/DB_XREF=gi:10518346 /UG=Hs.12321 sodium calcium exchanger /FL=gb:AF169257.2 gb:NM_020689.2
219099_at_HG-U133A	C12orf5	chromosome 12 open reading frame 5	gb:NM_020375.1 /DEF=Homo sapiens chromosome 12 open reading frame 5 (C12ORF5), mRNA, /FEA=mRNA /GEN=C12ORF5 /PROD=chromosome 12 open reading frame 5 /DB_XREF=gi:9966848 /UG=Hs.24792 chromosome 12 open reading frame 5 /FL=gb:NM_020375.1
219111_s_at_HG-U133A	MGC2835	ATP-dependent RNA helicase	gb:NM_024072.1 /DEF=Homo sapiens hypothetical protein MGC2835 (MGC2835), mRNA, /FEA=mRNA /GEN=MGC2835 /PROD=hypothetical protein MGC2835 /DB_XREF=gi:13129055 /UG=Hs.70582 hypothetical protein MGC2835 /FL=gb:BC001132.1 gb:BC001848.1 gb:NM_024072.1
219138_at_HG-U133A	RPL14	ribosomal protein L14	Consensus includes gb:BC000606.1 /DEF=Homo sapiens, Similar to ribosomal protein L14, clone MG:1644, mRNA, complete cds, /FEA=mRNA /PROD=Similar to ribosomal protein L14 /DB_XREF=gi:12653648 /UG=Hs.738 ribosomal protein L14 /FL=gb:BC000606.1 gb:NM_003973.1
219156_at_HG-U133A	FLJ11271	hypothetical protein FLJ11271	gb:NM_018373.1 /DEF=Homo sapiens hypothetical protein FLJ11271 (FLJ11271), mRNA, /FEA=mRNA /GEN=FLJ11271 /PROD=hypothetical protein FLJ11271 /DB_XREF=gi:8922963 /UG=Hs.109654 hypothetical protein FLJ11271 /FL=gb:NM_018373.1
219202_at_HG-U133A	FLJ22341	hypothetical protein FLJ22341	gb:NM_024599.1 /DEF=Homo sapiens hypothetical protein FLJ22341 (FLJ22341), mRNA, /FEA=mRNA /GEN=FLJ22341 /PROD=hypothetical protein FLJ22341 /DB_XREF=gi:13375798 /UG=Hs.25485 hypothetical protein FLJ22341 /FL=gb:NM_024599.1
219221_at_HG-U133A	FLJ22332	hypothetical protein FLJ22332	gb:NM_024724.1 /DEF=Homo sapiens hypothetical protein FLJ22332 (FLJ22332), mRNA, /FEA=mRNA /GEN=FLJ22332 /PROD=hypothetical protein FLJ22332 /DB_XREF=gi:13376033 /UG=Hs.111092 hypothetical protein FLJ22332 /FL=gb:NM_024724.1
219229_at_HG-U133A	SLC21A11	solute carrier family 21 (organic anion transporter), member 11	gb:NM_013272.2 /DEF=Homo sapiens solute carrier family 21 (organic anion transporter), member 11 (SLC21A11), mRNA, /FEA=mRNA /GEN=SLC21A11

		/PROD=solute carrier family 21 (organic aniontransporter), member 11 /DB_XREF=gi:7706713 /UG=Hs.14805 solute carrier family 21 (organic anion transporter), member 11 /FL=gb:AF205074.1 gb:AF187816.1 gb:AB031050.2 gb:NM_013272.2
219234_X_at_HG-U133A	FLJ23142	hypothetical protein FLJ23142 gb:NM_024583.1 /DEF=Homo sapiens hypothetical protein FLJ23142 /FEA=mRNA /GEN=FLJ23142 /PROD=hypothetical protein (FLJ23142), mRNA. /FEA=mRNA /GEN=FLJ23142 /PROD=hypothetical protein FLJ23142 /DB_XREF=gi:13375765 /UG=Hs.20999 hypothetical protein FLJ23142 /FL=gb:NM_024583.1
219271_at_HG-U133A	FLJ12691	hypothetical protein FLJ12691 gb:NM_024572.1 /DEF=Homo sapiens hypothetical protein FLJ12691 /FEA=mRNA /GEN=FLJ12691 /PROD=hypothetical protein FLJ12691 /DB_XREF=gi:13375743 /UG=Hs.15830 hypothetical protein FLJ12691 /FL=gb:NM_024572.1
219280_at_HG-U133A	WDR9	WD repeat domain 9 gb:NM_018963.1 /DEF=Homo sapiens WD repeat domain 9 (WDR9), mRNA. /FEA=mRNA /GEN=WDR9 /PROD=WD repeat domain 9 /DB_XREF=gi:11321643 /UG=Hs.225674 WD repeat domain 9 /FL=gb:NM_018963.1
219291_at_HG-U133A	MDS009	x 009 protein gb:NM_020234.1 /DEF=Homo sapiens x 009 protein (MDS009), mRNA. /FEA=mRNA /GEN=MDS009 /PROD=x 009 protein /DB_XREF=gi:9910425 /UG=Hs.64641 x 009 protein /FL=gb:AF168717.1 gb:NM_020234.1
219312_s_at_HG-U133A	RINZF	zinc finger protein RINZF gb:NM_023929.1 /DEF=Homo sapiens hypothetical protein FLJ12752 (FLJ12752), mRNA. /FEA=mRNA /GEN=FLJ12752 /PROD=hypothetical protein FLJ12752 /DB_XREF=gi:129865200 /UG=Hs.237146 hypothetical protein FLJ12752 /FL=gb:NM_023929.1
219329_s_at_HG-U133A	3-Apr	apoptosis related protein APR-3 gb:NM_016085.1 /DEF=Homo sapiens apoptosis related protein APR-3, mRNA. /FEA=mRNA /GEN=APR-3 /PROD=apoptosis related protein APR-3 /DB_XREF=gi:7706360 /UG=Hs.9527 apoptosis related protein APR-3 /FL=gb:AF144055.2 gb:NM_016085.1
219337_at_HG-U133A	FLJ20584	hypothetical protein FLJ20584 gb:NM_017891.1 /DEF=Homo sapiens hypothetical protein FLJ20584

		(FLJ20584), mRNA /FEA=mRNA /GEN=FLJ20584 /PROD=hypothetical protein FLJ20584 /FL=gb:NM_017891.1
219358_s_at_HG-U133A	CENTA2	gb:NM_018404.1 /DEF=Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA /FEA=mRNA /GEN=HSA272195 /PROD=centaurin-alpha 2 protein /DB_XREF=gi:8923762 /UG=Hs.28802 centaurin-alpha 2 protein /FL=gb:NM_018404.1
219360_s_at_HG-U133A	TRPM4	gb:NM_017636.1 /DEF=Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA /FEA=mRNA /GEN=FLJ20041 /PROD=hypothetical protein FLJ20041 /DB_XREF=gi:8923048 /UG=Hs.31608 hypothetical protein FLJ20041 /FL=gb:NM_017636.1
219362_at_HG-U133A	FLJ22643	gb:NM_024635.1 /DEF=Homo sapiens hypothetical protein FLJ22643 (FLJ22643), mRNA /FEA=mRNA /GEN=FLJ22643 /PROD=hypothetical protein FLJ22643 /DB_XREF=gi:13375865 /UG=Hs.43579 hypothetical protein FLJ22643 /FL=gb:NM_024635.1
219452_at_HG-U133A	LOC64174	gb:NM_022355.1 /DEF=Homo sapiens putative dipeptidase (LOC64174), mRNA /FEA=mRNA /GEN=LOC64174 /PROD=putative dipeptidase /DB_XREF=gi:11641268 /UG=Hs.115537 putative dipeptidase /FL=gb:NM_022355.1
219457_s_at_HG-U133A	RIN3	gb:NM_024832.1 /DEF=Homo sapiens hypothetical protein FLJ22439 (FLJ22439), mRNA /FEA=mRNA /GEN=FLJ22439 /PROD=hypothetical protein FLJ22439 /DB_XREF=gi:13376237 /UG=Hs.180040 hypothetical protein FLJ22439 /FL=gb:NM_024832.1
219463_at_HG-U133A	C20orf103	gb:NM_012261.1 /DEF=Homo sapiens similar to S68401 (cattle) glucose induced gene (HS1119D91), mRNA /FEA=mRNA /GEN=HS1119D91 /PROD=similar to S68401 (cattle) glucose induced gene /DB_XREF=gi:7110832 /UG=Hs.22920 similar to S68401 (cattle) glucose induced gene /FL=gb:NM_012261.1

219471_at_HG-U133A	FLJ21562	hypothetical protein FLJ21562	gb:NM_025113.1 /DEF=Homo sapiens hypothetical protein FLJ21562 /GEN=FLJ21562 /PROD=hypothetical protein FLJ21562 /DB_XREF=gi:13376686 /UG=Hs.288708 hypothetical protein FLJ21562 /FL=gb:NM_025113.1
219477_s_at_HG-U133A	LOC55901	TMTSP for transmembrane molecule with thrombospondin module	gb:NM_018676.1 /DEF=Homo sapiens TMTSP for transmembrane molecule with thrombospondin module (LOC55901), mRNA, /FEA=mRNA /GEN=LOC55901 /PROD=TMTSP for transmembrane molecule with thrombospondin module /DB_XREF=gi:8923893 /UG=Hs.325667 TMTSP for transmembrane molecule with thrombospondin module /FL=gb:AB044385.1
219478_at_HG-U133A	WFDC1	WAP four-disulfide core domain 1	gb:NM_021197.1 /DEF=Homo sapiens WAP four-disulfide core domain 1 (WFDC1), mRNA, /FEA=mRNA /GEN=WFDC1 /PROD=WAP four-disulfide core domain 1 /DB_XREF=gi:10864006 /UG=Hs.36688 WAP four-disulfide core domain 1 /FL=gb:AF302109.1 gb:AF169631.1 gb:NM_021197.1
219518_s_at_HG-U133A	FLJ22637	hypothetical protein FLJ22637	gb:NM_025165.1 /DEF=Homo sapiens hypothetical protein FLJ22637 /GEN=FLJ22637 /PROD=hypothetical protein (FLJ22637), mRNA, /FEA=mRNA /GEN=FLJ22637 /DB_XREF=gi:13376767 /UG=Hs.296178 hypothetical protein FLJ22637 /FL=gb:NM_025165.1
219574_at_HG-U133A	FLJ20668	hypothetical protein FLJ20668	gb:NM_017923.1 /DEF=Homo sapiens hypothetical protein FLJ20668 /GEN=FLJ20668 /PROD=hypothetical protein (FLJ20668), mRNA, /FEA=mRNA /GEN=FLJ20668 /DB_XREF=gi:89236112 /UG=Hs.12920 hypothetical protein FLJ20668 /FL=gb:NM_017923.1
219598_s_at_HG-U133A			gb:NM_016104.1 /DEF=Homo sapiens PTD013 protein (PTD013), mRNA, /FEA=mRNA /GEN=PTD013 /PROD=PTD013 protein /DB_XREF=gi:7706668 /UG=Hs.279857 PTD013 protein /FL=gb:AF092134.1 gb:NM_016104.1
219615_s_at_HG-U133A	KCNK5	potassium channel, subfamily K, member 5 (TASK-2)	gb:NM_003740.1 /DEF=Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5), mRNA, /FEA=mRNA /GEN=KCNK5 /PROD=potassium channel, subfamily K, member 5 (TASK-2)

			/DB_XREF=gi:4504850 /UG=Hs.127007 potassium channel, subfamily K, member 5 (TASK-2) /FL=gb:AF084830.1 gb:NM_003740.1
219631_at_HG-U133A	FLJ12929	hypothetical protein FLJ12929	gb:NM_024937.1 /DEF=Homo sapiens hypothetical protein FLJ12929 /PROD=hypothetical protein (FLJ12929), mRNA /FEA=mRNA /GEN=FLJ12929 /UG=Hs.278956 hypothetical protein /DB_XREF=gi:13376412 /UG=Hs.278956 hypothetical protein
219634_at_HG-U133A	C4ST	chondroitin 4-sulfotransferase	FLJ12929 /FL=gb:NM_024937.1 gb:NM_018413.1 /DEF=Homo sapiens chondroitin 4-sulfotransferase (C4ST), mRNA /FEA=mRNA /GEN=C4ST /PROD=chondroitin 4-sulfotransferase /DB_XREF=gi:8923757 /UG=Hs.287402 chondroitin 4-sulfotransferase /FL=gb:AB042326.1 gb:NM_018413.1 gb:AF239820.1
219641_at_HG-U133A	FLJ10103	hypothetical protein FLJ10103	gb:NM_017996.1 /DEF=Homo sapiens hypothetical protein FLJ10103 /PROD=hypothetical protein (FLJ10103), mRNA /GEN=FLJ10103 /PROD=hypothetical protein FLJ10103 /DB_XREF=gi:8922230 /UG=Hs.42140 hypothetical protein FLJ10103 /FL=gb:BC001242.1 gb:NM_017996.1
219654_at_HG-U133A	PTPLA	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a	gb:NM_014241.1 /DEF=Homo sapiens protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a (PTPLA), mRNA /FEA=mRNA /GEN=PTPLA /PROD=protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a /DB_XREF=gi:7657481 /UG=Hs.114062 protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a /FL=gb:AF114494.1 gb:NM_014241.1
219667_s_at_HG-U133A	BANK	hypothetical protein FLJ20706	gb:NM_017935.1 /DEF=Homo sapiens hypothetical protein FLJ20706 /PROD=hypothetical protein (FLJ20706), mRNA /FEA=mRNA /GEN=FLJ20706 /PROD=hypothetical protein FLJ20706 /DB_XREF=gi:8923635 /UG=Hs.193736 hypothetical protein FLJ20706 /FL=gb:NM_017935.1
219690_at_HG-U133A	FLJ22573	hypothetical protein FLJ22573	gb:NM_024660.1 /DEF=Homo sapiens hypothetical protein FLJ22573 /PROD=hypothetical protein (FLJ22573), mRNA /FEA=mRNA /GEN=FLJ22573 /PROD=hypothetical protein FLJ22573 /DB_XREF=gi:13375912 /UG=Hs.62406 hypothetical protein FLJ22573 /FL=gb:NM_024660.1

		hypothetical protein FLJ20174	gb:NM_017699.1 /DEF=Homo sapiens hypothetical protein FLJ20174 (FLJ20174), mRNA, /FEA=mRNA /GEN=FLJ20174 /PROD=hypothetical protein FLJ20174 /FL=gb:NM_017699.1
219734_at_HG-U133A	FLJ20174		gb:NM_012447.1 /DEF=Homo sapiens stromal antigen 3 (STAG3), mRNA (/FEA=mRNA /GEN=STAG3 /PROD=stromal antigen 3 /FL=gb:NM_012447.1 /UG=Hs.20132 stromal antigen 3 /FL=gb:NM_012447.1
219753_at_HG-U133A	STAG3	stromal antigen 3	gb:NM_024820.1 /DEF=Homo sapiens KIAA1608 protein (KIAA1608), mRNA (/FEA=mRNA /GEN=KIAA1608 /PROD=hypothetical protein FLJ21129 /DB_XREF=gi:13449264 /UG=Hs.300842 KIAA1608 protein /FL=gb:NM_024820.1
219763_at_HG-U133A	KIAA1608	KIAA1608 protein	gb:NM_013439.1 /DEF=Homo sapiens paired immunoglobulin-like receptor alpha (PILR(ALPHA)), mRNA, /FEA=mRNA /GEN=PILR(ALPHA) /PROD=paired immunoglobulin-like receptor alpha /DB_XREF=gi:7305384 /UG=Hs.122591 paired immunoglobulin-like receptor alpha /FL=gb:AF161080.1 /FL=gb:NM_024820.1
219788_at_HG-U133A	PILR	paired immunoglobulin-like receptor alpha	Consensus includes gb:AF628360 /FEA=EST /DB_XREF=gi:4665160 /DB_XREF=est:75e10.x1 /CLONE=IMAGE:2284938 /UG=Hs.123655 natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C) /FL=gb:M59305.1 gb:AF025998.1 gb:NM_000908.1
219789_at_HG-U133A	NPR3		gb:NM_022133.1 /DEF=Homo sapiens sorting nexin 16 (SNX16), mRNA /FEA=mRNA /GEN=sNX16 /PROD=sorting nexin 16 /DB_XREF=gi:11545864 /UG=Hs.128645 sorting nexin 16 /FL=gb:AF305779.1 gb:NM_022133.1
219793_at_HG-U133A	SNX16	sorting nexin 16	gb:NM_024070.1 /DEF=Homo sapiens hypothetical protein MGC2463 (MGC2463), mRNA, /FEA=mRNA /GEN=MGC2463 /PROD=hypothetical protein MGC2463 /DB_XREF=gi:13129051 /UG=Hs.323634 hypothetical protein MGC2463 /FL=gb:BC001129.1 gb:NM_024070.1
219812_at_HG-U133A	MGC2463	hypothetical protein MGC2463	gb:NM_014037.1 /DEF=Homo sapiens NTT5 protein (NTT5), mRNA
219820_at_HG-U133A	NTT5	NTT5 protein	

			/FEA=mRNA /GEN=NTT5 /PROD=NTT5 protein /DB_XREF=gi:7662517 /UG=Hs.59260 NTT5 protein /FL=gb:AF265578.1 gb:AL136856.1 gb:AF151977.1 gb:NM_014037.1
219837_s_at_HG-U133A	C17	cytokine-like protein C17	gb:NM_018659.1 /DEF=Homo sapiens cytokine-like protein C17 (C17). mRNA. /FEA=mRNA /GEN=C17 /PROD=cytokine-like protein C17 /DB_XREF=gi:8922107 /UG=Hs.13872 cytokine-like protein C17 /FL=gb:AF193766.1 gb:NM_018659.1
219846_at_HG-U133A	FLJ23040	hypothetical protein FLJ23040	gb:NM_025174.1 /DEF=Homo sapiens hypothetical protein FLJ23040 (FLJ23040), mRNA. /FEA=mRNA /GEN=FLJ23040 /PROD=hypothetical protein FLJ23040 /DB_XREF=gi:13375769 /UG=Hs.169813 hypothetical protein FLJ23040 /FL=gb:NM_025174.1
219868_s_at_HG-U133A	ANKHZN	ANKHZN protein	gb:NM_016376.1 /DEF=Homo sapiens ANKHZN protein (ANKHZN), mRNA. /FEA=mRNA /GEN=ANKHZN /PROD=ANKHZN protein /DB_XREF=gi:7705277 /UG=Hs.284163 ANKHZN protein /FL=gb:AB037360.1 gb:NM_016376.1
219869_s_at_HG-U133A	LOC64116	up-regulated by BCG-CWS	gb:NM_022154.1 /DEF=Homo sapiens up-regulated by BCG-CWS (LOC64116), mRNA. /FEA=mRNA /GEN=LOC64116 /PROD=up-regulated by BCG-CWS /DB_XREF=gi:11545899 /UG=Hs.284205 up-regulated by BCG- CWS /FL=gb:NM_022154.1
219891_at_HG-U133A	FLJ20208	hypothetical protein FLJ20208	gb:NM_017712.1 /DEF=Homo sapiens hypothetical protein FLJ20208 (FLJ20208), mRNA. /FEA=mRNA /GEN=FLJ20208 /PROD=hypothetical protein FLJ20208 /DB_XREF=gi:8923197 /UG=Hs.131776 hypothetical protein FLJ20208 /FL=gb:NM_017712.1
220000_at_HG-U133A	SIGLEC5	Ig-like lectin 5	gb:NM_003830.1 /DEF=Homo sapiens sialic acid binding Ig-like lectin 5 (SIGLEC5), mRNA. /FEA=mRNA /GEN=SIGLEC5 /PROD=sialic acid binding Ig- like lectin 5 /DB_XREF=gi:4502658 /UG=Hs.117005 sialic acid binding Ig- like lectin 5 /FL=gb:U71383.1 gb:NM_003830.1 gb:AF170484.1
220001_at_HG-U133A	PAD15	sialic acid binding Ig-like lectin 5	gb:NM_012387.1 /DEF=Homo sapiens peptidyl arginine deiminase, type V (PAD), mRNA. /FEA=mRNA /GEN=PAD /PROD=peptidyl arginine deiminase, type V

			type V /DB_XREF=gi:6912575 /UG=Hs.117232 peptidyl arginine deiminase, type V /FL=gb:AB017919.1 gb:NM_012387.1
220007_at_HG-U133A	FLJ13984	hypothetical protein FLJ13984	gb:NM_024770.1 /DEF=Homo sapiens hypothetical protein FLJ13984 /PROD=hypothetical protein (FLJ13984), mRNA. /FEA=mRNA /GEN=FLJ13984 /UG=Hs.135146 hypothetical protein FLJ13984 /DB_XREF=gi:13376116 /UG=Hs.135146 hypothetical protein FLJ13984 /FL=gb:NM_024770.1
220050_at_HG-U133A	C9orf9	chromosome 9 open reading frame 9	gb:NM_018956.1 /DEF=Homo sapiens chromosome 9 open reading frame 9 (C9ORF9), mRNA. /FEA=mRNA /GEN=C9ORF9 /PROD=chromosome 9 open reading frame 9 /DB_XREF=gi:9506440 /UG=Hs.62595 chromosome 9 open reading frame 9 /FL=gb:NM_018956.1
220059_at_HG-U133A	BRDG1	BCR downstream signaling 1	gb:NM_012108.1 /DEF=Homo sapiens BCR downstream signaling 1 (BRDG1), mRNA. /FEA=mRNA /GEN=BRDG1 /PROD=BCR downstream signaling 1 /DB_XREF=gi:6912271 /UG=Hs.121128 BCR downstream signaling 1 /FL=gb:AB023483.1 gb:NM_012108.1
220118_at_HG-U133A	TZFP	testis zinc finger protein	gb:NM_014383.1 /DEF=Homo sapiens testis zinc finger protein (TZFP), mRNA. /FEA=mRNA /GEN=TZFP /PROD=testis zinc finger protein /DB_XREF=gi:7657664 /UG=Hs.99430 testis zinc finger protein /FL=gb:AF130255.1 gb:AF165097.1 gb:NM_014383.1
220307_at_HG-U133A	CD244	natural killer cell receptor 2B4	gb:NM_016382.1 /DEF=Homo sapiens natural killer cell receptor 2B4 (CD244), mRNA. /FEA=mRNA /GEN=CD244 /PROD=natural killer cell receptor 2B4 /DB_XREF=gi:7706528 /UG=Hs.157872 natural killer cell receptor 2B4 /FL=gb:AF242540.1 gb:AF105261.1 gb:AF145782.1 gb:AF107761.2 gb:AF117711.1 gb:NM_016382.1
220338_at_HG-U133A	FLJ10244	hypothetical protein FLJ10244	gb:NM_018037.1 /DEF=Homo sapiens hypothetical protein FLJ10244 (FLJ10244), mRNA. /FEA=mRNA /GEN=FLJ10244 /PROD=hypothetical protein FLJ10244 /DB_XREF=gi:8922306 /UG=Hs.274419 hypothetical protein FLJ10244 /FL=gb:NM_018037.1
220564_at_HG-U133A	FLJ11218	hypothetical protein FLJ11218	gb:NM_018863.1 /DEF=Homo sapiens hypothetical protein FLJ11218

		(FLJ11218), mRNA. /FEA=mRNA /GEN=FLJ11218 /PROD=hypothetical protein FLJ11218 /FL=gb:NM_018363.1
		gb:NM_015363.1 /DEF=Homo sapiens zinc finger, imprinted 2 (ZIM2), mRNA. /FEA=mRNA /GEN=ZIM2 /PROD=zinc finger, imprinted 2 /DB_XREF=gi:8922945 /UG=Hs.274413 hypothetical protein
220653_at_HG-U133A	ZIM2	zinc finger, imprinted 2 gb:NM_018262.1 /DEF=Homo sapiens hypothetical protein FLJ10897 (FLJ10897), mRNA. /FEA=mRNA /GEN=FLJ10897 /PROD=hypothetical protein FLJ10897 /DB_XREF=gi:8922747 /UG=Hs.70202 WD repeat domain 10 /FL=gb:NM_018262.1
220744_s_at_HG-U133A	WDR10	WD repeat domain 10 gb:NM_016947.1 /DEF=Homo sapiens G8 protein (G8), mRNA. /FEA=mRNA /GEN=G8 /PROD=G8 protein /DB_XREF=gi:8393383 /UG=Hs.109798-G8 protein /FL=gb:NM_016947.1
220755_s_at_HG-U133A		protein phosphatase 4 regulatory subunit 2 gb:NM_019853.1 /DEF=Homo sapiens protein phosphatase 4 regulatory subunit 2 (PPP4R2), mRNA. /FEA=mRNA /GEN=PPP4R2 /PROD=protein phosphatase 4 regulatory subunit 2 /DB_XREF=gi:9790172 /UG=Hs.1256682
220764_at_HG-U133A	PPP4R2	protein phosphatase 4 regulatory subunit 2 gb:NM_004384.1 /DEF=Homo sapiens casein kinase 1, gamma 3 (CSNK1G3), mRNA. /FEA=mRNA /GEN=CSNK1G3 /PROD=casein kinase 1, gamma 3 /DB_XREF=gi:4758079 /UG=Hs.129206 casein kinase 1, gamma 3 /FL=gb:AF049089.1 gb:NM_004384.1
220768_s_at_HG-U133A	CSNK1G3	casein kinase 1, gamma 3 gb:NM_024881.1 /DEF=Homo sapiens hypothetical protein FLJ14251 (FLJ14251), mRNA. /FEA=mRNA /GEN=FLJ14251 /PROD=hypothetical protein FLJ14251 /DB_XREF=gi:13376323 /UG=Hs.214178 hypothetical protein FLJ14251 /FL=gb:NM_024881.1
220796_x_at_HG-U133A	FLJ14251	hypothetical protein FLJ14251 gb:NM_024888.1 /DEF=Homo sapiens hypothetical protein FLJ11535
220798_x_at_HG-U133A	FLJ11535	hypothetical protein FLJ11535 (FLJ11535), mRNA. /FEA=mRNA /GEN=FLJ11535 /PROD=hypothetical protein

			FLJ11535 /DB_XREF=gi:13376338 /UG=Hs.225170 hypothetical protein FLJ11535 /FL=gb:AL136596.1 gb:NM_024888.1
220924_s_at_HG-U133A	SLC38A2	solute carrier family 38, member 2	gb:NM_018976.1 /DEF=Homo sapiens amino acid transporter 2 (KIAA1382), mRNA, /FEA=mRNA /GEN=KIAA1382 /PROD=amino acid transporter 2 /DB_XREF=gi:95066836 /UG=Hs.298275 amino acid transporter 2 /FL=gb:NM_018976.1
220987_s_at_HG-U133A	DKFZP434J037	hypothetical protein DKFZp434J037	gb:NM_030952.1 /DEF=Homo sapiens hypothetical protein DKFZp434J037 gb:NM_030952.1 /DEF=Homo sapiens hypothetical protein DKFZp434J037, mRNA, /GEN=DKFZP434J037 /PROD=hypothetical protein DKFZp434J037 /DB_XREF=gi:13569521 /FL=gb:NM_030952.1
220999_s_at_HG-U133A	PRO1331	hypothetical protein PRO1331	gb:NM_030978.1 /DEF=Homo sapiens hypothetical protein PRO1331 gb:NM_030978.1 /DEF=Homo sapiens mRNA /GEN=PRO1331 /PROD=hypothetical protein (PRO1331), mRNA, /FEA=mRNA /GEN=PRO1331 /PROD=hypothetical protein PRO1331 /DB_XREF=gi:13562115 /FL=gb:NM_030978.1
221004_s_at_HG-U133A	ITM3	integral membrane protein 3	gb:NM_030926.1 /DEF=Homo sapiens integral membrane protein 3 (ITM3), mRNA, /FEA=mRNA /GEN=ITM3 /PROD=integral membrane protein 3 /DB_XREF=gi:13569884 /FL=gb:NM_030926.1
221006_s_at_HG-U133A	MY014	hypothetical protein My014	gb:NM_030918.1 /DEF=Homo sapiens hypothetical protein My014 (MY014), mRNA, /FEA=mRNA /GEN=MY014 /PROD=hypothetical protein My014 /DB_XREF=gi:13569876 /FL=gb:NM_030918.1
221011_s_at_HG-U133A	DKFZP566J091	hypothetical protein DKFZp566J091	gb:NM_030915.1 /DEF=Homo sapiens hypothetical protein DKFZp566J091 (DKFZP566J091), mRNA, /FEA=mRNA /GEN=DKFZP566J091 /PROD=hypothetical protein DKFZp566J091 /DB_XREF=gi:13569871 /FL=gb:NM_030915.1
221030_s_at_HG-U133A	DKFZP564B1162	hypothetical protein DKFZp564B1162	gb:NM_031305.1 /DEF=Homo sapiens hypothetical protein DKFZp564B1162 (DKFZP564B1162), mRNA, /FEA=mRNA /GEN=DKFZP564B1162 /PROD=hypothetical protein DKFZp564B1162 /DB_XREF=gi:13775229 /FL=gb:NM_031305.1
221188_s_at_HG-CIDE8		cell death-inducing DFFA-like effector b	gb:NM_014430.1 /DEF=Homo sapiens cell death-inducing DFFA-like effector

U133A		b (CIDEB), mRNA. /FEA=mRNA /GEN=CIDEB /PROD=cell death-inducing DFFA-like effector b /DB_XREF=gi:7656978 /UG=Hs.288835 cell death-inducing DFFA-like effector b /FL=gb:AF190901.1 gb:NM_014430.1
		gb:NM_024521.1 /DEF=Homo sapiens hypothetical protein FLJ21459 (FLJ21459), mRNA. /FEA=mRNA /GEN=FLJ21459 /PROD=hypothetical protein FLJ21459 /DB_XREF=gi:13375661 /UG=Hs.3769 hypothetical protein FLJ21459 /FL=gb:NM_024521.1
221206_at_HG-U133A	FLJ21459	hypothetical protein FLJ21459
221234_s_at_HG-U133A	BACH2	BTB and CNC homology 1, basic leucine zipper transcription factor 2 /DB_XREF=gi:13540489 /FL=gb:NM_021813.1 zipper transcription factor 2 /DB_XREF=gi:13540489 /FL=gb:NM_021813.1
221239_s_at_HG-U133A	SPAP1	SH2 domain-containing phosphatase anchor protein 1 /SPAP1, mRNA. /FEA=mRNA /GEN=SPAP1 /PROD=SH2 domain-containing phosphatase anchor protein1 /DB_XREF=gi:13540524 /FL=gb:NM_030764.1
221253_s_at_HG-U133A	MGC3178	thioredoxin related protein MGC3178 /DB_XREF=gi:13540603 /FL=gb:NM_030810.1
221268_s_at_HG-U133A	LOC81537	sphingosine-1-phosphatase LOC81537 /DB_XREF=gi:13540568 /FL=gb:NM_030791.1
221331_x_at_HG-U133A	CTLA4	cytotoxic T-lymphocyte-associated protein 4 /CTLA4, mRNA. /FEA=CDS /GEN=CTLA4 /PROD=cytotoxic T-lymphocyte-associated protein 4 /DB_XREF=gi:4885166 /UG=Hs.247824 /FL=gb:NM_005214.1
221486_at_HG-U133A		cytotoxic T-lymphocyte-associated protein 4 /FL=gb:NM_005214.1 gb:AF051770.1 /DEF=Homo sapiens alpha endosulfine mRNA, complete cds. /FEA=mRNA /PROD=alpha endosulfine /DB_XREF=gi:4894373 /UG=Hs.111680 endosulfine alpha /FL=gb:AF067170.1 gb:AF157510.1

221543_s_at_HG-U133A	C8orf2	chromosome 8 open reading frame 2	gb:AL442077.1 /DEF=Homo sapiens mRNA; cDNA DKFZp667H242 (from clone DKFZp667H242); complete cds. /FEA=mRNA /GEN=DKFZ4667H242 /PROD=hypothetical protein /DB_XREF=gi:10241715 /UG=Hs_125849 chromosome 8 open reading frame 2 /FL=gb:AL442077.1 gb:NM_007175.1
221555_x_at_HG-U133A	CDC14B	CDC14 cell division cycle 14 homolog B (S. cerevisiae)	Consensus includes gb:AU145941 /CLONE=HEMBA1006337 /UG=Hs_22116 CDC14 /DB_XREF=est:AU145941 /GEN=cdc14b /PROD=gi:11007462 (cell division cycle 14, S. cerevisiae) homolog B /FL=gb:AF064104.1
221558_s_at_HG-U133A	LEF1	lymphoid enhancer-binding factor 1	gb:AF288571.1 /DEF=Homo sapiens lymphoid enhancer factor-1 (LEF1) mRNA, complete cds. /FEA=mRNA /GEN=LEF1 /PROD=lymphoid enhancer binding factor-1 /DB_XREF=gi:9858157 /UG=Hs_44865 lymphoid enhancer binding factor-1 /FL=gb:AF198532.1 gb:NM_016269.1 gb:AF288571.1
221581_s_at_HG-U133A	WBSCR5	Williams-Beuren syndrome chromosome region 5	gb:AF257135.1 /DEF=Homo sapiens WBSCR15 protein (WBSCR15) mRNA, complete cds. /FEA=mRNA /GEN=WBSCR15 /PROD=WBSCR15 protein /DB_XREF=gi:9651998 /UG=Hs_56607 Williams-Beuren syndrome chromosome region 5 /FL=gb:NM_022040.1 gb:BC001699.1 gb:AF257135.1
221586_s_at_HG-U133A	E2F5	E2F transcription factor 5, p130-binding	gb:U15642.1 /DEF=Human transcription factor E2F-5 mRNA, complete cds. /FEA=mRNA /PROD=E2F-5 /DB_XREF=gi:758415 /UG=Hs_2331 E2F transcription factor 5, p130-binding /FL=gb:NM_001951.2 gb:U15642.1 gb:U31556.1
221601_s_at_HG-U133A	TOSO	regulator of Fas-induced apoptosis	Consensus includes gb:AI084226 /FEA=EST /DB_XREF=gi:3422649 /DB_XREF=est:oy72g09.x1 /CLONE=IMAGE:1671424 /UG=Hs_58831 regulator of Fas-induced apoptosis /FL=gb:AF057557.1 gb:NM_005449.1
221602_s_at_HG-U133A	TOSO	regulator of Fas-induced apoptosis	gb:AF057557.1 /DEF=Homo sapiens anti-Fas-induced apoptosis (TOSO) mRNA, complete cds. /FEA=mRNA /GEN=TOSO /PROD=anti-Fas-induced apoptosis /DB_XREF=gi:3169232 /UG=Hs_58831 regulator of Fas-induced apoptosis /FL=gb:AF057557.1 gb:NM_005449.1
221617_at_HG-U133A			Consensus includes gb:AF077053.1 /DEF=Homo sapiens neuronal cell death-related protein mRNA, complete cds. /FEA=mRNA /PROD=neuronal cell

			death-related protein /DB_XREF=gi:4689153 /UG=Hs.171723 neuronal cell
			death-related protein /FL=gb:AF077053.1 gb:NM_015975.1 gb:AF220509.1
221642_at_HG-U133A	TREX1	three prime repair exonuclease 1	gb:BC002903.1 /DEF=Homo sapiens, clone MGC:10323, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:10323) /DB_XREF=gi:12804100 /UG=Hs.23595 three prime repair exonuclease 1 /FL=gb:BC002903.1
221731_x_at_HG-U133A	CSPG2	chondroitin sulfate proteoglycan 2 (versican)	Consensus includes gb:BF218922 /FEA=EST /DB_XREF=gi:11112418 /DB_XREF=est:601885091F1 /CLONE=IMAGE:4103447 /UG=Hs.81800
221739_at_HG-U133A	IL27	interleukin 27	Consensus includes gb:AL524093 /FEA=EST /DB_XREF=gi:12787586 /DB_XREF=est:AL524093 /CLONE=CS0DC002Y104 (5 prime) /UG=Hs.10927 hypothetical protein EUROIMAGE1875335
221755_at_HG-U133A	ADSS	Homo sapiens mRNA for FLJ00043 protein, partial cds	Consensus includes gb:BG334196 /FEA=EST /DB_XREF=gi:13140634 /DB_XREF=est:602461680F1 /CLONE=IMAGE:4578666 /UG=Hs.325852 Homo sapiens mRNA for FLJ00043 protein, partial cds
221761_at_HG-U133A	RPE	adenylosuccinate synthase	Consensus includes gb:AA628948 /FEA=EST /DB_XREF=gi:2541335 /DB_XREF=est:a28f07.s1 /CLONE=IMAGE:1032997 /UG=Hs.90011 adenylosuccinate synthase /FL=gb:NM_001126.1
221770_at_HG-U133A	KIAA1718	ribulose-5-phosphate-3-epimerase	Consensus includes gb:BE964473 /FEA=EST /DB_XREF=gi:11767942 /DB_XREF=est:601658180R1 /CLONE=IMAGE:3876354 /UG=Hs.125845 ribulose-5-phosphate-3-epimerase
221778_at_HG-U133A	KIAA1718	KIAA1718 protein	Consensus includes gb:BE217882 /FEA=EST /DB_XREF=gi:8905200 /DB_XREF=est:tv31b02.x1 /CLONE=IMAGE:3174987 /UG=Hs.222707 KIAA1718 protein
221802_s_at_HG-U133A	KIAA1598	KIAA1598 protein	Consensus includes gb:AU157109 /FEA=EST /DB_XREF=gi:110118630 /DB_XREF=est:AU157109 /CLONE=PLACE1006159 /UG=Hs.23740 KIAA1598 protein
221834_at_HG-U133A		Homo sapiens cDNA FLJ31489 f1, clone	Consensus includes gb:AV700132 /FEA=EST /DB_XREF=gi:10302103

		NT2NE2003308	/DB_XREF=est:AV700132 /CLONE=GKCGSE03 /UG=Hs.295923 seven in absentia (Drosophila) homolog 1
221858_at_HG-U133A	KIAA0608	KIAA0608 protein Homo sapiens clone 23579 mRNA sequence	Consensus includes gb:N34407 /FEA=EST /DB_XREF=gi:1155549 /DB_XREF=est:yy53g10.s1 /CLONE=IMAGE:277314 /UG=Hs.100360 KIAA0608 protein
221865_at_HG-U133A			Consensus includes gb:BF969986 /FEA=EST /DB_XREF=gi:12337201 /DB_XREF=est:602272821F1 /CLONE=IMAGE:4360804 /UG=Hs.170226 Homo sapiens clone 23579 mRNA sequence
221902_at_HG-U133A	RPL38	ESTs ribosomal protein L38	Consensus includes gb:AL567940 /FEA=EST /DB_XREF=gi:12921802 /DB_XREF=est:AL567940 /CLONE=CS0DF036YK19 (3 prime) /UG=Hs.7967 ESTs
221943_x_at_HG-U133A	PAX5	paired box gene 5 (B-cell lineage specific activator protein)	Consensus includes gb:AW303136 /FEA=EST /DB_XREF=gi:6712816 /DB_XREF=est:xr59cd8.x1 /CLONE=IMAGE:2764430 /UG=Hs.2017 ribosomal protein L38
221969_at_HG-U133A			Consensus includes gb:BF510692 /FEA=EST /DB_XREF=gi:11539390 /DB_XREF=est:Ui-H-BI4-adff-12-0-Ui.s1 /CLONE=IMAGE:3084815 /UG=Hs.22030 paired box gene 5 (B-cell lineage specific activator protein)
221980_at_HG-U133A	NXPH3		Consensus includes gb:AL117592.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586H1921 (from clone DKFZp586H1921). /FEA=mRNA /DB_XREF=gi:5912156 /UG=Hs.179765 Homo sapiens mRNA; cDNA DKFZp586H1921 (from clone DKFZp586H1921)
221991_at_HG-U133A		neurexophilin 3	Consensus includes gb:AI937333 /FEA=EST /DB_XREF=gi:5676203 /DB_XREF=est:wp75h10.x1 /CLONE=IMAGE:2467651 /UG=Hs.55069 neurexophilin 3
222062_at_HG-U133A	WSX1		Consensus includes gb:AI983115 /FEA=EST /DB_XREF=gi:5810334 /DB_XREF=est:wu18b02.x1 /CLONE=IMAGE:2517291 /UG=Hs.132781 class 1 cytokine receptor
222073_at_HG-U133A	COL4A3	class I cytokine receptor collagen, type IV, alpha 3 (Goodpasture	Consensus includes gb:AI694562 /FEA=EST /DB_XREF=gi:4971902

		antigen)	/DB_XREF=est:wd72g08.x1 /CLONE=IMAGE:2337182 /UG=Hs.150318 ESTs
222108_at_HG-U133A			Consensus includes gb:AC004010 /DEF=Human BAC clone GS1-99HB /FEA=CDS /DB_XREF=gi:2781385 /UG=Hs.121520 Human BAC clone GS1-99HB
222146_s_at_HG-U133A			Consensus includes gb:AK026674.1 /DEF=Homo sapiens cDNA: FLJ23021 fis, clone LNG0104, highly similar to HUMSEF21B Human SEF2-1B protein (SEF2-1B) mRNA. /FEA=mRNA /DB_XREF=gi:10439577 /UG=Hs.3226198 transcription factor 4
222147_s_at_HG-U133A			Consensus includes gb:AL133519 /DEF=Human DNA sequence from clone RP11-122O1 on chromosome 20 Contains a novel gene encoding a protein orthologous to the mouse vesicular inhibitory amino acid transporter (VIAAT), a novel gene similar to the yeast actin-like protein ARP5, 3 CpG island... /FEA=CDS /DB_XREF=gi:10045268 /UG=Hs.302092 Human DNA sequence from clone RP11-122O1 on chromosome 20 Contains a novel gene encoding a protein orthologous to the mouse vesicular inhibitory amino acid transporter (VIAAT), a novel gene similar to the yeast actin-like protein ARP5, 3 CpG islands, ESTs
222150_s_at_HG-U133A			Consensus includes gb:AK026747.1 /DEF=Homo sapiens cDNA: FLJ23094 fis, clone LNG0739, highly similar to HST000007 Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 293605. /FEA=mRNA /DB_XREF=gi:10439670 /UG=Hs.12969 hypothetical protein
222154_s_at_HG-U133A	DKFZP564A2416	DKFZP564A2416 protein	Consensus includes gb:AK002064.1 /DEF=Homo sapiens cDNA FLJ11202 fis, clone PLACE1007746. /FEA=mRNA /DB_XREF=gi:7023720 /UG=Hs.5297 DKFZP564A2416 protein
222163_s_at_HG-U133A	MGC5347	hypothetical protein MGC5347	Consensus includes gb:BE890973 /FEA=EST /DB_XREF=gi:10349835 /DB_XREF=est:601431962F1 /CLONE=IMAGE:3917319 /UG=Hs.5555 hypothetical protein MGC5347
222166_at_HG-U133A			Consensus includes gb:AK022985.1 /DEF=Homo sapiens cDNA FLJ12823 fis,

		clone NT2RP2002752. /FEA=mRNA /DB_XREF=gi:10434538 /UG=Hs.95867 hypothetical protein EST00098
222203_s_at_HG-U133A		Consensus includes gb:AK023625.1 /DEF=Homo sapiens cDNA FLJ13563 fs, clone PLACE1008111, weakly similar to PROBABLE OXIDOREDUCTASE (EC 1.-.-). /FEA=mRNA /DB_XREF=gi:10435607 /UG=Hs.288880 PAN2 protein
222229_x_at_HG-U133A		Consensus includes gb:AL121871 /DEF=Human DNA sequence from clone RP13-258O15 on chromosome Xq21.2-Xq21.33 Contains a pseudogene similar to ribosomal protein L26, STSs and GSSs /FEA=CDS /DB_XREF=gi:6855342 /UG=Hs.272344 Human DNA sequence from clone RP13-258O15 on chromosome Xq21.2-Xq21.33 Contains a pseudogene similar to ribosomal protein L26, STSs and GSSs
222237_s_at_HG-U133A		Consensus includes gb:AC084239 /DEF=Homo sapiens chromosome 19, BAC CTC-512J12 (BC347040), complete sequence /FEA=mRNA_2 /DB_XREF=gi:10864171 /UG=Hs.48589 zinc finger protein 228
222275_at_HG-U133A	ESTs	Consensus includes gb:AI039469 /FEA=EST /DB_XREF=gi:3278863 /DB_XREF=est:ox41a08.s1 /CLONE=IMAGE:1658870 /UG=Hs.27362 ESTs
222282_at_HG-U133A	ESTs	Consensus includes gb:AV761453 /CLONE=MDSBZA03 /UG=Hs.294014 ESTs /DB_XREF=est:AV761453 /FEA=EST /DB_XREF=gi:10919301 /DB_XREF=est:AW972359 /CLONE=MDSBZA03 /UG=Hs.294014 ESTs /DB_XREF=est:AW972359 /FEA=EST /DB_XREF=gi:8162205
222313_at_HG-U133A	ESTs	Consensus includes gb:BG025063 /FEA=EST /DB_XREF=gi:12411278 /DB_XREF=est:602276408F1 /CLONE=IMAGE:4364304 /UG=Hs.44888 ESTs
222335_at_HG-U133A	ESTs	Consensus includes gb:AW167859 /FEA=EST /DB_XREF=gi:6399308 /DB_XREF=est:xg55a05.x1 /CLONE=IMAGE:2632208 /UG=Hs.9788 hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5 /FL=gb:BC004317.1 gb:NM_030571.1
222422_s_at_HG-U133B	MGC10924	hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5 /FL=gb:BC004317.1 gb:NM_030571.1
222448_s_at_HG-	UMP-CMPK	gb:AF112216.1 /DEF=Homo sapiens UMP-CMP kinase mRNA, complete cds.

U133B			/FEA=mRNA /PROD=UMP-CMP kinase /DB_XREF=gi:6563219 /UG=Hs.11463 UMP-CMP kinase /FL=gb:AF259961.1 gb:AF110643.1 gb:AF112216.1
			gb:AF070416.1 gb:NM_016308.1 gb:AF165521.1 /DEF=Homo sapiens ribosomal protein L30 isolog (L30) mRNA, complete cds. /FEA=mRNA /GEN=L30 /PROD=ribosomal protein L30 isolog /DB_XREF=gi:9294748 /UG=Hs.284162 60S ribosomal protein L30 isolog /FL=gb:NM_016304.1 gb:AF060926.1 gb:AF212226.1 gb:BC005344.1
222465_at_HG-U133B	C15orf15	chromosome 15 open reading frame 15	gb:AF201949.1 gb:AF165521.1 gb:BC005176.1 /DEF=Homo sapiens, seven transmembrane protein TM7SF3, clone MGc:847, mRNA, complete cds. /FEA=mRNA /PROD=seven transmembrane protein TM7SF3 /DB_XREF=gi:13477393 /UG=Hs.10071 seven transmembrane protein TM7SF3 /FL=gb:BC005176.1 gb:AB032470.1 gb:NM_016551.1
222477_s_at_HG-U133B	TM7SF3	seven transmembrane protein TM7SF3	Consensus includes gb:AW262867 /FEA=EST /DB_XREF=gi:6639683 /DB_XREF=east:xq96d11.x1 /CLONE=IMAGE:2758485 /UG=Hs.4746 hypothetical protein FLJ21324 /FL=gb:NM_021941.1 gb:BC003651.1
222492_at_HG-U133B	FLJ21324	hypothetical protein FLJ21324	gb:AF139576.1 /DEF=Homo sapiens MHS4R2 (MHS4R2) mRNA, complete cds. /FEA=mRNA /GEN=MHS4R2 /PROD=MHS4R2 /DB_XREF=gi:13171100 /UG=Hs.170318 hypothetical protein FLJ10147 /FL=gb:AF139576.1
222520_s_at_HG-U133B	ESRRBL1	estrogen-related receptor beta like 1	gb:AF245220.1 gb:NM_018010.1 Consensus includes gb:AU150752 /FEA=EST /DB_XREF=gi:11012273 /DB_XREF=east:AU150752 /CLONE=NT2RP2003522 /UG=Hs.59757 zinc finger protein 281 /FL=gb:AF125158.1 gb:NM_012482.1
222619_at_HG-U133B	ZNF281	zinc finger protein 281	Consensus includes gb:AK001261.1 /DEF=Homo sapiens cDNA FLJ10399 fis, clone NT2RM4000354, weakly similar to LETHAL(2)DENTICLELESS PROTEIN. /FEA=mRNA /DB_XREF=gi:7022404 /UG=Hs.126774 L2DTL
222680_s_at_HG-U133B	RAMP	RA-regulated nuclear matrix-associated protein	protein /FL=gb:AF195765.1 gb:NM_016448.1
222692_s_at_HG-	FLJ23399	hypothetical protein FLJ23399	Consensus includes gb:BF444916 /FEA=EST /DB_XREF=gi:11510054

U133B			/DB_XREF=est:nad19a09.x1 /CLONE=IMAGE:3365681 /UG=Hs.299883 hypothetical protein FLJ23399 /FL=gb:NM_022763.1
222698_s_at_HG-U133B	IMPACT	hypothetical protein IMPACT	gb:AF208894.1 /DEF=Homo sapiens IMPACT (IMPACT) mRNA, complete cds. /FEA=mRNA /GEN=IMPACT /PROD=IMPACT /DB_XREF=gi:11494011 /UG=Hs.284245 hypothetical protein IMPACT /FL=gb:AF208894.1
222862_s_at_HG-U133B	AK5	adenylate kinase 5	gb:AB026264.1 gb:NM_018439.1 Consensus includes gb:BG169832 /FEA=EST /DB_XREF=gi:12676535 /DB_XREF=est:602324480F1 /CLONE=IMAGE:4427755 /UG=Hs.18268 adenylate kinase 5 /FL=gb:AF062959.1 gb:NM_012093.1
222915_s_at_HG-U133B	BANK	hypothetical protein FLJ20706	Consensus includes gb:AA811540 /FEA=EST /DB_XREF=gi:2881151 /DB_XREF=est:ab73e02.s1 /CLONE=IMAGE:1337018 /UG=Hs.193736 hypothetical protein FLJ20706 /FL=gb:NM_017935.1
222916_s_at_HG-U133B			Consensus includes gb:AF116718.1 /DEF=Homo sapiens PRO2900 mRNA, complete cds. /FEA=mRNA /PROD=PRO2900 /DB_XREF=gi:7959934 /UG=Hs.283473 hypothetical protein PRO2900 /FL=gb:AF116718.1
222955_s_at_HG-U133B	HT011	uncharacterized hypothalamus protein HT011	gb:NM_018635.1 gb:AF168713.1 /DEF=Homo sapiens x 004 protein mRNA, complete cds. /FEA=mRNA /PROD=x 004 protein /DB_XREF=gi:9437340 /UG=Hs.267923 uncharacterized hypothalamus protein HT011 /FL=gb:AF220185.1
222976_s_at_HG-U133B	NTRK1	neurotrophic tyrosine kinase, receptor, type 1	gb:BC000771.1 /DEF=Homo sapiens, Similar to tropomyosin 4, clone MGC:3261, mRNA, complete cds. /FEA=mRNA /PROD=Similar to tropomyosin 4 /DB_XREF=gi:12653954 /UG=Hs.85844 neurotrophic tyrosine kinase, receptor, type 1 /FL=gb:BC000771.1
222977_at_HG-U133B	SURF4	surfcat 4	Consensus includes gb:AL518882 /FEA=EST /DB_XREF=gi:127782375 /DB_XREF=est:AL518882 /CLONE=CS0DA011YM11 (3 prime) /UG=Hs.284296 Homo sapiens cDNA: FLJ22993 fis, clone KAT11914 /FL=gb:AF078886.1
222979_s_at_HG-			gb:AF078866.1 /DEF=Homo sapiens SURF-4 mRNA, complete cds.

U133B			/FEA=mRNA /PROD=SURF-4 /DB_XREF=gi:5531846 /UG=Hs.284296 Homo sapiens cDNA: FLJ22993 fis, clone KAT11914 /FL=gb:AF078866.1
222982_x_at_HG-U133B	SLC38A2	solute carrier family 38, member 2	gb:AF298897.1 /DEF=Homo sapiens amino acid transporter system A (ATA2) mRNA, complete cds. /FEA=mRNA /GEN=ATA2 /PROD=amino acid transporter system A /DB_XREF=gi:10945620 /UG=Hs.298275 amino acid transporter 2 /FL=gb:AF298897.1
222996_s_at_HG-U133B	HSPC195	hypothetical protein HSPC195	gb:BC002490.1 /DEF=Homo sapiens hypothetical protein, clone MGC:915, mRNA, complete cds. /FEA=mRNA /PROD=hypothetical protein /DB_XREF=gi:12803342 /UG=Hs.15093 hypothetical protein /FL=gb:BC002490.1 gb:AF151029.1 gb:NM_016463.1
223036_at_HG-U133B	FRSB	phenylalanyl-tRNA synthetase beta-subunit	gb:DB4430.1 /DEF=Homo sapiens mRNA for phenylalanyl tRNA synthetase complete cds. /FEA=mRNA /PROD=phenylalanyl tRNA synthetase beta-subunit /DB_XREF=gi:7768937 /UG=Hs.9081 phenylalanyl-tRNA synthetase beta-subunit /FL=gb:AF042346.1 gb:NM_005687.1 gb:AF161521.1 gb:DB4430.1
223044_at_HG-U133B	SLC11A3	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 3	gb:AL136944.1 /DEF=Homo sapiens mRNA, cDNA DKFZp586J0624 (from clone DKFZp586J0624); complete cds. /FEA=mRNA /GEN=DKFZp586J0624 /PROD=hypothetical protein /DB_XREF=gi:12053382 /UG=Hs.5944 solute carrier family 11 (proton-coupled divalent metal ion transporters), member 3 /FL=gb:AL136944.1 gb:AF226614.1 gb:NM_014555.1 gb:AF215636.1
223054_at_HG-U133B	DNAJB11		gb:BC001144.1 /DEF=Homo sapiens, ER-associated DNAJ; ER-associated Hsp40 co-chaperone; hDj9; ER3, clone MGC:1169, mRNA, complete cds. /FEA=mRNA /PROD=ER-associated DNAJ; ER-associated Hsp40 co-chaperone; hDj9; ER3 /DB_XREF=gi:12654614 /UG=Hs.278605 Dnaj (Hsp40) homolog, subfamily B, member 11 /FL=gb:BC001144.1
223226_x_at_HG-U133B	MGC3181	Dnaj (Hsp40) homolog, subfamily B, member 11	gb:AB028859.1 gb:AF228505.1 gb:NM_016306.1
		hypothetical protein MGC3181	gb:BC000274.1 /DEF=Homo sapiens, Similar to single-stranded-DNA-binding protein, clone MGC:3181, mRNA, complete cds. /FEA=mRNA /PROD=Similar

		to single-stranded-DNA-binding protein /DB_XREF=gi:12653022 /UG=Hs.324618 Homo sapiens, Similar to single-stranded-DNA-binding protein, clone MGC:3181, mRNA, complete cds /FL=gb:BC00274.1
223246_s_at_HG-U133B	STRBP	spermatic perinuclear RNA binding protein gb:BC002693.1 /DEF=Homo sapiens, Similar to spermatic perinuclear RNA-binding protein, clone MGC:3405, mRNA, complete cds. /FEA=mRNA /PROD=Similar to spermatic perinuclear RNA-binding protein FLJ11307 /DB_XREF=gi:12803714 /UG=Hs.8215 hypothetical protein FLJ11307 /FL=gb:AL136866.1 gb:BC002693.1 gb:NM_018387.1
223253_at_HG-U133B	UCC1	upregulated in colorectal cancer gene 1 gb:AY027862.1 /DEF=Homo sapiens, UCC1 protein, alone MGc:1185, mRNA, complete cds. /FEA=mRNA /PROD=UCC1 protein /DB_XREF=gi:12653794 /UG=Hs.46721 UCC1 protein /FL=gb:BC000686.1
223276_at_HG-U133B	NID67	putative small membrane protein NID67 gb:AF313413.1 /DEF=Homo sapiens putative small membrane protein NID67 mRNA, complete cds. /FEA=mRNA /PROD=putative small membrane protein NID67 /DB_XREF=gi:12484085 /UG=Hs.29444 Homo sapiens putative small membrane protein NID67 mRNA, complete cds /FL=gb:AF313413.1
223280_x_at_HG-U133B	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A gb:AF253977.1 /DEF=Homo sapiens HAIRB-iso mRNA, complete cds. /FEA=mRNA /PROD=HAIRB-iso /DB_XREF=gi:12005800 /UG=Hs.17914 membrane-spanning 4-domains, subfamily A, member 6A, member /FL=gb:AF212240.1 gb:AF261136.1
223287_s_at_HG-U133B	FOXP1	forkhead box P1 gb:AF14696.1 /DEF=Homo sapiens clone pAB195 FOXP1 (FOXP1) mRNA, complete cds. /FEA=mRNA /GEN=FOXP1 /PROD=FOXP1 /DB_XREF=gi:12043713 /UG=Hs.274344 hypothetical protein /FL=gb:AF14696.1 gb:AF15109.1 gb:NM_016477.1
223314_at_HG-U133B	MGC11352	Consensus includes gb:BF025955 /FEA=EST /DB_XREF=gi:10733667 /DB_XREF=est:601669947F1 /CLONE=IMAGE:3953075 /UG=Hs.101395 hypothetical protein MGC11352 /FL=gb:AL136638.1
223318_s_at_HG-	MGC10974	gb:BC00393.1 /DEF=Homo sapiens, Similar to RIKEN cDNA 23T0045B01 hypothetical protein MGC10974

U133B		gene, clone MGC:10974, mRNA, complete cds. /FEA=mRNA /PROD=Similar to RIKEN cDNA 2310045B01 gene /DB_XREF=gi:13325151 /UG=Hs.111099 Homo sapiens, Similar to RIKEN cDNA 2310045B01 gene, clone MGC:10974, mRNA, complete cds /FL=gb:BC004393.1
223321_s_at_HG-U133B	FGFRL1	fibroblast growth factor receptor-like 1 gb:AF312678.1 /DEF=Homo sapiens FGF homologous factor receptor (FHFR) mRNA, complete cds. /FEA=mRNA /GEN=FHFR /PROD=FGF homologous factor receptor /DB_XREF=gi:13183617 /UG=Hs.193326 fibroblast growth factor receptor-like 1 /FL=gb:AF312678.1
223382_s_at_HG-U133B	NIN283	nerve injury gene 283 cytochrome P450, subfamily II, polypeptide 1 gb:AF335278.1 /DEF=Homo sapiens cytochrome P450 2S1 (CYP2S1) mRNA, complete cds. /FEA=mRNA /GEN=CYP2S1 /PROD=cytochrome P450 2S1 /DB_XREF=gi:13161183 /UG=Hs.98370 cytochrome P450, subfamily II, polypeptide 1 /FL=gb:AF335278.1 gb:NM_030822.2
223385_at_HG-U133B	CYP2S1	Consensus includes gb:BE880703 /FEA=EST /DB_XREF=gi:10329479 /DB_XREF=est601490317F1 /CLONE=IMAGE:3892493 /UG=Hs.24678 sphingosine-1-phosphatase /FL=gb:AF349315.1
223391_at_HG-U133B	LOC81537	gb:BC001294.1 /DEF=Homo sapiens, Similar to x 006 protein, clone MGC:5294, mRNA, complete cds. /FEA=mRNA /PROD=Similar to x 006 protein /DB_XREF=gi:12654898 /UG=Hs.47668 x 006 protein /FL=gb:BC001294.1
223401_at_HG-U133B	MDS006	x 006 protein
223422_s_at_HG-U133B	DKFZP564B1162	hypothetical protein DKFZp564B1162 Consensus includes gb:AI743534 /FEA=EST /DB_XREF=gi:5111822 /DB_XREF=estwf72e03.x2 /CLONE=IMAGE:2361148 /UG=Hs.93589 Homo sapiens mRNA; cDNA DKFZp564B1162 (from clone DKFZp564B1162); complete cds /FL=gb:AL136646.1

223449_at_HG-U133B	SEMA6A	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	gb:AF225425.1 /DEF=Homo sapiens HT018 mRNA, complete cds. /FEA=mRNA /PROD=HT018 /DB_XREF=gi:9963852 /UG=Hs.108920 HT018 protein /FL=gb:NM_020681.1 gb:AF225425.1
			gb:BC005158.1 /DEF=Homo sapiens, Similar to RIKEN cDNA 3010001K23 gene, clone MGC:4618, mRNA, complete cds. /FEA=mRNA /PROD=Similar to RIKEN cDNA 3010001K23 gene /DB_XREF=gi:13477362 /UG=Hs.89072 Homo sapiens, Similar to RIKEN cDNA 3010001K23 gene, clone MGC:4618, mRNA, complete cds /FL=gb:BC005158.1
223462_at_HG-U133B	MGC4618	hypothetical protein MGC4618	gb:AF069506.1 /DEF=Homo sapiens activator of G protein signaling (AGS1) mRNA, complete cds. /FEA=mRNA /GEN=AGS1 /PROD=activator of G protein signaling /DB_XREF=gi:4959037 /UG=Hs.25829 ras-related protein /FL=gb:AF069506.1 gb:AF172846.1 gb:NM_016084.1
223467_at_HG-U133B	RASD1	RAS, dexamethasone-induced 1	gb:BC004942.1 /DEF=Homo sapiens, clone MGC:10812, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:10812) /DB_XREF=gi:13438298 /UG=Hs.4188 Homo sapiens, clone MGC:10812, mRNA, complete cds /FL=gb:BC004942.1
223469_at_HG-U133B	MGC10812	hypothetical protein MGC10812	gb:BC002556.1 /DEF=Homo sapiens, hypothetical protein FLJ22548 similar to gene trap PAT 12, clone MGC:759, mRNA, complete cds. /FEA=mRNA /PROD=hypothetical protein FLJ22548 similar to gene trap PAT 12 /DB_XREF=gi:12803462 /UG=Hs.103267 hypothetical protein FLJ22548 similar to gene trap PAT 12 /FL=gb:NM_022456.1 gb:BC002556.1
223471_at_HG-U133B			Consensus includes gb:AI932310 /FEA=EST /DB_XREF=gi:5671047 /DB_XREF=est:wd26h03.x1 /CLONE=IMAGE:2329301 /UG=Hs.179260 chromosome 14 open reading frame 4 /FL=gb:AF063597.1
223474_at_HG-U133B	C14orf4	chromosome 14 open reading frame 4	gb:AF327923.1 /DEF=Homo sapiens transmembrane protein induced by tumor necrosis factor alpha (TMPII) mRNA, complete cds. /FEA=mRNA /GEN=TMPII /PROD=transmembrane protein induced by tumor necrosis factor alpha /DB_XREF=gi:13241760 /UG=Hs.314243 Homo sapiens transmembrane
223482_at_HG-U133B	TMPII		

			protein induced by tumor necrosis factor alpha (TNF) mRNA, complete cds /FL=gb:AF327923.1
223498_at_HG-U133B	Homo sapiens, clone IMAGE:3614358, mRNA, partial cds		gb:AB041533.1 /DEF=Homo sapiens HCMOGT-1 mRNA for sperm antigen, complete cds. /FEA=mRNA /GEN=HCMOGT-1 /PROD=sperm antigen /DB_XREF=gi:10798803 /UG=Hs.15053 Homo sapiens HCMOGT-1 mRNA for sperm antigen, complete cds /FL=gb:AB041533.1
223514_at_HG-U133B	CARD11		gb:AF322641.1 /DEF=Homo sapiens caspase recruitment domain protein 11 mRNA, complete cds. /FEA=mRNA /PROD=caspase recruitment domain protein 11 /DB_XREF=gi:12382772 /UG=Hs.293867 Homo sapiens caspase recruitment domain protein 11 mRNA, complete cds /FL=gb:AF322641.1
223522_at_HG-U133B	GL012		gb:AF251293.1 /DEF=Homo sapiens GL012 mRNA, complete cds. /FEA=mRNA /PROD=GL012 /DB_XREF=gi:12005727 /UG=Hs.21379 hypothetical protein GL012 /FL=gb:AF251293.1
223595_at_HG-U133B	AD031		gb:AF247167.1 /DEF=Homo sapiens AD031 mRNA, complete cds. /FEA=mRNA /PROD=AD031 /DB_XREF=gi:12005634 /UG=Hs.44004 Homo sapiens AD031 mRNA, complete cds /FL=gb:AF247167.1
223703_at_HG-U133B	CDA017		gb:AF267860.1 /DEF=Homo sapiens CDA017 mRNA, complete cds. /FEA=mRNA /PROD=CDA017 /DB_XREF=gi:12006046 /UG=Hs.39780 Homo sapiens CDA017 mRNA, complete cds /FL=gb:AF267860.1
223712_at_HG-U133B	DCOHM		gb:AL136721.1 /DEF=Homo sapiens cDNA DKFZp566K1946 (from clone DKFZp566K1946); complete cds. /FEA=mRNA /GEN=DKFZp566K1946 /PROD=hypothetical protein /DB_XREF=gi:12052960 /UG=Hs.150186 Homo sapiens mRNA; cDNA DKFZp566K1946 (from clone DKFZp566K1946); complete cds /FL=gb:AL136721.1
223785_at_HG-U133B	FLJ10719		gb:BC004277.1 /DEF=Homo sapiens, Similar to hypothetical protein FLJ10719, clone MGIC:10837, mRNA, complete cds. /FEA=mRNA /PROD=Similar to hypothetical protein FLJ10719 /DB_XREF=gi:13279100 /UG=Hs.134734 Homo sapiens, Similar to hypothetical protein FLJ10719,

			clone MGC:10837, mRNA, complete cds /FL=gb:BC004277.1 gb:AF222694.1 /DEF=Homo sapiens galectin-related inhibitor of proliferation isoform b (GRIP1) mRNA, complete cds. /FEA=mRNA /GEN=GRIP1 /PROD=galectin-related inhibitor of proliferation isoform b /DB_XREF=gi:6979866 /UG=Hs.284183 Homo sapiens galectin-related inhibitor of proliferation isoform a (GRIP1) mRNA, complete cds /FL=gb:AF222694.1 gb:AF222695.1
223828_s_at_HG-U133B	LGALS12	lectin, galactoside-binding, soluble, 12 (galectin 12)	gb:AF132203.1 /DEF=Homo sapiens PRO1933 mRNA, complete cds. /FEA=mRNA /PROD=PRO1933 /DB_XREF=gi:11495551 /UG=Hs.119597 stearoyl-CoA desaturase (delta-9-desaturase) /FL=gb:AF132203.1
223839_s_at_HG-U133B			gb:BC001134.1 /DEF=Homo sapiens, hypothetical protein FLJ13258 similar to fused toes, clone MGC:2845, mRNA, complete cds. /FEA=mRNA /PROD=hypothetical protein FLJ13258 similar to fused toes /DB_XREF=gi:12654596 /UG=Hs.2888929 hypothetical protein FLJ13258 similar to fused toes /FL=gb:BC001134.1
223894_s_at_HG-U133B	FTS	fused toes homolog (mouse)	gb:AF348078.1 /DEF=Homo sapiens G-protein coupled receptor 91 (GPR91) mRNA, complete cds. /FEA=mRNA /GEN=GPR91 /PROD=G-protein coupled receptor 91 /DB_XREF=gi:13517982 /UG=Hs.279575 Homo sapiens G-protein coupled receptor 91 (GPR91) mRNA, complete cds /FL=gb:AF348078.1
223939_at_HG-U133B	GPR91	G protein-coupled receptor 91	gb:AF223937.1 /DEF=Homo sapiens ninein isotype 1 mRNA, complete cds. /FEA=mRNA /PROD=ninein isotype 1 /DB_XREF=gi:12655859 /UG=Hs.44054 ninein (GSK3B interacting protein) /FL=gb:AF223937.1
223981_at_HG-U133B	NIN	ninein (GSK3B interacting protein)	gb:AB041261.1 /DEF=Homo sapiens iPLA2 mRNA for calcium-independent phospholipase A2, complete cds. /FEA=mRNA /GEN=iPLA2 /PROD=calcium- independent phospholipase A2 /DB_XREF=gi:7670057 /UG=Hs.44198 intracellular membrane-associated calcium-independent phospholipase A2 gamma /FL=gb:AB041261.1
223982_s_at_HG-U133B	IPLA2	intracellular membrane-associated calcium-independent phospholipase A2 gamma	gb:AL136929.1 /DEF=Homo sapiens mRNA; cDNA DkFZp586D0222 (from
224044_at_HG-U133B	FLJ1040	hypothetical protein FLJ11040	

			clone DKFZp586D0222; complete cds. /FEA=mRNA /GEN=DKFZp586D0222 /PROD=hypothetical protein /DB_XREF=gi:12053352 /UG=Hs.14202 hypothetical protein FLJ11040 /FL=gb:AL136929.1
			gb:AF339912.1 /DEF=Homo sapiens potassium channel TASK-4 mRNA, complete cds. /FEA=mRNA /PROD=potassium channel TASK-4 /DB_XREF=gi:13507376 /UG=Hs.162282 Homo sapiens potassium channel TASK-4 mRNA, complete cds /FL=gb:AF339912.1
224049_at_HG-U133B	KCNK17		potassium channel subfamily K, member 17 (TASK-4) gb:AF25649.1 /DEF=Homo sapiens DC28 mRNA, complete cds. /FEA=mRNA /PROD=DC28 /DB_XREF=gi:12005822 /UG=Hs.27721 Wolf-Hirschhorn syndrome candidate 1-like 1 /FL=gb:AF25649.1
224076_s_at_HG-U133B	WHSC1L1		Wolf-Hirschhorn syndrome candidate 1-like 1 gb:AF118886.1 /DEF=Homo sapiens VAV-3 protein beta isoform (VAV-3) mRNA, alternatively spliced, complete cds. /FEA=mRNA /GEN=/AV-3 /PROD=VAV-3 protein beta isoform /DB_XREF=gi:4416405 /UG=Hs.267659 vav 3 oncogene /FL=gb:AF118886.1
224221_s_at_HG-U133B	VAV3		gb:AF116635.1 /DEF=Homo sapiens PRO2221 mRNA, complete cds. /FEA=mRNA /PROD=PRO2221 /DB_XREF=gi:7959888 /UG=Hs.296442 hypothetical protein PRO2221 /FL=gb:AF116695.1
224254_x_at_HG-U133B			gb:AB042647.1 /DEF=Homo sapiens B29 mRNA, complete cds. /FEA=mRNA /GEN=B29 /DB_XREF=gi:13603411 /FL=gb:AB042647.1
224324_at_HG-U133B	B29	B29 protein	gb:AF237908.1 /DEF=Homo sapiens MS4A6A protein mRNA, complete cds. /FEA=mRNA /PROD=MS4A6A protein /DB_XREF=gi:13649404
224356_x_at_HG-U133B	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A	gb:AF293341.1 /DEF=Homo sapiens collagen-like Alzheimer amyloid plaque component precursor type II mRNA, complete cds. /FEA=mRNA - /PROD=collagen-like Alzheimer amyloid plaque component precursor type II /DB_XREF=gi:13625305 /FL=gb:AF293341.1
224389_s_at_HG-U133B	LOC84570	collagen-like Alzheimer amyloid plaque component precursor	gb:AF343662.1 /DEF=Homo sapiens immunoglobulin receptor translocation associated protein 2a (IRTA2) mRNA, complete cds, alternatively spliced.
224404_s_at_HG-U133B	IRTA2	immunoglobulin superfamily receptor translocation associated 2a (IRTA2)	

			/FEA=mRNA /GEN=IRTA2 /PROD=immunoglobulin receptor translocation associatedprotein 2a /DB_XREF=gi:13591709 /FL=gb:AF343662.1
224405_at_HG-U133B	IRTA2	immunoglobulin superfamily receptor translocation associated 2	gb:AF343663.1 /DEF=Homo sapiens immunoglobulin receptor translocation associated protein 2b (IRTA2) mRNA, complete cds, alternatively spliced. /FEA=mRNA /GEN=IRTA2 /PROD=immunoglobulin receptor translocation associatedprotein 2b /DB_XREF=gi:13591711 /FL=gb:AF343663.1
224406_s_at_HG-U133B	IRTA2	immunoglobulin superfamily receptor translocation associated 2	gb:AF343664.1 /DEF=Homo sapiens immunoglobulin receptor translocation associated protein 2c (IRTA2) mRNA, complete cds, alternatively spliced. /FEA=mRNA /GEN=IRTA2 /PROD=immunoglobulin receptor translocation associatedprotein 2c /DB_XREF=gi:13591713 /FL=gb:AF343664.1
224407_s_at_HG-U133B	MST4	Mst3 and SOK1-related kinase	gb:AF344882.1 /DEF=Homo sapiens serine/threonine protein kinase MST4 (MST4) mRNA, complete cds, alternatively spliced. /FEA=mRNA /GEN=MST4 /PROD=serine/threonine protein kinase MST4 /DB_XREF=gi:13549066 /FL=gb:AF344882.1
224435_at_HG-U133B	MGC4248	hypothetical protein MGC4248	gb:BC005871.1 /DEF=Homo sapiens, Similar to RIKEN cDNA 5730469M10 gene, clone MGC:4248, mRNA, complete cds. /FEA=mRNA /PROD=Similar to RIKEN cDNA 5730469M10 gene /DB_XREF=gi:13543426 /FL=gb:BC005871.1
224482_s_at_HG-U133B	MGC11316	hypothetical protein MGC11316	gb:BC006240.1 /DEF=Homo sapiens, clone MGC:11316, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:11316) /DB_XREF=gi:13623278 /FL=gb:BC0062240.1
224516_s_at_HG-U133B	HSPC195	hypothetical protein HSPC195	gb:BC006428.1 /DEF=Homo sapiens, hypothetical protein, clone MGC:12969, mRNA, complete cds. /FEA=mRNA /PROD=hypothetical protein /DB_XREF=gi:13623618 /FL=gb:BC006428.1
224520_s_at_HG-U133B	MGC13168	hypothetical protein MGC13168	gb:BC006440.1 /DEF=Homo sapiens, clone MGC:13168, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:13168) /DB_XREF=gi:13623640 /FL=gb:BC006440.1
224553_s_at_HG-	TNFRSF18	tumor necrosis factor receptor	gb:AF117297.1 /DEF=Homo sapiens TNF receptor superfAMILY activation-

U133B		superfamily, member 18	inducible protein mRNA, complete cds. /FEA=CDS /PROD=TNF receptor superfamily activation-inducibleprotein /DB_XREF=gi:4378799 /UG=Hs.212680 tumor necrosis factor receptor superfamily, member 18 /FL=gb:AF117297.1
224559_at_HG-U133B			Consensus includes gb:AF001540 /FEA=EST /DB_XREF=gi:2529712 /DB_XREF=est:AF001540 /CLONE=alpha1 /UG=Hs.42346 calcineurin-binding protein cal sarcin-1
224570_s_at_HG-U133B		Homo sapiens, clone IMAGE:3882977, mRNA, partial cds	Consensus includes gb:AA166686 /FEA=EST /DB_XREF=gi:1745160 /DB_XREF=est:2085e03.s1 /CLONE=IMAGE:593692 /UG=Hs.279009 matrix Gla protein
224609_at_HG-U133B	CTL2	CT12 gene	Consensus includes gb:AI264216 /FEA=EST /DB_XREF=gi:3872419 /DB_XREF=est:qk02h01.x1 /CLONE=IMAGE:1867825 /UG=Hs.105509 CT12 gene /FL=gb:NM_020428.1
224664_at_HG-U133B		Homo sapiens, RIKEN cDNA 2310005G07 gene, clone MGc:10049 IMAGE:3890955, mRNA, complete cds	Consensus includes gb:BE982336 /FEA=EST /DB_XREF=gi:11765135 /DB_XREF=est:601655601R1 /CLONE=IMAGE:3846049 /UG=Hs.178485 Homo sapiens cDNA FLJ13919 fis, clone Y79AA1000410
224681_at_HG-U133B	GNA12	guanine nucleotide binding protein (G protein) alpha 12	Consensus includes gb:BG028884 /FEA=EST /DB_XREF=gi:12417979 /DB_XREF=est:602292385F1 /CLONE=IMAGE:4387292 /UG=Hs.182874 /FL=gb:L01694.1 guanine nucleotide binding protein (G protein) alpha 12. /FL=gb:NM_007353.1
224710_at_HG-U133B	RAB34	RAB34, member RAS oncogene family	Consensus includes gb:AF322067.1 /DEF=Homo sapiens RAB39 (RAB39) mRNA, complete cds. /FEA=CDS /GEN=RAB39 /PROD=RAB39 /DB_XREF=gi:12958664 /UG=Hs.301853 Homo sapiens RAB39 (RAB39) mRNA, complete cds /FL=gb:AF322067.1
224724_at_HG-U133B	KIAA1247	similar to glucosamine-6-sulfatases	Consensus includes gb:AL133001.1 /DEF=Novel human gene on chromosome 20, similar to GLUCOSAMINE-6-SULFATASES. /FEA=mRNA /PROD=hypothetical protein /DB_XREF=gi:6453340 /UG=Hs.43857 similar to glucosamine-6-sulfatases
224727_at_HG-U133B		Homo sapiens mRNA; cDNA	Consensus includes gb:AL045545 /FEA=EST /DB_XREF=gi:5433676

	DKFZp434E2023 (from clone DKEZp434E2023)	/DB_XREF=est:DKFZp434K095_r1 /CLONE=DKFZp434K095 /UG=Hs.250465 Homo sapiens mRNA; cDNA DKFZp434E2023 (from clone DKEZp434E2023)
	Homo sapiens cDNA FLJ32189 fis, clone PLACE6002084, weakly similar to CYTOCHROME B561	Consensus includes gb:AA683481 /FEA=EST /DB_XREF=gi:2670079 /DB_XREF=est:z155b03.s1 /CLONE=IMAGE:505805 /UG=Hs.22546 Homo sapiens cDNA: FLJ22217 fis, clone HRC01591
224735_at_HG-U133B	porcupine	Consensus includes gb:BE778706 /FEA=EST /DB_XREF=gi:10199993 /DB_XREF=est:601466232F1 /CLONE=IMAGE:3869516 /UG=Hs.5326 amino acid system N transporter 2; porcupine
224739_at_HG-U133B	MG61	Consensus includes gb:AB037845.1 /DEF=Homo sapiens mRNA for KIAA1424 protein, partial cds. /FEA=mRNA /GEN=KIAA1424 /PROD=KIAA1424 protein /DB_XREF=gi:7243228 /UG=Hs.11611 KIAA1424 protein
224764_at_HG-U133B	ARHGAP10	Rho-GTPase activating protein 10 Consensus includes gb:AB032977.1 /DEF=Homo sapiens mRNA for KIAA151 protein, partial cds. /FEA=mRNA /GEN=KIAA151 /PROD=KIAA151 protein /DB_XREF=gi:6382017 /UG=Hs.6298 KIAA151 protein
224772_at_HG-U133B	MGC14961	hypothetical protein MGC14961 Consensus includes gb:AA654142 /FEA=EST /DB_XREF=gi:2590296 /DB_XREF=est:nt10d06.s1 /CLONE=IMAGE:1192715 /UG=Hs.23954 cerebral cell adhesion molecule /FL=gb:AF177203.1 qb:NM_016174.1
224794_s_at_HG-U133B	LOC51148	cerebral cell adhesion molecule Consensus includes gb:AU152410 /FEA=EST /DB_XREF=gi:11013931 /DB_XREF=est:AU152410 /CLONE=NT2RP3000901 /UG=Hs.10647 FLJ00005 protein
224804_s_at_HG-U133B	FLJ00005	FLJ00005 protein Consensus includes gb:BF1112093 /FEA=EST /DB_XREF=gi:10941783 /DB_XREF=est:7140b07.x1 /CLONE=IMAGE:3523908 /UG=Hs.5724 sclerostin DFNEs2000011
224811_at_HG-U133B		Consensus includes gb:AA526844 /FEA=EST /DB_XREF=gi:2268913 /DB_XREF=est:n192d10.s1 /CLONE=IMAGE:984307 /UG=Hs.288985 Homo sapiens cDNA: FLJ22300 fis, clone HRC04759
224823_at_HG-U133B		Consensus includes qb:BE218980 /FEA=EST /DB_XREF=gi:8906298
224833_at_HG-U133B	ET51	v-ets erythroblastosis virus E26

		oncogene homolog 1 (avian)	/DB_XREF=est:hv47a05.x1 /CLONE=IMAGE:3176528 /UG=Hs.18063 Homo sapiens cDNA FLJ10768 fis, clone NT2RP4000150
224837_at_HG-U133B	FOXP1	forkhead box P1	Consensus includes gb:AV080845 /FEA=EST /DB_XREF=gi:6035997 /DB_XREF=est:xc38c08.x1 /CLONE=IMAGE:2586542 /UG=Hs.108327 damage-specific DNA binding protein 1 (127kD)
224838_at_HG-U133B			Consensus includes gb:AK026898.1 /FEA=EST /DB_XREF=gi:13135436 /DB_XREF=est:xc38c08.x1 /CLONE=IMAGE:10439865 /UG=Hs.108327
224839_s_at_HG-U133B	GPT2	glutamic pyruvate transaminase (alanine aminotransferase) 2	Consensus includes gb:BG328998 /FEA=EST /DB_XREF=gi:13135436 /DB_XREF=est:602428659F1 /CLONE=IMAGE:4558454 /UG=Hs.79265 suppression of tumorigenicity 5
224847_at_HG-U133B		Homo sapiens cDNA FLJ31360 fis, clone MESAN2000572	Consensus includes gb:AV051349 /FEA=EST /DB_XREF=gi:5913619 /DB_XREF=est:wy89g02.x1 /CLONE=IMAGE:2555762 /UG=Hs.180059, Homo sapiens cDNA FLJ20653 fis, clone KAT01739
224848_at_HG-U133B		Homo sapiens cDNA FLJ31360 fis, clone MESAN2000572	Consensus includes gb:AA922068 /FEA=EST /DB_XREF=gi:3069377 /DB_XREF=est:om45d11.s1 /CLONE=IMAGE:1543989 /UG=Hs.180059 Homo sapiens cDNA FLJ20653 fis, clone KAT01739
224872_at_HG-U133B	KIAA1463	KIAA1463 protein	Consensus includes gb:AB040896.1 /DEF=Homo sapiens mRNA for KIAA1463 protein, partial cds. /FEA=mRNA /GEN=KIAA1463 /PROD=KIAA1463 protein /DB_XREF=gi:7959186 /UG=Hs.21104 KIAA1463 protein
224918_x_at_HG-U133B	MGST1	microsomal glutathione S-transferase 1	Consensus includes gb:AI220117 /FEA=EST /DB_XREF=gi:3802320 /DB_XREF=est:qg89h11.x1 /CLONE=IMAGE:1842405 /UG=Hs.790 microsomal glutathione S-transferase 1
224928_at_HG-U133B	PRSS2	protease, serine, 2 (trypsin 2)	Consensus includes gb:AK024846.1 /DEF=Homo sapiens cDNA: FLJ21193 /DB_XREF=gi:10437253 /UG=Hs.78521 KIAA1717 protein
224932_at_HG-U133B			Consensus includes gb:AI814909 /FEA=EST /DB_XREF=gi:5426124

			/DB_XREF=est:wk68e04.x1 /CLONE=IMAGE:2420574 /UG=Hs.66915 ESTs Weakly similar to 16.7kd protein H.sapiens
			Consensus includes gb:BG165815 /FEA=EST /DB_XREF=gi:12672518
224935_at_HG-U133B	EIF2S3	eukaryotic translation initiation factor 2, subunit 3 (gamma, 52kD)	/DB_XREF=est:602344486F1 /CLONE=IMAGE:4454565 /UG=Hs.30376 hypothetical protein
224967_at_HG-U133B		Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1287006	Consensus includes gb:W72338 /FEA=EST /DB_XREF=gi:1382943 /DB_XREF=est:zd62a08.s1 /CLONE=IMAGE:345206 /UG=Hs.23703 ESTs
224970_at_HG-U133B	NFIA	nuclear factor I/A	Consensus includes gb:AA419275 /FEA=EST /DB_XREF=gi:2078988 /DB_XREF=est:zv35e01.s1 /CLONE=IMAGE:755640 /UG=Hs.173933 nuclear factor IA
224975_at_HG-U133B	NFIA	nuclear factor I/A	Consensus includes gb:AB037860.1 /DEF=Homo sapiens mRNA for KIAA1439 protein, partial cds. /FEA=mRNA /GEN=KIAA1439 /PROD=KIAA1439 protein /DB_XREF=gi:7243275 /UG=Hs.173933 nuclear factor IA
224976_at_HG-U133B	NFIA	nuclear factor I/A	Consensus includes gb:R37335 /FEA=EST /DB_XREF=gi:794791 /DB_XREF=est:yf56105.s1 /CLONE=IMAGE:26230 /UG=Hs.173933 nuclear factor IA
224994_at_HG-U133B	CAMK2D	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	Consensus includes gb:AA777512 /FEA=EST /DB_XREF=gi:2836991 /DB_XREF=est:zj02g07.s1 /CLONE=IMAGE:449148 /UG=Hs.111460 Homo sapiens cDNA: FLJ21175 fis, clone COL10287, highly similar to AF071569 Homo sapiens multifunctional calcium/calmodulin-dependent protein kinase II delta2 isoform mRNA
225003_at_HG-U133B	MBC3205	hypothetical protein MBC3205	Consensus includes gb:BF343862 /FEA=EST /DB_XREF=gi:11291061 /DB_XREF=est:602015541F1 /CLONE=IMAGE:4150954 /UG=Hs.43621 ESTs
225010_at_HG-U133B			Consensus includes gb:AK024913.1 /DEF=Homo sapiens cDNA: FLJ21260 fis, clone COL01441. /FEA=mRNA /DB_XREF=gi:10437328 /UG=Hs.288862 Homo sapiens cDNA: FLJ21260 1s, clone COL01441
225014_at_HG-U133B		Homo sapiens, clone IMAGE:4247529,	Consensus includes gb:BF508958 /FEA=EST /DB_XREF=gi:11592256

		mRNA, partial cds	/DB_XREF=est:U1-H-B14-aos-g-12-o-U1.s1 /CLONE=IMAGE:30886038 /UG=Hs.235026 ESTs
			Consensus includes gb:BF797381 /FEA=EST /DB_XREF=gi:12102435 /DB_XREF=est:602257023F1 /CLONE=IMAGE:4340525 /UG=Hs.111460 Homo sapiens cDNA: FLJ21715 fis, clone COL10287, highly similar to AF071569
225019_at_HG-U133B	CAMK2D	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	Homo sapiens multifunctional calcium/calmodulin-dependent protein kinase II delta2 isoform mRNA
225025_at_HG-U133B	IGSF8	immunoglobulin superfamily, member 8	Consensus includes qb:BC004108.1 /DEF=Homo sapiens, clone IMAGE:3687782, mRNA, partial cds. /FEA=mRNA /PROD=Unknown (protein for IMAGE:3687782) /DB_XREF=gi:13278850 /UG=Hs.332012 Homo sapiens, clone IMAGE:3687782, mRNA, partial cds
225051_at_HG-U133B	FLJ10120	hypothetical protein FLJ10120	Consensus includes qb:AA522435 /FEA=EST /DB_XREF=gi:2264267 /DB_XREF=est:ng30g04.s1 /CLONE=IMAGE:936342 /UG=Hs.268024 Homo sapiens mRNA; cDNA DKFZp434C184 (from clone DKFZp434C184)
225055_at_HG-U133B	DKFZp434N2412	hypothetical protein FLJ10120	Consensus includes qb:AV735241 /FEA=EST /DB_XREF=gi:10852786 /DB_XREF=est:AV735241 /CLONE=cdAAJB04 /UG=Hs.190488 hypothetical protein FLJ10120
225064_at_HG-U133B	DKFZp434N2412	Hom sapiens mRNA; cDNA DKFZp434N2412 (from clone DKFZp434N2412)	Consensus includes qb:R60018 /FEA=EST /DB_XREF=gi:830713 /DB_XREF=est:yh12b01.s1 /CLONE=IMAGE:42905 /UG=Hs.250535 Homo sapiens mRNA; cDNA DKFZp434N2412 (from clone DKFZp434N2412)
225065_x_at_HG-U133B		Hom sapiens, clone IMAGE:4154219, mRNA, partial cds	Consensus includes qb:AI826279 /FEA=EST /DB_XREF=gi:5446950 associated protein 1 (negative cofactor 2 alpha)
225073_at_HG-U133B	HSPC232		Consensus includes qb:NM_016488.1 /DEF=Homo sapiens hypothetical protein (HSPC232), mRNA. /FEA=CDS /GEN=HSPC232 /PROD=hypothetical protein HSPC232 /DB_XREF=gi:7705526 /UG=Hs.281428 hypothetical protein /FL=gb:AF151040.1 qb:AF151066.1 qb:NM_016488.1
225080_at_HG-U133B	MYO1C	myosin IC	Consensus includes qb:BG251821 /FEA=EST /DB_XREF=gi:12761637

		/DB_XREF=est:602364436F1 /CLONE=IMAGE:4472864 /UG=Hs.297939
		cathepsin B
		Consensus includes gb:AA522888 /FEA=EST /DB_XREF=gi:2263600
		/DB_XREF=est:ni41b09.s1 /CLONE=IMAGE:979385 /UG=Hs.96513 ESTs,
		Highly similar to unnamed protein product H.sapiens
		Consensus includes gb:AW170571 /FEA=EST /DB_XREF=gi:6402096
		/DB_XREF=est:xn63f11.x1 /CLONE=IMAGE:2698413 /UG=Hs.96144 copine II
		Consensus includes gb:BF968578 /FEA=EST /DB_XREF=gi:12335793
		/DB_XREF=est:602271184F1 /CLONE=IMAGE:4359237 /UG=Hs.18585 ESTs,
		Moderately similar to ALU4_HUMAN ALU SUBFAMILY SB2 SEQUENCE
		CONTAMINATION WARNING ENTRY H.sapiens
		Consensus includes gb:AI457436 /FEA=EST /DB_XREF=gi:4310305
		/DB_XREF=est:tl73e06.x1 /CLONE=IMAGE:2152738 /UG=Hs.28959 ESTs
		Consensus includes gb:AI569503 /FEA=EST /DB_XREF=gi:4532877
		/DB_XREF=est:tn87h05.x1 /CLONE=IMAGE:2176569 /UG=Hs.105509 CTL2 gene
		gene
		Consensus includes gb:AI735261 /FEA=EST /DB_XREF=gi:5056785
		/DB_XREF=est:at0b05.x1 /CLONE=IMAGE:2354505 /UG=Hs.125031
		cholineethanolaminephosphotransferase
		Consensus includes gb:T97323 /FEA=EST /DB_XREF=gi:746668
		/DB_XREF=est:y57b07.s1 /CLONE=IMAGE:121813 /UG=Hs.278894 KIAA1482 protein
		stromal interaction molecule 2
		Consensus includes gb:N48266 /FEA=EST /DB_XREF=gi:1189432
		/DB_XREF=est:y205b10.s1 /CLONE=IMAGE:282139 /UG=Hs.278894 KIAA1482
		protein
		Consensus includes gb:AL355708.1 /DEF=Homo sapiens mRNA full length
		insert cDNA clone EUROIMAGE 44260. /FEA=mRNA /DB_XREF=gi:7799100
		/UG=Hs.284169 Homo sapiens mRNA full length insert cDNA clone
		225270_at_HG-U133B

			EUROIMAGE 44260 Consensus includes gb:AL525780 /FEA=EST /DB_XREF=gi:12789273 /DB_XREF=est:AL525780 /CLONE=CS0DC013YG11 (3 prime) /UG=Hs.9070 Homo sapiens mRNA; cDNA DKFZp434A109 (from clone DKFZp434A109)
225277_at_HG-U133B			Consensus includes gb:AK025615.1 /DEF=Homo sapiens cDNA: FLJ21962 fis, clone HEP05564. /FEA=mRNA /DB_XREF=gi:10438186 /UG=Hs.7567 Homo sapiens cDNA: FLJ21962 fis, clone HEP05564
225285_at_HG-U133B			Consensus includes gb:AI826268 /FEA=EST /DB_XREF=gi:5446939 /DB_XREF=est:wk33d06.x1 /CLONE=IMAGE:2417195 /UG=Hs.27769 ESTs, Weakly similar to MCAT_HUMAN MITOCHONDRIAL CARNITINE/ACYLCARNITINE CARRIER PROTEIN H.sapiens
225305_at_HG-U133B			Consensus includes gb:AI826268 /FEA=EST /DB_XREF=gi:5446939 /DB_XREF=est:wk33d06.x1 /CLONE=IMAGE:2417195 /UG=Hs.27769 ESTs, Weakly similar to MCAT_HUMAN MITOCHONDRIAL CARNITINE/ACYLCARNITINE CARRIER PROTEIN H.sapiens
225306_s_at_HG-U133B			Consensus includes gb:BG291649 /FEA=EST /DB_XREF=gi:13049586 /DB_XREF=est:602385778F1 /CLONE=IMAGE:4514827 /UG=Hs.95835 ESTs, Weakly similar to unnamed protein product H.sapiens
225314_at_HG-U133B			Consensus includes gb:AB037732.1 /DEF=Homo sapiens mRNA for KIAA1311 protein, partial cds. /FEA=mRNA /GEN=KIAA1311 /PROD=KIAA1311 protein /DB_XREF=gi:7242976 /UG=Hs.61441 KIAA1311 protein
225326_at_HG-U133B	KIAA1311	KIAA1311 protein	Consensus includes gb:AB037791.1 /DEF=Homo sapiens mRNA for KIAA1370 protein, partial cds. /FEA=mRNA /GEN=KIAA1370 /PROD=KIAA1370 protein /DB_XREF=gi:5432319 protein FLJ10980
225327_at_HG-U133B	FLJ10980	hypothetical protein FLJ10980	Consensus includes gb:AL044092 /FEA=EST /DB_XREF=gi:5432319
225330_at_HG-U133B		Homo sapiens, clone MGC:18216 IMAGE:4156235, mRNA, complete cds	/DB_XREF=est:DKFZp434M1328_s1 /CLONE=DKFZp434M1328

			/UG=Hs.293960 ESTs
			Consensus includes gb:BF941088 /FEA=EST /DB_XREF=gi:12358408 /DB_XREF=est:7d92e07.x1 /CLONE=IMAGE:3280596 /UG=Hs.170307 Ral
225331_at_HG-U133B	ESTs		guanine nucleotide exchange factor RaIGPS1A
			Consensus includes gb:AL035689 /DEF=Human DNA sequence from clone RP1-187111 on chromosome 6q11.1-22.33. Contains the gene for a novel protein similar to <i>S. pombe</i> and <i>S. cerevisiae</i> predicted proteins, the gene for a novel protein similar to protein kinase C inhibitors, the 3' end of... /FEA=mRNA_3 /DB_XREF=gi:8218045 /UG=Hs.6966 Human DNA sequence from clone RP1-187111 on chromosome 6q11.1-22.33. Contains the gene for a novel protein similar to <i>S. pombe</i> and <i>S. cerevisiae</i> predicted proteins, the gene for a novel protein similar to protein kinase C inhibitors, the 3' end of the gene
225344_at_HG-U133B			Consensus includes gb:AI559701 /FEA=EST /DB_XREF=gi:4509906 /DB_XREF=est:tg51e03.x1 /CLONE=IMAGE:2212348 /UG=Hs.91684 Homo sapiens mRNA; cDNA DKFZp6671103 (from clone DKFZp6671103)
225386_s_at_HG-U133B	LOC92906		hypothetical protein BC008217
225406_at_HG-U133B	TSG		twisted gastrulation
225426_at_HG-U133B	ESTs		gastrulation
225452_at_HG-U133B	PPARBP		Consensus includes gb:AW195360 /FEA=EST /DB_XREF=gi:6474436 /DB_XREF=est:xn37d08.x1 /CLONE=IMAGE:2695887 /UG=Hs.7256 integral inner nuclear membrane protein
225469_at_HG-U133B	KRAS2		Consensus includes gb:AI423072 /FEA=EST /DB_XREF=gi:4269003 /DB_XREF=est:tf18b02.x1 /CLONE=IMAGE:2096523 /UG=Hs.10130 ESTs
225510_at_HG-U133B	CHN1		v-Ki-ras2 Kirsten rat sarcoma 2 viral oncogene homolog Kirsten rat sarcoma 2 viral oncogene homolog Consensus includes gb:BG033561 /FEA=EST /DB_XREF=gi:12425979

		/DB_XREF=est:602302173F1 /CLONE=IMAGE:4403610 /UG=Hs.22660 Homo sapiens cDNA FLJ11658 fis, clone HEMBA1004577
225512_at_HG-U133B	Homo sapiens cDNA FLJ31131 fis, clone IMR32200935	Consensus includes gb:AI005245 /FEA=EST /DB_XREF=gi:3214755 /DB_XREF=est:ol98h02.x1 /CLONE=IMAGE:1624851 /UG=Hs.23653 ESTs
225547_at_HG-U133B	Homo sapiens cDNA FLJ32554 fis, clone SPLEM1000106	Consensus includes gb:BG169443 /FEA=EST /DB_XREF=gi:12676146 /DB_XREF=est:602321129F1 /CLONE=IMAGE:4424526 /UG=Hs.292815 ESTs
225553_at_HG-U133B	Homo sapiens cDNA FLJ12874 fis, clone NT2RP2003769	Consensus includes gb:AL042817 /FEA=EST /DB_XREF=gi:5935564 /DB_XREF=est:DKFZp434F1922_s1 /CLONE=DKFZp434F1922 /UG=Hs.56847 Homo sapiens cDNA FLJ12874 fis, clone NT2RP2003769
225563_at_HG-U133B	ESTs	Consensus includes gb:AI970788 /FEA=EST /DB_XREF=gi:5767614 /DB_XREF=est:wr19g02.x1 /CLONE=IMAGE:2482034 /UG=Hs.30348 ESTs
225565_at_HG-U133B	ESTs, Weakly similar to SFRB_HUMAN SPlicing Factor Arginine/Serine-Rich 11 [H.sapiens]	Consensus includes gb:AA769455 /FEA=EST /DB_XREF=gi:2820693 /DB_XREF=est:zr41g11.s1 /CLONE=IMAGE:1290404 /UG=Hs.22315 ESTs
2255692_at_HG-U133B	NRM	Consensus includes gb:D81046 /FEA=EST /DB_XREF=gi:1178925 /DB_XREF=est:HUM127A03A /CLONE=GEN-127A03 /UG=Hs.57222 nurim (nuclear envelope membrane protein)
225624_at_HG-U133B		Consensus includes gb:AL044019 /FEA=EST /DB_XREF=gi:5432247 /DB_XREF=est:DKFZp434J1128_s1 /CLONE=DKFZp434J1128 /UG=Hs.194478 Homo sapiens mRNA, cDNA DKFZp434O1572 (from clone DKFZp434O1572)
225629_s_at_HG-U133B	KIAA1538	Consensus includes gb:AI669498 /FEA=EST /DB_XREF=gi:4834272 /DB_XREF=est:wb88e05.x1 /CLONE=IMAGE:2312768 /UG=Hs.35096 KIAA1538 protein
225635_s_at_HG-U133B		Consensus includes gb:BG535378 /FEA=EST /DB_XREF=gi:13526923 /DB_XREF=est:602563038F1 /CLONE=IMAGE:4688000 /UG=Hs.94109 Homo sapiens cDNA FLJ13634 fis, clone PLACE1011133
225640_at_HG-U133B		Consensus includes gb:AA875998 /FEA=EST /DB_XREF=gi:2984839 /DB_XREF=est:ob93b09.s1 /CLONE=IMAGE:1338905 /UG=Hs.94109 Homo

		consensus includes gb:AV755269 /FEA=EST /DB_XREF=gi:10913117 /DB_XREF=est:AV755269 /CLONE=BMFARD01 /UG=Hs.105664 hypothetical protein FLJ22294
225653_at_HG-U133B	Homo sapiens, clone IMAGE:3448872, mRNA, partial cds	Consensus includes gb:W92748 /FEA=EST /DB_XREF=gi:1421920 /DB_XREF=est:zd92h03.s1 /CLONE=IMAGE:356981 /UG=Hs.263395 sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A
225660_at_HG-U133B	SEMA6A	Consensus includes gb:AL384017 /FEA=EST /DB_XREF=gi:4196798 /DB_XREF=est:te35h10.x1 /CLONE=IMAGE:2088739 /UG=Hs.18955 Homo sapiens cDNA FLJ20667 fis, clone KIAA596
225670_at_HG-U133B		Consensus includes gb:AC006042 /DEF=Homo sapiens BAC clone RP11-505D17 from 7p22-p21 /FEA=CDS_2 /DB_XREF=gi:4508120 /UG=Hs.18987 Homo sapiens BAC clone RP11-505D17 from 7p22-p21
225700_at_HG-U133B		Consensus includes gb:AV727346 /FEA=EST /DB_XREF=gi:10836767 /DB_XREF=est:AV727346 /CLONE=HTCACCC11 /UG=Hs.22410 ESTs
225713_at_HG-U133B	KIAA1898	Consensus includes gb:AL110131.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564H122 (from clone DKFZp564H122). /FEA=mRNA /DB_XREF=gi:5817026 /UG=Hs.28783 KIAA1223 protein
225735_at_HG-U133B		Consensus includes gb:BF203664 /CLONE=IMAGE:4098670 /UG=Hs.181073 ESTs /DB_XREF=est:601865696F1 /CLONE=IMAGE:4098670 /UG=Hs.181073 ESTs
225772_s_at_HG-U133B	MGC14288	Consensus includes gb:AV205585 /FEA=EST /DB_XREF=gi:6505059 /DB_XREF=est:U1-H-B1-af1-a-08-0-UI.s1 /CLONE=IMAGE:2722479 /UG=Hs.20340 ESTs, Moderately similar to ALU1_HUMAN_ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
225776_at_HG-U133B	BAZ2A	ESTs, Moderately similar to ZN91_HUMAN_ZINC FINGER PROTEIN domain, 2A
225782_at_HG-U133B		Consensus includes gb:AW027333 /FEA=EST /DB_XREF=gi:5086089 /DB_XREF=est:wt73d02.x1 /CLONE=IMAGE:2513091 /UG=Hs.35092 ESTs

225790_at_HG-U133B	ESTs, Moderately similar to ZN91_HUMAN ZINC FINGER PROTEIN 91 [H.sapiens]	Consensus includes gb:AL048386 /FEA=EST /DB_XREF=gi:4727526 /DB_XREF=est:DKFZp586F1624_s1 /CLONE=DKFZp586F1624 /UG=Hs.35092 ESTs
	Homo sapiens cDNA: FLJ23597 fis, clone LNG15281	Consensus includes gb:AA618420 /FEA=EST /DB_XREF=gi:2505625 /DB_XREF=est:n03a10.s1 /CLONE=IMAGE:928314 /UG=Hs.299254 Homo sapiens cDNA: FLJ23597 fis, clone LNG15281
225792_at_HG-U133B		Consensus includes gb:AW006123 /FEA=EST /DB_XREF=gi:5854901 /DB_XREF=est:zw92f05.x1 /CLONE=IMAGE:2566305 /UG=Hs.61661 ESTs, weakly similar to AF174605_1 F-box protein Fbx25 H.sapiens
225803_at_HG-U133B	FBXO32	Consensus includes gb:BE044480 /FEA=EST /DB_XREF=gi:8361533 /DB_XREF=est:ha46b12.x1 /CLONE=IMAGE:3040415 /UG=Hs.75410 heat shock 70kD protein 5 (glucose-regulated protein, 78kd)
225804_at_HG-U133B		Consensus includes gb:BF75280 /FEA=EST /DB_XREF=gi:11546107 /DB_XREF=est:7q19n05.x1 /CLONE=IMAGE:3698936 /UG=Hs.285833 Homo sapiens cDNA: FLJ22135 fis, clone HEP20858
225889_at_HG-U133B		Consensus includes gb:AI709406 /FEA=EST /DB_XREF=gi:4999182 /DB_XREF=est:as37d05.x1 /CLONE=IMAGE:2319369 /UG=Hs.330716 Homo sapiens cDNA FLJ14368 fis, clone HEMBA1001122
225897_at_HG-U133B		ESTs, Weakly similar to SFR4_HUMAN SPLICING FACTOR, ARGININE/SERINE-RICH 4 [H.sapiens] Consensus includes gb:AW194716 /FEA=EST /DB_XREF=gi:6473610 /DB_XREF=est:xn43c08.x1 /CLONE=IMAGE:2686462 /UG=Hs.35274 ESTs
225902_at_HG-U133B		Consensus includes gb:AA766897 /FEA=EST /DB_XREF=gi:2818135 /DB_XREF=est:nz80c09.s1 /CLONE=IMAGE:1301776 /UG=Hs.122444 ESTs
225917_at_HG-U133B	DKFZp762B226	hypothetical protein DKFZp762B226 mitogen-activated protein kinase kinase 1
225927_at_HG-U133B	MAP3K1	Consensus includes gb:BF432625 /FEA=EST /DB_XREF=gi:2287913 /DB_XREF=est:n189d12.s1 /CLONE=IMAGE:984023 /UG=Hs.170610 ESTs
225959_s_at_HG-U133B	NIN283	Consensus includes gb:BF432625 /FEA=EST /DB_XREF=gi:11444777 /DB_XREF=est:nac58b01.x1 /CLONE=IMAGE:3406417 /UG=Hs.49657 Homo sapiens mRNA; cDNA DKFZp547N084 (from clone DKFZp547N084) nerve injury gene 283

226005_at_HG-U133B	Homo sapiens, clone IMAGE:4431242, mRNA	Consensus includes gb:BG170762 /FEA=EST /DB_XREF=gi:12677465 /DB_XREF=est:6022323878F1 /CLONE=IMAGE:4426914 /UG=Hs.296273 ESTs
	hepatocellular carcinoma-associated protein HCA4	Consensus includes gb:AA627644 /FEA=EST /DB_XREF=gi:2539739 /DB_XREF=est:nq51d02.s1 /CLONE=IMAGE:1147395 /UG=Hs.94011 ESTs, Weakly similar to MGb4_HUMAN MELANOMA-ASSOCIATED ANTIGEN B4 H.sapiens
226008_at_HG-U133B	Homo sapiens cDNA FLJ13900 fis, clone THYRO1001746	Consensus includes gb:AW451452 /FEA=EST /DB_XREF=gi:6992228 /DB_XREF=est:U1-H-B13-all-d-02-0-U1.s1 /CLONE=IMAGE:2736818 /UG=Hs.89474 ADP-ribosylation factor 6
226013_at_HG-U133B	eukaryotic translation initiation factor 3, subunit 5 (epsilon, 47kD)	Consensus includes gb:BF115977 /FEA=EST /DB_XREF=gi:10985453 /DB_XREF=est:7n7ng02.x1 /CLONE=IMAGE:3570603 /UG=Hs.7811 eukaryotic translation initiation factor 3, subunit 5 (epsilon, 47kD)
226014_at_HG-U133B	likely ortholog of rat activator of G-protein signaling 3	Consensus includes gb:AI242661 /FEA=EST /DB_XREF=gi:3838058 /DB_XREF=est:q18a10.x1 /CLONE=IMAGE:1856826 /UG=Hs.239370 DKFZP727/051 protein
226043_at_HG-U133B	putative endoplasmic reticulum multispan transmembrane protein	Consensus includes gb:BF475369 /FEA=EST /DB_XREF=gi:11546196 /DB_XREF=est:nna17f06.x1 /CLONE=IMAGE:3255298 /UG=Hs.324473 mitogen-activated protein kinase 1
226060_at_HG-U133B	Homo sapiens PP3781 mRNA, complete cds	Consensus includes gb:AA481141 /FEA=EST /DB_XREF=gi:2210693 /DB_XREF=est:aa34e11.s1 /CLONE=IMAGE:815180 /UG=Hs.4248 vav 2 oncogene
226063_at_HG-U133B		Consensus includes gb:AL11763.1 /DEF=homo sapiens mRNA; cDNA DKFZp586C0224 (from clone DKFZp586C0224). /FEA=mRNA /DB_XREF=gi:5912245 /UG=Hs.5884 Homo sapiens mRNA; cDNA DKFZp586C0224 (from clone DKFZp586C0224)
226066_at_HG-U133B		Consensus includes gb:AI093546 /FEA=EST /DB_XREF=gi:3432522 /DB_XREF=est:qb08h06.x1 /CLONE=IMAGE:1695707 /UG=Hs.24379 MUM2 protein
226101_at_HG-U133B	ESTs	

226120_at_HG-U133B	LOC123016	hypothetical protein BC001563	Consensus includes gb:AW293939 /FEA=EST /DB_XREF=gi:6700575 /DB_XREF=est:U1-H-BW0-alk-b-11-0-U1.s1 /CLONE=IMAGE:2729444 /UG=Hs.55158 ESTs, Weakly similar to weak similarity to TPR domains C.elegans
226122_at_HG-U133B			Consensus includes gb:AL035086 /DEF=Human DNA sequence from clone 44A20 on chromosome 6q23.1-24.3. Contains a gene for a novel protein similar to MTHFD1 (methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase... /FEA=mRNA_2 /DB_XREF=gi:4741478 /UG=Hs.51965 KIAA1209 protein
226147_s_at_HG-U133B		Homo sapiens cDNA: FLJ22667 fis, clone HS108385	Consensus includes gb:AA838075 /FEA=EST /DB_XREF=gi:2913732 /DB_XREF=est:oe93h05.s1 /CLONE=IMAGE:1419225 /UG=Hs.205126 Homo sapiens cDNA: FLJ22667 fis, clone HS108385
226156_at_HG-U133B	AKT2	v-akt murine thymoma viral oncogene homolog 2	Consensus includes gb:BE866854 /FEA=EST /DB_XREF=gi:10315630 /DB_XREF=est:601442669F1 /CLONE=IMAGE:3847000 /UG=Hs.1822778 calmodulin 2 (phosphorylase kinase, delta)
226165_at_HG-U133B	E2F5	E2F transcription factor 5, p130-binding	Consensus includes gb:BF674436 /FEA=EST /DB_XREF=gi:11948331 /DB_XREF=est:602137204F1 /CLONE=IMAGE:4273584 /UG=Hs.286124 CD24 antigen (small cell lung carcinoma cluster 4 antigen)
226188_at_HG-U133B			Consensus includes gb:AK025603.1 /DEF=Homo sapiens cDNA: FLJ21950 fis, clone HEP0499. /FEA=mRNA /DB_XREF=gi:10438711 /UG=Hs.7149 Homo sapiens cDNA: FLJ21950 fis, clone HEP04949
226190_at_HG-U133B		ESTs, Moderately similar to I38022 hypothetical protein [H.sapiens]	Consensus includes gb:BG029496 /FEA=EST /DB_XREF=gi:12418592 /DB_XREF=est:602297045F1 /CLONE=IMAGE:4391507 /UG=Hs.57776 ESTs
226210_s_at_HG-U133B		ESTs, Moderately similar to hypothetical protein FLJ20489 [Homo sapiens] [H.sapiens]	Consensus includes gb:AI291123 /FEA=EST /DB_XREF=gi:3933897 /DB_XREF=est:qm15e11.x1 /CLONE=IMAGE:1881932 /UG=Hs.279789 histone deacetylase 3
226236_at_HG-U133B		ESTs, Weakly similar to A42442 integrin	Consensus includes gb:BF675218 /FEA=EST /DB_XREF=gi:11949113

	beta-1 chain, splice form beta-1-S [H.sapiens]	/DB_XREF=est602138154F1 /CLONE=IMAGE:4274820 /UG=Hs.3709 16w molecular mass ubiquitine-binding protein (9.5kD)
	ESTs, Highly similar to AF161403 1 HSPC285 [H.sapiens]	Consensus includes gb:BF059395 /FEA=EST /DB_XREF=gi:10813213 /DB_XREF=est7k59a05.x1 /CLONE=IMAGE:3479696 /UG=Hs.293815 Homo sapiens HSPC285 mRNA, partial cds
226244_at_HG-U133B	Homo sapiens mRNA, cDNA DKFZp434E1515 (from clone DKFZp434E1515)	Consensus includes gb:AI346026 /FEA=EST /DB_XREF=gi:4083232 /DB_XREF=est:qp48b01.x1 /CLONE=IMAGE:1926217 /UG=Hs.287830 Homo sapiens mRNA; cDNA DKFZp434E1515 (from, clone DKFZp434E1515)
226247_at_HG-U133B	ESTs	Consensus includes gb:AU144961 /FEA=EST /DB_XREF=gi:11006482 /DB_XREF=est:AU144961 /CLONE=HEMBA1003463 /UG=Hs.104627 Homo sapiens cDNA FLJ10158 fis, clone HEMBA1003463
226250_at_HG-U133B	ESTs	Consensus includes gb:AA058578 /FEA=EST /DB_XREF=gi:1551385 /DB_XREF=est:zf55h02.s1 /CLONE=IMAGE:380883 /UG=Hs.104627 Homo sapiens cDNA FLJ10158 fis, clone HEMBA1003463
226252_at_HG-U133B	ESTs, Weakly similar to T08680 hypothetical protein DKFZp564P0622.1 [H.sapiens]	Consensus includes gb:BG031897 /FEA=EST /DB_XREF=gi:12422649 /DB_XREF=est:602300785F1 /CLONE=IMAGE:4402293 /UG=Hs.12296 ESTs, Weakly similar to T08680 hypothetical protein DKFZp564P0622.1 Homo sapiens
226258_at_HG-U133B	protein kinase PKNbeta	Consensus includes gb:AB046783.1 /DEF=Homo sapiens mRNA for KIAA1563 protein, partial cds. /FEA=mRNA /GEN=KIAA1563 /PROD=KIAA1563 protein /DB_XREF=gi:10047190 /UG=Hs.27669 KIAA1563 protein
226291_at_HG-U133B	ALS2	Consensus includes gb:NM_013355.1 /DEF=Homo sapiens protein kinase PKNbeta (pknbeta), mRNA. /FEA=CDS /GEN=pknbeta /PROD=protein kinase PKNbeta /DB_XREF=gi:7019488 /UG=Hs.44101 protein kinase PKNbeta /FL=gb:AB019692.1 gb:NM_013355.1
226299_at_HG-U133B	pknbeta	Consensus includes gb:AV729072 /FEA=EST /DB_XREF=gi:10838493 /DB_XREF=est:AV729072 /CLONE=HTCBBG11 /UG=Hs.43627 SRY (sex determining region Y)-box 22
226301_at_HG-U133B	dJ55C23.6	dJ55C23.6 gene

226324_s_at_HG-U133B	SLB	selective LIM binding factor, rat homolog Homo sapiens cDNA FLJ31063 fis, clone HSYRA2001105	Consensus includes gb:AI798098 /FEA=EST /DB_XREF=gi:5363581 /DB_XREF=est:wh81c10.x1 /CLONE=IMAGE:2387154 /UG=Hs.11356 ESTs
226326_at_HG-U133B		Homo sapiens mRNA; cDNA DKFZp564N1063 (from clone DKFZp564N1063)	Consensus includes gb:AW593244 /FEA=EST /DB_XREF=gi:7280502 /DB_XREF=est:hg11e10.x1 /CLONE=IMAGE:2945322 /UG=Hs.236443 Homo sapiens mRNA; cDNA DKFZp564N1063 (from clone DKFZp564N1063)
226342_at_HG-U133B		HTPAP protein	Consensus includes gb:BE858787 /FEA=EST /DB_XREF=gi:10374184 /DB_XREF=est:795603.x1 /CLONE=IMAGE:3304709 /UG=Hs.8841 ESTs
226384_at_HG-U133B	HTPAP		Consensus includes gb:AA905942 /FEA=EST /DB_XREF=gi:3041065 /DB_XREF=est:qj83b12.s1 /CLONE=IMAGE:1504895 /UG=Hs.153053 CD37 antigen
226408_at_HG-U133B	TEAD2	TEA domain family member 2 Homo sapiens mRNA; cDNA DKFZp434F053 (from clone DKFZp434F053)	Consensus includes gb:AU145309 /FEA=EST /DB_XREF=gi:11006830 /DB_XREF=est:AU145309 /CLONE=HEMBA1004460 /UG=Hs.301152 Homo sapiens mRNA; cDNA DKFZp434F053 (from clone DKFZp434F053)
226435_at_HG-U133B			Consensus includes gb:AK025100.1 /DEF=Homo sapiens cDNA: FLJ21447 fis, clone COL04468. /FEA=mRNA /DB_XREF=gi:10437548 /UG=Hs.44241 Homo sapiens cDNA: FLJ21447 fis, clone COL04468.
226438_at_HG-U133B			Consensus includes gb:AI130705 /FEA=EST /DB_XREF=gi:3600721 /CLONE=qc12d05.x1 /UG=Hs.38516 ESTs, /DB_XREF=est:qc12d05.x1 Weekly similar to A46302 PTB-associated splicing factor, long form H.sapiens
226448_at_HG-U133B		Homo sapiens, clone MGC:15887 IMAGE:3530481, mRNA, complete cds	Consensus includes gb:AV703054 /FEA=EST /DB_XREF=gi:10719384 /DB_XREF=est:AV703054 /CLONE=ADBCMB05 /UG=Hs.98401 Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 926491
226450_at_HG-U133B			Consensus includes gb:BF508604 /FEA=EST /DB_XREF=gi:11591902
226454_at_HG-U133B	LOC92979	hypothetical protein BC009489	

		/DB_XREF=est:U1-H-BI4-aoo-f-08-0-Ui.s1 /CLONE=IMAGE:3085598 /UG=Hs.65377 ESTs, Moderately similar to KIAA1399 protein H.sapiens Consensus includes gb:BG291039 /FEA=EST /DB_XREF=gi:13048607
		Hom sapiens, Similar to hypothetical protein FLJ22611, clone MGC24716 IMAGE:4277726, mRNA, complete cds
226496_at_HG-U133B	ESTs	/DB_XREF=est:602386841F1 /CLONE=IMAGE:4515730 /UG=Hs.27774 ESTs, Highly similar to AF161349_1 HSPC086 H.sapiens Consensus includes gb:W72331 /FEA=EST /DB_XREF=gi:1383086 /DB_XREF=est:zd62c11.s1 /CLONE=IMAGE:345236 /UG=Hs.21812 ESTs
226499_at_HG-U133B		Consensus includes gb:AI042019 /FEA=EST /DB_XREF=gi:3281213 /DB_XREF=est:oy34h10.x1 /CLONE=IMAGE:1667779 /UG=Hs.25328 ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens -
226508_at_HG-U133B		Consensus includes gb:AL530596 /FEA=EST /DB_XREF=gi:12794089 /DB_XREF=est:AL530596 /CLONE=CS0DD008YD03 (5 prime) /UG=Hs.55148 ESTs
226531_at_HG-U133B	FLJ14466	hypothetical protein FLJ14466 mannosidase, alpha, class 2A, member 1 Consensus includes gb:AV700323 /FEA=EST /DB_XREF=gi:10302294 /DB_XREF=est:AV700323 /CLONE=GKCBSC12 /UG=Hs.63368 ESTs
226538_at_HG-U133B	MAN2A1	Consensus includes gb:AL110152.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586E1624 (from clone DKFZp586E1624). /FEA=mRNA /DB_XREF=gi:5817054 /UG=Hs.94030 Homo sapiens mRNA; cDNA DKFZp586E1624 (from clone DKFZp586E1624)
226545_at_HG-U133B	ESTs	Consensus includes gb:BG477064 /FEA=EST /DB_XREF=gi:13409343 /DB_XREF=est:602324421F1 /CLONE=IMAGE:4642660 /UG=Hs.90286 ESTs
226546_at_HG-U133B	ESTs	- Consensus includes gb:AI672159 /FEA=EST /DB_XREF=gi:4851890 /DB_XREF=est:wa04c04.x1 /CLONE=IMAGE:2297094 /UG=Hs.91389 ESTs
226550_at_HG-U133B		Consensus includes gb:AA576959 /FEA=EST /DB_XREF=gi:2354433 /DB_XREF=est:nm82d05.s1 /CLONE=IMAGE:1074729 /UG=Hs.13234 ESTs
226560_at_HG-U133B	ESTs	Consensus includes gb:AA910497 /FEA=EST /DB_XREF=gi:3049787 /DB_XREF=est:ok44g07.s1 /CLONE=IMAGE:1516860 /UG=Hs.241334 ESTs
226590_at_HG-U133B		Homo sapiens mRNA full length insert cDNA clone EUROMAGE 1517766

226607_at_HG-U133B	L3MBTL	I(3)mbt-like (Drosophila)	Consensus includes gb:AI498144 /FEA=EST /DB_XREF=gi:4390126 /DB_XREF=est:tm90001.x1 /CLONE=IMAGE:2165376 /UG=Hs.323795 ESTs
	TGFBR3	transforming growth factor, beta receptor III (betaglycan, 300kD)	Consensus includes gb:AW193688 /FEA=EST /DB_XREF=gi:6472397 /DB_XREF=est:xm29e06.x1 /CLONE=IMAGE:2685634 /UG=Hs.79059 transforming growth factor, beta receptor III (betaglycan, 300kD)
226625_at_HG-U133B		Homo sapiens cDNA FLJ12292 fis, clone MAMMA1001812	Consensus includes gb:AA776892 /FEA=EST /DB_XREF=gi:2836223 /DB_XREF=est:ac40c01.s1 /CLONE=IMAGE:858912 /UG=Hs.98613 Homo sapiens cDNA FLJ12292 fis, clone MAMMA1001812
226634_at_HG-U133B		Homo sapiens cDNA FLJ13634 fis, clone PLACE1011133	Consensus includes gb:BG170478 /FEA=EST /DB_XREF=gi:12677181 /DB_XREF=est:602322848F1 /CLONE=IMAGE:4426211 /UG=Hs.94109 Homo sapiens cDNA FLJ13634 fis, clone PLACE1011133
226635_at_HG-U133B		Homo sapiens cDNA FLJ11570 fis, clone HEMBA1003309	Consensus includes gb:AU157224 /FEA=EST /DB_XREF=gi:11018745 /DB_XREF=est:AU157224 /CLONE=PLACE1006780 /UG=Hs.11571 Homo sapiens cDNA FLJ11570 fis, clone HEMBA1003309
226641_at_HG-U133B	KLF2	Kruppel-like factor 2 (lung)	Consensus includes gb:AI831932 /FEA=EST /DB_XREF=gi:5452603 /DB_XREF=est:wh89b08.x1 /CLONE=IMAGE:2387895 /UG=Hs.107740 Kruppel-like factor 2 (lung)
226646_at_HG-U133B		Homo sapiens cDNA FLJ31090 fis, clone IMR321000102	Consensus includes gb:AI247881 /FEA=EST /DB_XREF=gi:3843278 /DB_XREF=est:oh58d08.x1 /CLONE=IMAGE:1848879 /UG=Hs.10198 ESTs
226713_at_HG-U133B	LOC129642	hypothetical protein BC016005	Consensus includes gb:W163676 /FEA=EST /DB_XREF=gi:1371257 /DB_XREF=est:zd30b03.s1 /CLONE=IMAGE:342125 /UG=Hs.15641 ESTs
226726_at_HG-U133B		Homo sapiens cDNA: FLJ23586 fis, clone LNG14376	Consensus includes gb:AW242220 /FEA=EST /DB_XREF=gi:6575974 /DB_XREF=est:x023g03.x1 /CLONE=IMAGE:2704852 /UG=Hs.306915 Homo sapiens cDNA: FLJ23586 fis, clone LNG14376
226734_at_HG-U133B		Homo sapiens cytomegalovirus partial fusion receptor mRNA, partial cds	Consensus includes gb:AI23899 /FEA=EST /DB_XREF=gi:3835296 /DB_XREF=est:qh38a02.x1 /CLONE=IMAGE:1846970 /UG=Hs.25119 ESTs
226735_at_HG-U133B		hypothetical protein LOC51234	Consensus includes gb:N21320 /FEA=EST /DB_XREF=gi:1126490 /DB_XREF=est:estyx53h07.s1 /CLONE=IMAGE:265501 /UG=Hs.250905
226741_at_HG-U133B			

			hypothetical protein
			Consensus includes gb:AW003459 /FEA=EST /DB_XREF=gi:5850364 /DB_XREF=est:wq66a10.x1 /CLONE=IMAGE:2476218 /UG=Hs.235709 Homo sapiens mRNA; cDNA DKFZP667B0711 (from clone DKFZP667B0711)
226743_at_HG-U133B	Homo sapiens mRNA for FLJ00257 protein		Consensus includes gb:AW193693 /FEA=EST /DB_XREF=gi:6472392 /DB_XREF=est:xml29d12.x1 /CLONE=IMAGE:2685623 /UG=Hs.26358
226751_at_HG-U133B	DKFZP566K1924	DKFZP566K1924 protein	DKFZP566K1924 protein
			Consensus includes gb:AI762154 /FEA=EST /DB_XREF=gi:5177821 /DB_XREF=est:w90e02.x1 /CLONE=IMAGE:2388026 /UG=Hs.54982 Homo sapiens cDNA FLJ14014 fis, clone HEMBA1000290
226783_at_HG-U133B			Consensus includes gb:AW007739 /FEA=EST /DB_XREF=gi:5856517 /DB_XREF=est:w168e08.x1 /CLONE=IMAGE:2512646 /UG=Hs.118913 ESTs
226795_at_HG-U133B			Consensus includes gb:AT64884 /FEA=EST /DB_XREF=gi:673929 /DB_XREF=est:yd10b06.s1 /CLONE=IMAGE:66707 /UG=Hs.288581 Homo sapiens cDNA FLJ14296 fis, clone PLACE1008455
226818_at_HG-U133B	Homo sapiens mRNA for FLJ00239 protein		Consensus includes gb:BF590697 /FEA=EST /DB_XREF=gi:11682943 /DB_XREF=est:7h39dd02.x1 /CLONE=IMAGE:3318339 /UG=Hs.288581 Homo sapiens cDNA FLJ14296 fis, clone PLACE1008455
226841_at_HG-U133B	Homo sapiens mRNA for FLJ00239 protein		Consensus includes gb:AI375115 /FEA=EST /DB_XREF=gi:4175105 /DB_XREF=est:tc09610.x1 /CLONE=IMAGE:2063370 /UG=Hs.293849 ESTs
226844_at_HG-U133B		ESTs	Consensus includes gb:AI961778 /FEA=EST /DB_XREF=gi:5754491 /DB_XREF=est:w167d10.x1 /CLONE=IMAGE:2512531 /UG=Hs.124707 ESTs
226876_at_HG-U133B	Homo sapiens, clone IMAGE:4564684, mRNA, partial cds		Consensus includes gb:AL581873 /FEA=EST /DB_XREF=gi:12949303 /DB_XREF=est:AL581873 /CLONE=CS0DG006YK17 (3 prime) /UG=Hs.11135 major histocompatibility complex, class II, DN alpha
	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1964662		Consensus includes gb:BG036514 /FEA=EST /DB_XREF=gi:12431757 /DB_XREF=est:602323471F1 /CLONE=IMAGE:4428089 /UG=Hs.187932 ESTs
226878_at_HG-U133B	Homo sapiens, clone IMAGE:4554684, mRNA, partial cds		Consensus includes gb:BG492359 /FEA=EST /DB_XREF=gi:13453871 ESTs
226905_at_HG-U133B			
226936_at_HG-U133B			

			/DB_XREF=est:602536279F1 /CLONE=IMAGE:4655418 /UG=Hs35962 ESTs
226939_at_HG-U133B	ESTs	Homo sapiens mRNA; cDNA DKFZp434P228 (from clone DKFZp434P228)	Consensus includes gb:AI202327 /FEA=EST /DB_XREF=gi:3754933 /DB_XREF=est:qs66a07.x1 /CLONE=IMAGE:1943028 /UG=Hs.44833 ESTs
226989_at_HG-U133B		ESTs, Weakly similar to Z195_HUMAN ZINC FINGER PROTEIN 195 [H.sapiens]	Consensus includes gb:BE855765 /FEA=EST /DB_XREF=gi:10367981 /DB_XREF=est:7g12d02.x1 /CLONE=IMAGE:3306243 /UG=Hs.108972 Homo sapiens mRNA; cDNA DKFZp434P228 (from clone DKFZp434P228)
227030_at_HG-U133B			Consensus includes gb:BG231773 /FEA=EST /DB_XREF=gi:12726899 /DB_XREF=est:naf3b12.x1 /CLONE=IMAGE:4142542 /UG=Hs.318893 ESTs
227038_at_HG-U133B	ESTs		Consensus includes gb:AI963083 /FEA=EST /DB_XREF=gi:5755796 /DB_XREF=est:wt27a06.x1 /CLONE=IMAGE:2508658 /UG=Hs.29567 ESTs
227039_at_HG-U133B	AKAP13	A kinase (PRKA) anchor protein 13	Consensus includes gb:AI674926 /FEA=EST /DB_XREF=gi:4875406 /DB_XREF=est:wc73g12.x1 /CLONE=IMAGE:2324326 /UG=Hs.29893 Homo sapiens mRNA full length insert cDNA clone EUROMAGE 146397
227041_at_HG-U133B		Homo sapiens cDNA FLJ31513 f1s, clone NT2R11000127	Consensus includes gb:BE466145 /FEA=EST /DB_XREF=gi:9511920 /DB_XREF=est:hy10h02.x1 /CLONE=IMAGE:3196947 /UG=Hs.30977 ESTs
227046_at_HG-U133B	C17orf26	chromosome 17 open reading frame 26	Consensus includes gb:BF062384 /FEA=EST /DB_XREF=gi:10821294 /DB_XREF=est:7k77e12.x1 /CLONE=IMAGE:3481462 /UG=Hs.3402 ESTs
227047_x_at_HG-U133B	KIAA1538	KIAA1538 protein	Consensus includes gb:N63748 /FEA=EST /DB_XREF=gi:12111577 /DB_XREF=est:za18f10.s1 /CLONE=IMAGE:292939 /UG=Hs.35096 KIAA1538 protein
227056_at_HG-U133B	KIAA0141	KIAA0141 gene product	Consensus includes gb:AA181172 /FEA=EST /DB_XREF=gi:1764639 /DB_XREF=est:zp6sf10.s1 /CLONE=IMAGE:625483 /UG=Hs.633510 KIAA0141 gene product
227065_at_HG-U133B	COL5A2	collagen, type V, alpha 2	Consensus includes gb:AA523105 /FEA=EST /DB_XREF=gi:2263817 /DB_XREF=est:ni44b04.s1 /CLONE=IMAGE:979663 /UG=Hs.82985 collagen, type V, alpha 2
227121_at_HG-U133B		ESTs	Consensus includes gb:BF476076 /FEA=EST /DB_XREF=gi:11546903

			/DB_XREF=est:hr77a10.x1 /CLONE=IMAGE:3134490 /UG=Hs.193784 Homo sapiens mRNA; cDNA DKFZp586K1922 (from clone DKFZp586K1922)
			Consensus includes gb:AW190565 /FEA=EST /DB_XREF=gi:6465045 /DB_XREF=est:xi40b02.x1 /CLONE=IMAGE:2677131 /UG=Hs.306814 Homo sapiens cDNA: FLJ21889 fis, clone HEP03178
			Consensus includes gb:AW873348 /FEA=EST /DB_XREF=gi:8007401 /DB_XREF=est:hi92d03.x1 /CLONE=IMAGE:3009413 /UG=Hs.30853 ESTs, /DB_XREF=est:hs87g04.x1 /CLONE=IMAGE:3144246 /UG=Hs.32365 ESTs, weakly similar to AF121859 1 sorting nexin 9. Homo sapiens
			Consensus includes gb:AI979334 /FEA=EST /DB_XREF=gi:5804353 /DB_XREF=est:wi03g02.x1 /CLONE=IMAGE:2515922 /UG=Hs.323822 Homo sapiens mRNA for KIAA1551 protein, partial cds
			Consensus includes gb:AW511319 /FEA=EST /DB_XREF=gi:7149397 /DB_XREF=est:hd45c10.x1 /CLONE=IMAGE:2912466 /UG=Hs.61426 ESTs
			Consensus includes gb:AW450901 /FEA=EST /DB_XREF=gi:6991677 /DB_XREF=est:U1-H-B13-all-d-04-0-U1.s1 /CLONE=IMAGE:2737183
			BTB and CNC homology 1, basic leucine zipper transcription factor 2
			Consensus includes gb:AB046819.1 /DEF=Homo sapiens mRNA for KIAA1599 protein, partial cds. /FEA=mRNA /GEN=KIAA1599 /PROD=KIAA1599 protein /DB_XREF=gi:10047272 /UG=Hs.285714 KIAA1599 protein
			Consensus includes gb:AW085505 /FEA=EST /DB_XREF=gi:6040657 /DB_XREF=est:wy66c12.x1 /CLONE=IMAGE:2553526 /UG=Hs.125019 ESTs, highly similar to KIAA0886 protein H.sapiens
			Consensus includes gb:BE465462 /FEA=EST /DB_XREF=gi:9511237 /DB_XREF=est:hw20e10.x1 /CLONE=IMAGE:3183498 /UG=Hs.108593 Homo clone HEP04081
227145_at_HG-U133B	LOXL4	lysyl oxidase-like 4	Homo sapiens mRNA full length insert cDNA clone EUR0IMAGE 1644069
227146_at_HG-U133B			Homo sapiens, clone MGC:32065 IMAGE:4869639, mRNA, complete cds
227151_at_HG-U133B			Homo sapiens mRNA for KIAA1551 protein, partial cds
227152_at_HG-U133B			Homo sapiens mesenchymal stem cell protein DSC95 mRNA, partial cds
227167_s_at_HG-U133B			BTB and CNC homology 1, basic leucine zipper transcription factor 2
227173_s_at_HG-U133B	BACH2		Consensus includes gb:AB046819.1 /DEF=Homo sapiens mRNA for KIAA1599 protein, partial cds. /FEA=mRNA /GEN=KIAA1599 /PROD=KIAA1599 protein /DB_XREF=gi:10047272 /UG=Hs.285714 KIAA1599 protein
227189_at_HG-U133B	KIAA1599	KIAA1599 protein	Consensus includes gb:AW085505 /FEA=EST /DB_XREF=gi:6040657 /DB_XREF=est:wy66c12.x1 /CLONE=IMAGE:2553526 /UG=Hs.125019 ESTs, highly similar to KIAA0886 protein H.sapiens
227198_at_HG-U133B			Consensus includes gb:BE465462 /FEA=EST /DB_XREF=gi:9511237 /DB_XREF=est:hw20e10.x1 /CLONE=IMAGE:3183498 /UG=Hs.108593 Homo clone HEP04081

		sapiens cDNA: FLI21923 fis, clone HEPO4081 -
227212_s_at_HG-U133B	Homo sapiens, Similar to RIKEN cDNA 3321402G02 gene, clone MGc:23929 IMAGE:4807540, mRNA, complete cds	Consensus includes gb:BE544837 /FEA=EST /DB_XREF=gi:9773482 /DB_XREF=est:601078832F1 /CLONE=IMAGE:3464694 /UG=Hs.119960 DKFP77G051 protein
227224_at_HG-U133B	ESTs	Consensus includes gb:AW003297 /FEA=EST /DB_XREF=gi:5850213 /DB_XREF=est:wg65b01.x1 /CLONE=IMAGE:2476105 /UG=Hs.174104 ESTs
227230_s_at_HG-U133B	KIAA1211	Consensus includes gb:BE855799 /FEA=EST /DB_XREF=gi:10368049 /DB_XREF=est:7g07a07.x1 /CLONE=IMAGE:3305748 /UG=Hs.205293 KIAA1211 protein
227237_x_at_HG-U133B	KIAA1273	Consensus includes gb:AW593303 /FEA=EST /DB_XREF=gi:7280561 /DB_XREF=est:hg12g12.x1 /CLONE=IMAGE:2945446 /UG=Hs.23413 KIAA1273 protein
227242_s_at_HG-U133B		Consensus includes gb:BF592034 /FEA=EST /DB_XREF=gi:11684358 /DB_XREF=est:7n98c03.x1 /CLONE=IMAGE:3572716 /UG=Hs.240559 Human DNA sequence from clone RP11-234G16 on chromosome 10. Contains ESTs, STSSs, GSSs and CpG islands. Contains a gene for two isoforms of a novel transcription factor similar to early B-cell factor (EBF)
227243_s_at_HG-U133B		Consensus includes gb:AL354950 /DEF=Human DNA sequence from clone RP11-234G16 on chromosome 10. Contains ESTs, STSSs, GSSs and CpG islands. Contains a gene for two isoforms of a novel transcription factor similar to early B-cell factor (EBF) /FEA=mRNA_2 /DB_XREF=gi:9908994 /UG=Hs.240559 Human DNA sequence from clone RP11-234G16 on chromosome 10. Contains ESTs, STSSs, GSSs and CpG islands. Contains a gene for two isoforms of a novel transcription factor similar to early B-cell factor (EBF)
227249_at_HG-U133B	NUDE1	Consensus includes gb:AI857385 /FEA=EST /DB_XREF=gi:5511301 /DB_XREF=est:wk96d1.x1 /CLONE=IMAGE:2423253 /UG=Hs.263925 LIS1-interacting protein NUDE1, rat interacting protein NUDE1, rat homolog

227261_at_HG-U133B	KLF12	Kruppel-like factor 12 tumor endothelial marker 7-related precursor	Consensus includes gb:AA020010 /FEA=EST /DB_XREF=gi:1483683 /DB_XREF=est:ze6210.s1 /CLONE=IMAGE:363595 /UG=Hs.294018 ESTs
227276_at_HG-U133B	TEM7R	ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY J. SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]	Consensus includes gb:AI264121 /FEA=EST /DB_XREF=gi:3872324 /DB_XREF=est:qk03a01.x1 /CLONE=IMAGE:1867848 /UG=Hs.33033 ESTs
227277_at_HG-U133B			Consensus includes gb:BG530089 /FEA=EST /DB_XREF=gi:13521626 /DB_XREF=est:602558749F1 /CLONE=IMAGE:4696597 /UG=Hs.33074 ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
227279_at_HG-U133B	MGC15737	hypothetical protein MGC15737	Consensus includes gb:AA847654 /FEA=EST /DB_XREF=gi:2934172 /DB_XREF=est:oe49e05.s1 /CLONE=IMAGE:1414976 /UG=Hs.39122 ESTs, Weakly similar to CENB MOUSE MAJOR CENTROMERE AUTOANTIGEN B M.musculus
227299_at_HG-U133B	CCNI	cyclin I	Consensus includes gb:AA020986 /FEA=EST /DB_XREF=gi:1484739 /DB_XREF=est:ze65e08.s1 /CLONE=IMAGE:3633878 /UG=Hs.79933 cyclin I
227326_at_HG-U133B	DTX1	ESTs, Weakly similar to hypothetical protein FLJ20489 [Homo sapiens] [H.sapiens]	Consensus includes gb:BE966768 /FEA=EST /DB_XREF=gi:11772526 /DB_XREF=est:601661268R1 /CLONE=IMAGE:3916097 /UG=Hs.11924 ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
227336_at_HG-U133B		deltex homolog 1 (Drosophila)	Consensus includes gb:AW578405 /FEA=EST /DB_XREF=gi:7247944 /DB_XREF=est:Ui-HF-BN0-ala-c-10-0-U1.s1 /CLONE=IMAGE:3078907 /UG=Hs.124024 deltex (Drosophila) homolog 1 /FL=gb:AE053700.1 gb:NM_004416.1
227353_at_HG-U133B		Homo sapiens, clone MGC:40121 IMAGE:5216355, mRNA, complete cds	Consensus includes gb:BEG71663 /FEA=EST /DB_XREF=gi:10032204 /DB_XREF=est:7a55g10.x1 /CLONE=IMAGE:3222690 /UG=Hs.15284 ESTs
227367_at_HG-U133B		ESTs	Consensus includes gb:AW976431 /FEA=EST /DB_XREF=gi:8167659 /DB_XREF=est:EST388540 /UG=Hs.184067 ESTs
227375_at_HG-U133B	DKFZP566D1346	hypothetical protein DKFZP566D1346	Consensus includes gb:AA152232 /FEA=EST /DB_XREF=gi:1721433 /DB_XREF=est:zo04c10.s1 /CLONE=IMAGE:566706 /UG=Hs.22612

		Homo sapiens, similar to putative, clone IMAGE:5190302, mRNA, partial cds	hypothetical protein DKFZp566D1346
227388_at_HG-U133B		Homo sapiens cDNA: FLJ23270 fis, clone COL10309, highly similar to HSU33271 Human normal keratinocyte mRNA	Consensus includes gb:AA479016 /FEA=EST /DB_XREF=gi:2205379 /DB_XREF=est:zu3903.s1 /CLONE=IMAGE:740381 /UG=Hs.26268 ESTs
227393_at_HG-U133B			Consensus includes gb:AW084755 /FEA=EST /DB_XREF=gi:6038907 /DB_XREF=est:xc57d02.x1 /CLONE=IMAGE:2588355 /UG=Hs.28455 Homo sapiens cDNA: FLJ23270 fis, clone COL10309, highly similar to HSU33271 Human normal keratinocyte mRNA
227396_at_HG-U133B		ESTs	Consensus includes gb:AI631833 /FEA=EST /DB_XREF=gi:4683163 /DB_XREF=est:wa36fr2.x1 /CLONE=IMAGE:2300207 /UG=Hs.306163 hypothetical protein AL110115
227407_at_HG-U133B			Consensus includes gb:AI341541 /FEA=EST /DB_XREF=gi:4078468 /DB_XREF=est:qq94e07.x1 /CLONE=IMAGE:1939044 /UG=Hs.5324 hypothetical protein
227408_s_at_HG-U133B	MSTP043	MSTP043 protein	Consensus includes gb:AW008976 /FEA=EST /DB_XREF=gi:5857754 /DB_XREF=est:ws75f08.x1 /CLONE=IMAGE:2503815 /UG=Hs.42768 hypothetical protein DKFZp76100113
227414_at_HG-U133B	DKFZp547E052	hypothetical protein DKFZp547E052	Consensus includes gb:AI869373 /FEA=EST /DB_XREF=gi:5594537 /DB_XREF=est:wm98d06.x1 /CLONE=IMAGE:2443979 /UG=Hs.49359 Homo sapiens mRNA: cDNA DKFZp547E052 (from clone DKFZp547E052)
227415_at_HG-U133B	FEBR22004099	Homo sapiens cDNA FLJ30865 fis, clone FEBR22004099	Consensus includes gb:BF109303 /FEA=EST /DB_XREF=gi:10938993 /DB_XREF=est:7161b10.x1 /CLONE=IMAGE:3625835 /UG=Hs.47084 ESTs
227478_at_HG-U133B		ESTs	Consensus includes gb:BF739885 /FEA=EST /DB_XREF=gi:12066549 /DB_XREF=est:7040c11.x1 /CLONE=IMAGE:3576573 /UG=Hs.128052 ESTs
227497_at_HG-U133B		Homo sapiens cDNA FLJ11723 fis, clone HEMBA1005314	Consensus includes gb:BE326808 /FEA=EST /DB_XREF=gi:9200584 /DB_XREF=est:hr65b11.x1 /CLONE=IMAGE:3133341 /UG=Hs.196008 Homo sapiens cDNA FLJ11723 fis, clone HEMBA1005314
227525_at_HG-U133B	LOC113263	hypothetical protein BC011254	Consensus includes gb:AA058770 /FEA=EST /DB_XREF=gi:1551643 /DB_XREF=est:zf66a09.s1 /CLONE=IMAGE:381880 /UG=Hs.5510 ESTs

227527_at_HG-U133B	Homo sapiens mRNA; cDNA DKFZp762P1915 (from clone DKFZp762P1915)	Consensus includes gb:AI394529 /FEA=EST /DB_XREF=gi:4224076 /DB_XREF=est:tt77b05.x1 /CLONE=IMAGE:2105265 /UG=Hs.3640 Homo sapiens mRNA; cDNA DKFZp762P1915 (from clone DKFZp762P1915)
227533_at_HG-U133B	ESTs	Consensus includes gb:AA732944 /FEA=EST /DB_XREF=gi:2754303 /DB_XREF=est:zg78d04.s1 /CLONE=IMAGE:399463 /UG=Hs.5415 ESTs
227536_at_HG-U133B	ATP1B1	Consensus includes gb:AI094580 /FEA=EST /DB_XREF=gi:3433566 /DB_XREF=est:oy64c02.s1 /CLONE=IMAGE:1670594 /UG=Hs.78629 ATPase, Na+K+ transporting, beta 1 polypeptide
227568_at_HG-U133B		Consensus includes gb:AF131793.1 /DEF=Homo sapiens clone 25142 mRNA sequence. /FEA=mRNA /DB_XREF=gi:4406821 /UG=Hs.25320 Homo sapiens clone 25142 mRNA sequence
227584_at_HG-U133B		Consensus includes gb:BF339566 /FEA=EST /DB_XREF=gi:11286021 /DB_XREF=ast:602039032F1 /CLONE=IMAGE:4186999 /UG=Hs.112461 ESTs, Weekly similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens [H.sapiens]
227587_at_HG-U133B	MGC15906	Consensus includes gb:N46431 /FEA=EST /DB_XREF=gi:1187597 /DB_XREF=est:yy75g12.s1 /CLONE=IMAGE:279430 /UG=Hs.104938 ESTs, Weekly similar to T12492 hypothetical protein DKFZp434C151.1 H.sapiens
227606_s_at_HG-U133B	KIAA1373	Consensus includes gb:AI638611 /FEA=EST /DB_XREF=gi:4690845 /DB_XREF=est:tt31b11.x1 /CLONE=IMAGE:2242365 /UG=Hs.16229 KIAA1373 protein
227607_at_HG-U133B	KIAA1373	Consensus includes gb:AI638611 /FEA=EST /DB_XREF=gi:4690845 /DB_XREF=est:tt31b11.x1 /CLONE=IMAGE:2242365 /UG=Hs.16229 KIAA1373 protein
227627_at_HG-U133B	SGKL	Consensus includes gb:AV690866 /FEA=EST /DB_XREF=gi:10292729 /DB_XREF=est:AV690866 /CLONE=GKCCXF03 /UG=Hs.24131 ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens

227646_at_HG-U133B	EBF	early B-cell factor	Consensus includes gb:BG435302 /FEA=EST /DB_XREF=gi:13341808 /DB_XREF=est:602508050F1 /CLONE=IMAGE:460532 /UG=Hs.32425 ESTs
227670_at_HG-U133B		Homo sapiens cDNA FLJ31529 fis, clone NT2R12000421, moderately similar to ZINC FINGER PROTEIN 75	Consensus includes gb:N74222 /FEA=EST /DB_XREF=gi:1231507 /DB_XREF=est:za59d08.s1 /CLONE=IMAGE:296847 /UG=Hs.50456 ESTs, Moderately similar to ZN75_HUMAN ZINC FINGER PROTEIN 75 H.sapiens
227680_at_HG-U133B		ESTs	Consensus includes gb:AI057121 /FEA=EST /DB_XREF=gi:3330997 /DB_XREF=est:oz23h05.x1 /CLONE=IMAGE:1676217 /UG=Hs.72087 ESTs
227700_x_at_HG-U133B	FLJ10709	hypothetical protein FLJ10709	Consensus includes gb:AL043161 /FEA=EST /DB_XREF=gi:5935774 /DB_XREF=est:DKFZp434F0123_s1 /CLONE=DKFZp434F0123 /UG=Hs.273357 hypothetical protein FLJ10709
227701_at_HG-U133B			Consensus includes gb:AK024739.1 /DEF=Homo sapiens cDNA: FLJ21086 fis, clone CAS03272. /FEA=mRNA /DB_XREF=gi:10437103 /UG=Hs.28538 Homo sapiens cDNA: FLJ21086 fis, clone CAS03272
227709_at_HG-U133B	RCN1.	reticulocalbin 1, EF-hand calcium binding domain	Consensus includes gb:BE670492 /FEA=EST /DB_XREF=gi:10031033 /DB_XREF=est:7e479c6.x1 /CLONE=IMAGE:3285658 /UG=Hs.167791 reticulocalbin 1, EF-hand calcium binding domain
227729_at_HG-U133B		ESTs	Consensus includes gb:AL038092 /FEA=EST /DB_XREF=gi:5407396 /DB_XREF=est:DKFZp566L011_s1 /CLONE=DKFZp566L011 /UG=Hs.107265 ESTs
227744_s_at_HG-U133B	HNRPD	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kD)	Consensus includes gb:AW005670 /FEA=EST /DB_XREF=gi:5854448 /DB_XREF=est:wz88f04.x1 /CLONE=IMAGE:2565919 /UG=Hs.303627 heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA-binding protein 1, 37kD)
227749_at_HG-U133B		ESTs	Consensus includes gb:AI703496 /FEA=EST /DB_XREF=gi:4991396 /DB_XREF=est:we24h07.x1 /CLONE=IMAGE:2342077 /UG=Hs.15085 ESTs
227767_at_HG-U133B	CSNK1G3	casein kinase 1, gamma 3	Consensus includes gb:AI073822 /FEA=EST /DB_XREF=gi:3400466 /DB_XREF=est:qa31h03.s1 /CLONE=IMAGE:1688405 /UG=Hs.30164 ESTs
227786_at_HG-U133B	TRAP25	TRAP/Mediator complex component	Consensus includes gb:AI026938 /FEA=EST /DB_XREF=gi:3244454

			/DB_XREF=est:ov8206.x1 /CLONE=IMAGE:1643843 /UG=Hs.298229 prefoldin 2
227812_at_HG-U133B	Homo sapiens clone HB-2 mRNA sequence		Consensus includes gb:BF432648 /FEA=EST /DB_XREF=gi:11444811 /DB_XREF=est:nac58a04.x1 /CLONE=IMAGE:3406567 /UG=Hs.48376 Homo sapiens clone HB-2 mRNA sequence
227817_at_HG-U133B	ESTs		Consensus includes gb:R51324 /FEA=EST /DB_XREF=gi:813226 /DB_XREF=est:yg72g01.s1 /CLONE=IMAGE:38786 /UG=Hs.6749 ESTs
227829_at_HG-U133B		Homo sapiens cDNA FLJ31267 fis, clone KIDNE2006053, moderately similar to Mus musculus mRNA for acetylglucosaminyltransferase-like protein	Consensus includes gb:AW272738 /FEA=EST /DB_XREF=gi:6659695 /DB_XREF=est:xu22b04.x1 /CLONE=IMAGE:2800879 /UG=Hs.86543 ESTs, Weakly similar to T00256 hypothetical protein KIAA0609 H.sapiens
227867_at_HG-U133B	ESTs	Weakly similar to T18967 hypothetical protein C05G5.5 - Caenorhabditis elegans [C.elegans]	Consensus includes gb:AA005361 /FEA=EST /DB_XREF=gi:1448394 /DB_XREF=est:zh97b01.s1 /CLONE=IMAGE:429193 /UG=Hs.36723 ESTs, Weakly similar to cDNA EST yk414c9.3 comes from this gene C.elegans
227900_at_HG-U133B	ESTs	Homo sapiens cDNA FLJ32270 fis, clone PUAE1000322	Consensus includes gb:AV701750 /CLONE=ADBANA03 /UG=Hs.144139 ESTs /DB_XREF=est:wb14c01.x1 /CLONE=IMAGE:2305632 /UG=Hs.280858 ESTs, Highly similar to A35661 DNA excision repair cross-complementing protein ERCC3 H.sapiens
227936_at_HG-U133B		chorea acanthocytosis	Consensus includes gb:AW629014 /FEA=EST /DB_XREF=gi:7375804 /DB_XREF=est:hi46e01.x1 /CLONE=IMAGE:2975352 /UG=Hs.65919 ESTs
227988_s_at_HG-U133B	CHAC		Consensus includes gb:AA045184 /FEA=EST /DB_XREF=gi:1523386 /DB_XREF=est:zk66c01.s1 /CLONE=IMAGE:487776 /UG=Hs.738 ribosomal protein L14
227998_at_HG-U133B	MGC17528	hypothetical protein MGC17528	Consensus includes gb:AI290476 /FEA=EST /DB_XREF=gi:3933250 /DB_XREF=est:q198b08.x1 /CLONE=IMAGE:1880343 /UG=Hs.87597 ESTs
227999_at_HG-U133B	LOC170394	hypothetical protein BC011630	

228003_at_HG-U133B	ESTs	Consensus includes gb:AW294640 /FEA=EST /DB_XREF=gi:6701276 /DB_XREF=est:U1-H-BW0-all-c-06-0-UI.s1 /CLONE=IMAGE:2729483 /UG=Hs.95898 ESTs
228007_at_HG-U133B		Consensus includes gb:AL133101.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434O0921 (from clone DKFZp434O0921). /FEA=mRNA /DB_XREF=gi:6453584 /UG=Hs.98508 Homo sapiens mRNA; cDNA DKFZp434O0921 (from clone DKFZp434O0921)
228024_at_HG-U133B	PAK1	Consensus includes gb:AW028100 /FEA=EST /DB_XREF=gi:5886856 /DB_XREF=est:ws63107.x1 /CLONE=IMAGE:2501917 /UG=Hs.290855 ESTs
228029_at_HG-U133B	KIAA1982	Consensus includes gb:AW513477 /FEA=EST /DB_XREF=gi:7151555 /DB_XREF=est:xo84f10.x1 /CLONE=IMAGE:2737579 /UG=Hs.22969. ESTs
228055_at_HG-U133B		Consensus includes gb:AI763426 /FEA=EST /DB_XREF=gi:5179093 /DB_XREF=est:wh92c02.x1 /CLONE=IMAGE:2388194 /UG=Hs.104433 Homo sapiens napsin 2 precursor, mRNA, partial sequence
228058_at_HG-U133B		Consensus includes gb:AI559190 /FEA=EST /DB_XREF=gi:4509395 /DB_XREF=est:tp42g08.x1 /CLONE=IMAGE:2211518 /UG=Hs.105887 ESTs, Weakly similar to Homolog of rat Zymogen granule membrane protein H.sapiens
228083_at_HG-U133B		Consensus includes gb:AL3879368, mRNA, complete cds IMAGE:3879368, mRNA, complete cds
228092_at_HG-U133B		Consensus includes gb:AI433691 /FEA=EST /DB_XREF=gi:4290952 /DB_XREF=est:ti88d06.x1 /CLONE=IMAGE:2139083 /UG=Hs.13768 Homo sapiens mRNA; cDNA DKFZp434I1216 (from clone DKFZp434I1216)
228174_at_HG-U133B	ESTs	Consensus includes gb:AL552470 /FEA=EST /DB_XREF=gi:12891398 /DB_XREF=est:AL552470 /CLONE=CS00D1070YJ22 (5 prime) /UG=Hs.155924 cAMP responsive element modulator
228176_at_HG-U133B	ESTs	Consensus includes gb:AI832363 /FEA=EST /DB_XREF=gi:5454275 /DB_XREF=est:af66c06.x1 /CLONE=IMAGE:2376970 /UG=Hs.48610 ESTs

	protein FLJ20489 [Homo sapiens] [H.sapiens]	/DB_XREF=est:nf81h07.s1 /CLONE=IMAGE:926365 /UG=Hs.55902 ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
228183_s_at_HG-U133B	hypothetical protein MGC4189 MGC4189	Consensus includes gb:BF342428 /FEA=EST /DB_XREF=gi:11289441 /DB_XREF=est:602013931F1 /CLONE=IMAGE:4149702 /UG=Hs.78614 complement component 1, q subcomponent binding protein
228193_s_at_HG-U133B	RGC32 protein RGC32	Consensus includes gb:AI744499 /FEA=EST /DB_XREF=gi:51112787 /DB_XREF=est:wg09a04.x1 /CLONE=IMAGE:2364558 /UG=Hs.76640 RGC32 protein
228211_at_HG-U133B	ESTs	Consensus includes gb:AI693726 /FEA=EST /DB_XREF=gi:4971066 /DB_XREF=est:wd44f03.x1 /CLONE=IMAGE:2331005 /UG=Hs.44367 ESTs
228242_at_HG-U133B	ESTs	Consensus includes gb:BF055201 /FEA=EST /DB_XREF=gi:10809097 /DB_XREF=est:776d08.x1 /CLONE=IMAGE:3392367 /UG=Hs.101624 ESTs
228266_s_at_HG-U133B	hepatoma-derived growth factor 2 CGI-142	Consensus includes gb:BE703418 /FEA=EST /DB_XREF=gi:10091160 /DB_XREF=est:MR2-NN1111-070800-008-a03 /UG=Hs.127842 CGI-142
228298_at_HG-U133B	LOC91523	Consensus includes gb:BF056501 /FEA=EST /DB_XREF=gi:10810797 /DB_XREF=est:7k11d11.x1 /CLONE=IMAGE:3444140 /UG=Hs.181261 ESTs
228328_at_HG-U133B	ESTs	Consensus includes gb:AI982758 /FEA=EST /DB_XREF=gi:5809977 /DB_XREF=est:w228h04.x1 /CLONE=IMAGE:2559415 /UG=Hs.7326 ESTs
228343_at_HG-U133B	POU domain, class 2, transcription factor 2 POU2F2	Consensus includes gb:AA805754 /FEA=EST /DB_XREF=gi:2874504 /DB_XREF=est:n43e05.s1 /CLONE=IMAGE:1186400 /UG=Hs.333040 ESTs
228345_at_HG-U133B	ESTs	Consensus includes gb:AI745136 /FEA=EST /DB_XREF=gi:5113424 /DB_XREF=est:tr19f03.x1 /CLONE=IMAGE:2218781 /UG=Hs.34656 ESTs
228361_at_HG-U133B	Homo sapiens, Similar to hypothetical protein PRO1722, clone MGIC:15692 IMAGE:3351479, mRNA, complete cds	Consensus includes gb:AL561296 /FEA=EST /DB_XREF=gi:12908585 /DB_XREF=est:AL561296 /CLONE=CS0DL010YF15 (5' prime) /UG=Hs.49047 ESTs
228377_at_HG-U133B	KIAA1384 protein KIAA1384	Consensus includes gb:AB037805.1 /DEF=Homo sapiens mRNA for KIAA1384 protein, partial cds. /GEN=mRNA /GEN=KIAA1384

		/PROD=KIAA1384 protein /DB_XREF=gi:7243148 /UG=Hs.88442_KIAA1384 protein
		Consensus includes gb:AW071847 /FEA=EST /DB_XREF=gi:6026772 /DB_XREF=est:ws54d05.x1 /CLONE=IMAGE:2501001 /UG=Hs.75968 thymosin, beta 4, X chromosome
228379_at_HG-U133B	ESTs	ESTs Consensus includes gb:AA489100 /FEA=EST /DB_XREF=gi:2218702 /DB_XREF=est:aa56h10.s1 /CLONE=IMAGE:824995 /UG=Hs.184430 ESTs
228390_at_HG-U133B	ESTs	ESTs Consensus includes gb:AI738666 /FEA=EST /DB_XREF=gi:5100647 /DB_XREF=est:wi11g03.x1 /CLONE=IMAGE:2389972 /UG=Hs.109045
228408_s_at_HG-U133B	FLJ10498	hypothetical protein FLJ10498 Consensus includes gb:AA495984 /FEA=EST /DB_XREF=gi:2229305 /DB_XREF=est:zw06d08.s1 /CLONE=IMAGE:768495 /UG=Hs.102630 ESTs
228410_at_HG-U133B	GAB3	GRB2-associated binding protein 3 N-acetylated alpha-linked acidic dipeptidase-like; ILEAL DIPEPTIDYLPEPTIDASE NAALADASEL Consensus includes gb:AW170591 /FEA=EST /DB_XREF=gi:6402116- /DB_XREF=est:xn64c01.x1 /CLONE=IMAGE:2698464 /UG=Hs.13967 ESTs
228424_at_HG-U133B		Highly similar to NAALADase L protein H.sapiens /DB_XREF=est:tny79e02.s1 /CLONE=IMAGE:1284506 /UG=Hs.145053 ESTs
228471_at_HG-U133B		ESTs Consensus includes gb:AW193515 /FEA=EST /DB_XREF=gi:6472214 /DB_XREF=est:xm17c03.x1 /CLONE=IMAGE:2684452 /UG=Hs.15370
228476_at_HG-U133B	KIAA1407	KIAA1407 protein KIAA1407 protein Consensus includes gb:AW165999 /FEA=EST /DB_XREF=gi:6397524 /DB_XREF=est:xf43e09.x1 /CLONE=IMAGE:2620840 /UG=Hs.179902
228485_s_at_HG-U133B	CDw92	CDw92 antigen transporter-like protein Consensus includes gb:AW243081 /FEA=EST /DB_XREF=gi:6576874 /DB_XREF=est:xf43e09.x1 /CLONE=IMAGE:2691643 /UG=Hs.19280 cysteine-rich motor neuron 1
228496_s_at_HG-U133B	CRIM1	cysteine-rich motor neuron 1 Consensus includes gb:AI279062 /FEA=EST /DB_XREF=gi:3917296 /DB_XREF=est:qm23ad6.x1 /CLONE=IMAGE:1882642 /UG=Hs.21710
228497_at_HG-U133B	DKFZp761G0313	hypothetical protein DKFZp761G0313

		hypothetical protein DKFZp761G0313
228518_at_HG-U133B	IGHG3	Consensus includes gb:AW575313 /FEA=EST /DB_XREF=gi:7246852 /DB_XREF=est:U1-HF-BL0-ac5-c12-0-U1.s1 /CLONE=IMAGE:3060095 /UG=Hs.278586 KIAA1108 protein
228551_at_HG-U133B		Consensus includes gb:AL137384.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434E0626 (from clone DKFZp434E0626). /FEA=mRNA /DB_XREF=gi:6807885 /UG=Hs.309857 Homo sapiens mRNA; cDNA DKFZp434E0626 (from clone DKFZp434E0626)
228555_at_HG-U133B		Consensus includes gb:AA029441 /FEA=EST /DB_XREF=gi:1496854 /DB_XREF=est:ze96c08.s1 /CLONE=IMAGE:3666830 /UG=Hs.32553 ESTs
228570_at_HG-U133B		Consensus includes gb:BF510581 /FEA=EST /DB_XREF=gi:11593879 /DB_XREF=est:U1-HB14-apk-b-03-0-U1.s1 /CLONE=IMAGE:3087676 /UG=Hs.5027 ESTs
228592_at_HG-U133B		Consensus includes gb:AW474852 /FEA=EST /DB_XREF=gi:7044958 /DB_XREF=est:xy0708.x1 /CLONE=IMAGE:2852463 /UG=Hs.86693 ESTs
228599_at_HG-U133B		Consensus includes gb:AI862674 /FEA=EST /DB_XREF=gi:5526781 /DB_XREF=est:wy2/1f01.x1 /CLONE=IMAGE:2404057 /UG=Hs.86693 ESTs
228652_at_HG-U133B		Consensus includes gb:AI279532 /FEA=EST /DB_XREF=gi:3917766 /DB_XREF=est:ql51ff03.x1 /CLONE=IMAGE:1875869 /UG=Hs.109540 ESTs, Weakly similar to Z189_HUMAN ZINC FINGER PROTEIN 189 H.sapiens [H.sapiens]
228660_X_at_HG-U133B	SEMA4F	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin)-4F hypothetical protein PRO2353
228663_at_HG-U133B		Consensus includes gb:AA523537 /FEA=EST /DB_XREF=gi:2264249 /DB_XREF=est:tg30e03.s1 /CLONE=IMAGE:936316 /UG=Hs.117612
228708_at_HG-U133B		Consensus includes gb:AI681307 /FEA=EST /DB_XREF=gi:4891489 /DB_XREF=est:tx45g07.x1 /CLONE=IMAGE:2272572 /UG=Hs.166674 ESTs
		Consensus includes gb:BF438386 /FEA=EST /DB_XREF=gi:11450903 /DB_XREF=est:7q08g08.x1 /CLONE=IMAGE:3677007 /UG=Hs.25318 Homo sequence

			consensus includes gb:AA211909 /FEA=EST /DB_XREF=gi:1810563
228737_at_HG-U133B	C20orf100	chromosome 20 open reading frame 100 ESTs, Weakly similar to cytokine receptor-like factor 2; cytokine receptor CRL2 precursor [Homo sapiens] [H.sapiens]	Consensus includes gb:AW289226 /FEA=EST /DB_XREF=gi:648364 /UG=Hs.26608 ESTs, /DB_XREF=est:zq95a03.s1 /CLONE=IMAGE:2772858 /UG=Hs.325823 ESTs, Moderately similar to ALU5_HUMAN ALU SUBFAMILY SC SEQUENCE
228766_at_HG-U133B		Homo sapiens clone 25023 mRNA sequence	Consensus includes gb:AI217416 /FEA=EST /DB_XREF=gi:3797231 /DB_XREF=est:qh22n01.x1 /CLONE=IMAGE:1845457 /UG=Hs.90858 Homo sapiens clone 25023 mRNA sequence
228827_at_HG-U133B			Consensus includes gb:BF240286 /FEA=EST /DB_XREF=gi:11154209 /DB_XREF=est:601905816F1 /CLONE=IMAGE:4133978 /UG=Hs.178137 transducer of ERBB2, 1
228834_at_HG-U133B	TCB1	transducer of ERBB2, 1	Consensus includes gb:AW510657 /FEA=EST /DB_XREF=gi:7148735 /DB_XREF=est:h8909.x1 /CLONE=IMAGE:2907161 /UG=Hs.156044 ESTs
228804_at_HG-U133B		Homo sapiens cDNA FLJ32343 fis, clone PROST2006260, weakly similar to SPLICING FACTOR, ARGININE/SERINE-RICH 4	Consensus includes gb:BE857467 /FEA=EST /DB_XREF=gi:10371522 /DB_XREF=est:7f97h11.x1 /CLONE=IMAGE:3304965 /UG=Hs.24380 ESTs
228816_at_HG-U133B		KIAA1394 protein	Consensus includes gb:AB037815.1 /DEF=Homo sapiens mRNA for KIAA1394 protein, partial cds. /FEA=mRNA /GEN=KIAA1394 /PROD=KIAA1394 protein /DB_XREF=gi:7243168 /UG=Hs.32156 KIAA1394 protein
228884_at_HG-U133B	KIAA1394	KIAA1394 protein	Consensus includes gb:AU157017 /FEA=EST /DB_XREF=gi:11018538 /DB_XREF=est:AU157017 /CLONE=PLACE1005740 /UG=Hs.323950 zinc finger protein 6 (CMPX1)
228888_at_HG-U133B	ZNF6	zinc finger protein 6 (CMPX1)	Consensus includes gb:BE259127 /FEA=EST /DB_XREF=gi:9129625 /DB_XREF=est:601115521F1 /CLONE=IMAGE:3356236 /UG=Hs.39911 Homo protein, partial cds
229001_at_HG-U133B			

		sapiens mRNA for FLJ00089 protein, partial cds
		Consensus includes gb:AI0955583 /FEA=EST /DB_XREF=gi:3434559 /DB_XREF=est:qb24aa02.x1 /CLONE=IMAGE:1697162 /UG=Hs.38509 ESTs, Weakly similar to CA13_HUMAN COLLAGEN ALPHA 1(III) CHAIN PRECURSOR H.sapiens
229003_x_at_HG-U133B	Homo sapiens mRNA full length insert cDNA clone EUROMAGE 1622425	Consensus includes gb:AW268880 /FEA=EST /DB_XREF=gi:6655910 /DB_XREF=est:qv24aa02.x1 /CLONE=IMAGE:2816381 /UG=Hs.9599 soluble carrier family 25, member 13 (citrin)
229061_s_at_HG-U133B	SLC25A13	Consensus includes gb:AA470369 /FEA=EST /DB_XREF=gi:2197678 /DB_XREF=est:ne10a12.s1 /CLONE=IMAGE:880798 /UG=Hs.72115 ESTs
229070_at_HG-U133B	MGC12335	Consensus includes gb:BF968097 /FEA=EST /DB_XREF=gi:12335312 /DB_XREF=est:602269272F1 /CLONE=IMAGE:4357504 /UG=Hs.26339 ESTs
229072_at_HG-U133B		Consensus includes gb:AV747166 /FEA=EST /DB_XREF=gi:10905014 /DB_XREF=est:AV747166 /CLONE=NPCATH06 /UG=Hs.59698 ESTs
229138_at_HG-U133B		Consensus includes gb:AI690433 /FEA=EST /DB_XREF=gi:4901735 /DB_XREF=est:tx87ff11.x1 /CLONE=IMAGE:2276589 /UG=Hs.55407 Homo sapiens mRNA; cDNA DKFZp434K0621 (from clone DKFZp434K0621); partial cds
229168_at_HG-U133B		Consensus includes gb:AL045882 /FEA=EST /DB_XREF=gi:5433989 /DB_XREF=est:DKFZp434J086_s1 /CLONE=DKFZp434J086 /UG=Hs.126695 ESTs
229194_at_HG-U133B		ESTs, Weakly similar to JC4296 ring finger protein - fruit fly [D.melanogaster]
		ESTs, Moderately similar to cytokine receptor-like factor 2; cytokine receptor CRL2 precursor [Homo sapiens] [H.sapiens]
229232_at_HG-U133B		Consensus includes gb:AI184512 /FEA=EST /DB_XREF=gi:3735150 /DB_XREF=est:qf29e10.x1 /CLONE=IMAGE:1751466 /UG=Hs.266155 ESTs
229253_at_HG-U133B	CTMP	Consensus includes gb:AK026189.1 /DEF=Homo sapiens cDNA: FLJ22536
229280_s_at_HG-		Consensus includes gb:AK026189.1 /DEF=Homo sapiens cDNA: FLJ22536

U133B			pis, clone HRC13155. /FEA=mRNA /DB_XREF=gi:10438959 /UG=Hs.43266 Homo sapiens cDNA: FLJ22536 pis, clone HRC13155
229302_at_HG-U133B	ESTs		Consensus includes gb:AA058832 /FEA=EST /DB_XREF=gi:1551675 /DB_XREF=est:zf65f12.s1 /CLONE=IMAGE:381839 /UG=Hs.40808 ESTs
229310_at_HG-U133B	KIAA1921	KIAA1921 protein	Consensus includes gb:BE465475 /FEA=EST /DB_XREF=gi:9511250 /DB_XREF=est:hw20g02.x1 /CLONE=IMAGE:3183566 /UG=Hs.272572 hemoglobin, alpha 2
229344_x_at_HG-U133B	KIAA1238	KIAA1238 protein	Consensus includes gb:AW135012 /FEA=EST /DB_XREF=gi:6138558 /DB_XREF=est:U1-H-B11-abt-d-05-0-Ui.s1 /CLONE=IMAGE:2712993 /UG=Hs.236463 KIAA1238 protein
229362_at_HG-U133B	ZNF216	Moderately similar to R3HU12 ribosomal protein S12, cytosolic [H.sapiens]	Consensus includes gb:AA878516 /FEA=EST /DB_XREF=gi:2987481 /DB_XREF=est:gi19hb8.s1 /CLONE=IMAGE:1492599 /UG=Hs.112830 ESTs. Moderately similar to R3HU12 ribosomal protein S12, cytosolic H.sapiens
229368_s_at_HG-U133B	ZNF216	zinc finger protein 216	Consensus includes gb:AI658995 /FEA=EST /DB_XREF=gi:4762565 /DB_XREF=est:lu23c12.x1 /CLONE=IMAGE:2251894 /UG=Hs.3776 zinc finger protein 216
229383_at_HG-U133B	ESTs	ribosomal protein L23a	Consensus includes gb:AI707896 /FEA=EST /DB_XREF=gi:4997672 /DB_XREF=est:as34a10.x1 /CLONE=IMAGE:2319066 /UG=Hs.107369 ESTs
229420_at_HG-U133B	RPL23A	-	Consensus includes gb:AI557425 /FEA=EST /DB_XREF=gi:4485788 /DB_XREF=est:PT2.1_7_B11.r /UG=Hs.184776 ribosomal protein L23a
229487_at_HG-U133B	ESTs	-	Consensus includes gb:W73890 /FEA=EST /DB_XREF=gi:1382285 /DB_XREF=est:zd65h02.s1 /CLONE=IMAGE:345555 /UG=Hs.120785 ESTs
229513_at_HG-U133B			Consensus includes gb:AK025613.1 /DEF=Homo sapiens cDNA: FLJ21960 pis, clone HEP05517. /FEA=mRNA /DB_XREF=gi:10438184 /UG=Hs.287687 Homo sapiens cDNA: FLJ21960 pis, clone HEP05517
229575_at_HG-U133B	ESTs		Consensus includes gb:AW271460 /FEA=EST /DB_XREF=gi:6658490 /DB_XREF=est:xs14g08.x1 /CLONE=IMAGE:2789662 /UG=Hs.122642 ESTs
229621_x_at_HG-		Homo sapiens cDNA FLJ31148 pis, clone	Consensus includes gb:N93227 /FEA=EST /DB_XREF=gi:1265536

U133B		IMR322001452	/DB_XREF=est:zb29d08.s1 /CLONE=IMAGE:305007 /UG=Hs.240559 Human DNA sequence from clone RP11-234G16 on chromosome 10. Contains ESTs, STSs, GSSs and CpG islands. Contains a gene for two isoforms of a novel transcription factor similar to early B-cell factor (EBF)
229637_at_HG-U133B	ESTs		Consensus includes gb:AA166891 /FEA=EST /DB_XREF=gi:1745055 /DB_XREF=est:zq39d08.s1 /CLONE=IMAGE:632079 /UG=Hs.25768 ESTs
229659_s_at_HG-U133B	Homo sapiens cDNA: FLJ22667 fis, clone HS108385		Consensus includes gb:BE501712 /FEA=EST /DB_XREF=gi:9704120 /DB_XREF=est:hw34c04.x1 /CLONE=IMAGE:3184806 /UG=Hs.205126 Homo sapiens cDNA: FLJ22667 fis, clone HS108385
229681_at_HG-U133B	ESTs		Consensus includes gb:AW449289 /FEA=EST /DB_XREF=gi:6990065 /DB_XREF=est:Ui-H-BI3-akh-1-09-0-U1.s1 /CLONE=IMAGE:2734241 /UG=Hs.17551 ESTs
229711_s_at_HG-U133B	MGC5370	hypothetical protein MGC5370	Consensus includes gb:AA902480 /FEA=EST /DB_XREF=gi:3037603 /DB_XREF=est:7n64a10.x1 /CLONE=IMAGE:1519367 /UG=Hs.332938 carboxypeptidase M protein
229722_at_HG-U133B	HSPOC072	HSPOC072 protein	Consensus includes gb:BF115733 /FEA=EST /DB_XREF=gi:10985209 /DB_XREF=est:7n64a10.x1 /CLONE=IMAGE:3569202 /UG=Hs.87329 HSPC072 protein
229745_x_at_HG-U133B		Homo sapiens, Similar to thymus expressed gene 3, clone MG:15476 IMAGE:2967514, mRNA, complete cds	Consensus includes gb:AI468629 /FEA=EST /DB_XREF=gi:4330719 /DB_XREF=est:lh83g03.x1 /CLONE=IMAGE:2125300 /UG=Hs.134185 ESTs, Weakly similar to Sf5 RAT 5E5 ANTIGEN R.norvegicus
229750_at_HG-U133B	ESTs		Consensus includes gb:BF510728 /FEA=EST /DB_XREF=gi:11594026 /DB_XREF=est:Ui-H-BI4-aoh-c-07-0-U1.s1 /CLONE=IMAGE:3084685 /UG=Hs.143087 ESTs
229779_at_HG-U133B	ESTs		Consensus includes gb:BF476080 /FEA=EST /DB_XREF=gi:11546907 /DB_XREF=est:hh77b03.x1 /CLONE=IMAGE:3134477 /UG=Hs.119471 ESTs
229790_at_HG-U133B	TERF2	telomeric repeat binding factor 2	Consensus includes gb:AW006852 /FEA=EST /DB_XREF=gi:5855610 /DB_XREF=est:wt07h12.x1 /CLONE=IMAGE:2506823 /UG=Hs.100030 telomeric

		repeat binding factor 2
229817_at_HG-U133B	DKFZP434M098	DKFZP434M098 protein
229833_at_HG-U133B		ESTs, Highly similar to A38283 arachidonate 12-lipoxygenase [H.sapiens]
229844_at_HG-U133B		ESTs
229848_at_HG-U133B	ZNF10	zinc finger protein 10 (KOX 1)
229872_s_at_HG-U133B	KIAA0493	KIAA0493 protein
229923_at_HG-U133B		-
229934_at_HG-U133B		ESTs
229937_x_at_HG-U133B		ESTs
230110_at_HG-U133B		ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]
230245_s_at_HG-U133B		Homo sapiens mRNA, cDNA DKFZp667L0210 (from clone
		Consensus includes gb:AI452715 /FEA=EST /DB_XREF=gi:4287293 /DB_XREF=est:ij56f10.x1 /CLONE=IMAGE:2145547 /UG=Hs.93738 DKFZP434M098 protein
		Consensus includes gb:BF507533 /FEA=EST /DB_XREF=gi:11590842 /DB_XREF=est:Ui-H-BW1-amr-f-06-0-Ui s1 /CLONE=IMAGE:3070979 /UG=Hs.33728 ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
		Consensus includes gb:AI699465 /FEA=EST /DB_XREF=gi:4987365 /DB_XREF=est:wa70109.x1 /CLONE=IMAGE:2301545 /UG=Hs.59368 ESTs
		Consensus includes gb:W72653 /FEA=EST /DB_XREF=gi:1382473 /DB_XREF=est:zd67c09.s1 /CLONE=IMAGE:345712 /UG=Hs.91226 ESTs
		Consensus includes gb:AA532655 /FEA=EST /DB_XREF=gi:2276909 /DB_XREF=est:ri17d09.s1 /CLONE=IMAGE:986609 /UG=Hs.295901 KIAA0493 protein
		Consensus includes gb:AK026322.1 /DEF=Homo sapiens cDNA: FLJ22669 fis, clone HS108594. /FEA=mRNA /DB_XREF=gi:10439147 /UG=Hs.44653 Homo sapiens cDNA: FLJ22669 fis, clone HS108594
		Consensus includes gb:N39230 /FEA=EST /DB_XREF=gi:1162437 /DB_XREF=est:yy50c03.s1 /CLONE=IMAGE:276964 /UG=Hs.38218 ESTs
		Consensus includes gb:AI681260 /FEA=EST /DB_XREF=gi:4831442 /DB_XREF=est:tx45c07.x1 /CLONE=IMAGE:2272524 /UG=Hs.149924 ESTs
		Consensus includes gb:AV713773 /FEA=EST /DB_XREF=gi:10795290 /DB_XREF=est:AV713773 /CLONE=DCBALC05 /UG=Hs.210792 ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
		Consensus includes gb:AI926479 /FEA=EST /DB_XREF=gi:5662443 /DB_XREF=est:wo45b06.x1 /CLONE=IMAGE:2458259 /UG=Hs.181297 ESTs

		DKFZ4667L0210)	Consensus includes gb:AA868809 /FEA=EST /DB_XREF=gi:2964254
		Homo sapiens cDNA FLJ25310 fis, clone SYN00991	/DB_XREF=est:al49h02.s1 /CLONE=IMAGE:1460691 /UG=Hs.25447 ESTs
230292_at_HG-U133B		Sac domain-containing inositol phosphatase 2	Consensus includes gb:BE858808 /FEA=EST /DB_XREF=gi:10374225
230363_s_at_HG-U133B	SAC2	RAD50 homolog (<i>S. cerevisiae</i>) ESTs, Weakly similar to T17233 hypothetical protein DKFZp434I216.1 [H.sapiens]	/DB_XREF=est:795h05.x1 /CLONE=IMAGE:3304761 /UG=Hs.52463 KIAA0966 protein
230405_at_HG-U133B	RAD50	CD5 antigen (p56-62) ESTs	Consensus includes gb:AI143416 /FEA=EST /DB_XREF=gi:36665225
230411_at_HG-U133B			/DB_XREF=est:qa55a10.s1 /CLONE=IMAGE:1690650 /UG=Hs.41587 RAD50 (<i>S. cerevisiae</i>) homolog
230489_at_HG-U133B	CD5	hypothetical protein DKFZp434I216.1 [H.sapiens]	Consensus includes gb:AI890356 /FEA=EST /DB_XREF=gi:5595520
230489_at_HG-U133B			/DB_XREF=est:wm84c05.x1 /CLONE=IMAGE:2442632 /UG=Hs.127804 ESTs, Weakly similar to T17233 hypothetical protein DKFZp434I216.1 H.sapiens
230526_at_HG-U133B	FLJ20015	hypothetical protein FLJ20015	Consensus includes gb:AI797836 /FEA=EST /DB_XREF=gi:35363393
230551_at_HG-U133B		ESTs	/DB_XREF=est:wh79f02.x1 /CLONE=IMAGE:2386971 /UG=Hs.58685 CD5 antigen (p56-62)
230588_s_at_HG-U133B	MCPR		Consensus includes gb:AA805622 /FEA=EST /DB_XREF=gi:2874372
230636_s_at_HG-U133B	BTEB1	basic transcription element binding protein 1	/DB_XREF=est:estoc19b11.s1 /CLONE=IMAGE:1341309 /UG=Hs.121572 ESTs
			Consensus includes gb:BF515959 /FEA=EST /DB_XREF=gi:11601138
			/DB_XREF=est:Ui-H-BW1-aoa-q-12-0-Ui.s1 /CLONE=IMAGE:3084119
			/UG=Hs.62529 ESTs
			Consensus includes gb:AI692426 /FEA=EST /DB_XREF=gi:4969766
			/DB_XREF=est:wd69c09.x1 /CLONE=IMAGE:2336848 /UG=Hs.107331 ESTs
			Consensus includes gb:AA906142 /FEA=EST /DB_XREF=gi:3041265
			/DB_XREF=est:oj93e12.s1 /CLONE=IMAGE:1505902 /UG=Hs.40137 anaphase-promoting complex 1; meiotic checkpoint regulator
			Consensus includes gb:AI458639 /FEA=EST /DB_XREF=gi:4311238
			/DB_XREF=est:ik13b12.x1 /CLONE=IMAGE:2150879 /UG=Hs.150557 basic transcription element binding protein 1

230048_at_HG-U133B	Homo sapiens mRNA; cDNA DKFZp667L0210 (from clone DKFZp667L0210)	Homo sapiens mRNA; cDNA gb:AI377398 /FEA=EST /DB_XREF=gi:4187251 /DB_XREF=est:tc35a11.x1 /CLONE=IMAGE:2066588 /UG=Hs.181297 ESTs
230050_at_HG-U133B	Homo sapiens cDNA FLJ12909 fis, clone NT2RP2004400	Consensus includes gb:AU151107 /FEA=EST /DB_XREF=gi:11012628 /DB_XREF=est:AU151107 /CLONE=NT2RP2004400 /UG=Hs.152460 Homo sapiens cDNA FLJ12909 fis, clone NT2RP2004400.
230059_at_HG-U133B	KIAA0212 gene product	Consensus includes gb:AW139300 /FEA=EST /DB_XREF=gi:6144018 /DB_XREF=est:U1-H-B1-ada-b-05-0-U1.s1 /CLONE=IMAGE:2715392 /UG=Hs.154332 KIAA0212 gene product
2300689_at_HG-U133B	KIAA0212 ESTs	Consensus includes gb:AA825243 /FEA=EST /DB_XREF=gi:2898542 /DB_XREF=est:oe5sg06.s1 /CLONE=IMAGE:1415962 /UG=Hs.163426 ESTs
230713_at_HG-U133B	ESTs, Moderately similar to ZN91_HUMAN ZINC FINGER PROTEIN 91 [H.sapiens]	Consensus includes gb:BF115786 /FEA=EST /DB_XREF=gi:10985262 /DB_XREF=est:7n64h03.x1 /CLONE=IMAGE:3569524 /UG=Hs.182185 ESTs
230743_at_HG-U133B	Homo sapiens, clone MGIC:10077 IMAGE:3896690, mRNA, complete cds	Consensus includes gb:AI743312 /FEA=EST /DB_XREF=gi:5111600 /DB_XREF=est:wgg91cd9.x1 /CLONE=IMAGE:2372464 /UG=Hs.183096 ESTs
230753_at_HG-U133B	ESTs	Consensus includes gb:R12665 /FEA=EST /DB_XREF=gi:765741 /DB_XREF=est:y40a04.s1 /CLONE=IMAGE:129294 /UG=Hs.11594 ESTs
230768_at_HG-U133B	ESTs	Consensus includes gb:BEG672541 /FEA=EST /DB_XREF=gi:10033082 /DB_XREF=est:7b68g10.x1 /CLONE=IMAGE:3233442 /UG=Hs.58753 ESTs
230775_s_at_HG-U133B	KIAA0610 protein	Consensus includes gb:BR590192 /FEA=EST /DB_XREF=gi:11682516 /DB_XREF=est:nab21a11.x1 /CLONE=IMAGE:3266229 /UG=Hs.118087 KIAA0610 protein
230793_at_HG-U133B	FLJ20048	Consensus includes gb:BE677038 /FEA=EST /DB_XREF=gi:10031579 /DB_XREF=est:7e45cd2.x1 /CLONE=IMAGE:3285410 /UG=Hs.116470 hypothetical protein FLJ20048
230795_at_HG-U133B	H4F2	Consensus includes gb:AI628075 /FEA=EST /DB_XREF=gi:5448746 /DB_XREF=est:wk31e04.x1 /CLONE=IMAGE:2413950 /UG=Hs.554668 ESTs

230802_at_HG-U133B	DKFZP564B1162	hypothetical protein DKFZp564B1162	Consensus includes gb:AI761947 /FEA=EST /DB_XREF=gi:5177614 /DB_XREF=est:wh50b09.x1 /CLONE=IMAGE:2384153 /UG=Hs.131587 ESTs, Weakly similar to Y053_HUMAN HYPOTHETICAL PROTEIN KIAA0053 H.sapiens
230803_s_at_HG-U133B	DKFZP564B1162	hypothetical protein DKFZp564B1162	Consensus includes gb:AI761947 /FEA=EST /DB_XREF=gi:5177614 /DB_XREF=est:wh50b09.x1 /CLONE=IMAGE:2384153 /UG=Hs.131587 ESTs, Weakly similar to Y053_HUMAN HYPOTHETICAL PROTEIN KIAA0053 H.sapiens
230834_at_HG-U133B			Consensus includes gb:BE348656 /FEA=EST /DB_XREF=gi:9260509 /DB_XREF=est:ht73g08.x1 /CLONE=IMAGE:3152414 /UG=Hs.114516 ESTs
			Consensus includes gb:AI492643 /FEA=EST /DB_XREF=gi:4393646 /DB_XREF=est:qz18a10.x1 /CLONE=IMAGE:2021850 /UG=Hs.284277 Homo sapiens immunoglobulin mu chain antibody MO30 (IgM) mRNA, complete cds
230877_at_HG-U133B	IGHG3	immunoglobulin heavy constant gamma 3 (G3m marker)	Consensus includes gb:AW611685 /FEA=EST /DB_XREF=gi:7316871 /DB_XREF=est:hg86a01.x1 /CLONE=IMAGE:2952456 /UG=Hs.6179 DEADH (Asp-Glu-Ala-AspHis) box poly(peptide 17 (72kD))
230917_at_HG-U133B		ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.sapiens]	Consensus includes gb:AI075039 /FEA=EST /DB_XREF=gi:3401683 /DB_XREF=est:ov1301.x1 /CLONE=IMAGE:1637209 /UG=Hs.130352 ESTs
230939_at_HG-U133B		ESTs	Consensus includes gb:AI740721 /FEA=EST /DB_XREF=gi:5109009 /DB_XREF=est:wg17d08.x1 /CLONE=IMAGE:2365359 /UG=Hs.128292 ESTs
230960_at_HG-U133B		Homo sapiens mRNA for FLJ00140	Consensus includes gb:BE646461 /FEA=EST /DB_XREF=gi:9970772 /DB_XREF=est:7e87b12.x1 /CLONE=IMAGE:3292127 /UG=Hs.137319 ESTs
230983_at_HG-U133B		Homo sapiens cDNA FLJ30065 fis, clone ADRG12000328	Consensus includes gb:AI821447 /FEA=EST /DB_XREF=gi:5440526 /DB_XREF=est:yp24d10.x5 /CLONE=IMAGE:1888371 /UG=Hs.141120 ESTs
230986_at_HG-U133B		ESTs	Consensus includes gb:AU149490 /FEA=EST /DB_XREF=gi:11011011 /DB_XREF=est:AU149490 /CLONE=NT2RRM4002430 /UG=Hs.15155 ESTs
230988_at_HG-U133B		ESTs, Weakly similar to T29012	Consensus includes gb:AI872303 /FEA=EST /DB_XREF=gi:5546352
230997_at_HG-U133B			

		hypothetical protein ZK328.7 - Caenorhabditis elegans [C.elegans]	/DB_XREF=est:wm57d10.x1 /CLONE=IMAGE:2440051 /UG=Hs.131816 ESTs,
231002_s_at_HG-U133B	NUF88	nucleoporin 88kD	Weakly similar to weak similarity to SP:YAD5 CLOAB C.elegans Consensus includes gb:AA778438 /FEA=EST /DB_XREF=gi:2837769
231050_at_HG-U133B	HRLP5	H-rev107-like protein 5	/DB_XREF=est:zr39g12.s1 /CLONE=IMAGE:379386 /UG=Hs.172108 nucleoporin 88kD Consensus includes gb:AW771586 /FEA=EST /DB_XREF=gi:7703843
231069_at_HG-U133B		ESTs, Weakly similar to T45117 hU1-70K protein [H.sapiens]	/DB_XREF=est:hn58g02.x1 /CLONE=IMAGE:3032114 /UG=Hs.12388 ESTs Consensus includes gb:AI768895 /FEA=EST /DB_XREF=gi:5235404 /DB_XREF=est:wh71f11.x1 /CLONE=IMAGE:23886221 /UG=Hs.295727 ESTs, Weakly similar to ALUB_HUMAN !!! ALU CLASS B WARNING ENTRY !!! H.sapiens Consensus includes gb:BF514552 /FEA=EST /DB_XREF=gi:11599731
231093_at_HG-U133B	FCRH3	Fc receptor-like protein 3	/DB_XREF=est:Ui-H-BW1-ang-b-12-0-Ui.s1 /CLONE=IMAGE:3081959 /UG=Hs.123296 ESTs Consensus includes gb:AI689803 /FEA=EST /DB_XREF=gi:4901097
231101_at_HG-U133B	PPP2R5E	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform	/DB_XREF=est:bx25h09.x1 /CLONE=IMAGE:2270657 /UG=Hs.122684 ESTs Consensus includes gb:AW511401 /FEA=EST /DB_XREF=gi:7149479
231118_at_HG-U133B		Homo sapiens cDNA FLJ25124 fs, clone CBR06414	/DB_XREF=est:hdB9e02.x1 /CLONE=IMAGE:2916698 /UG=Hs.133081 ESTs, Weakly similar to T08700 hypothetical protein DKF2p564G013.1 H.sapiens Consensus includes gb:AI683621 /FEA=EST /DB_XREF=gi:4893803
231181_at_HG-U133B		ESTs	/DB_XREF=est:tw52g09.x1 /CLONE=IMAGE:2263360 /UG=Hs.88651 ESTs Consensus includes gb:AI733145 /FEA=EST /DB_XREF=gi:5054558
231215_at_HG-U133B		ESTs	/DB_XREF=est:ol91005.x5 /CLONE=IMAGE:1536969 /UG=Hs.126962 ESTs Consensus includes gb:AW469714 /FEA=EST /DB_XREF=gi:7039820
231241_at_HG-U133B		ESTs, Moderately similar to PCAF associated factor 65 beta [Homo sapiens] [H.sapiens]	/DB_XREF=est:hd33d10.x1 /CLONE=IMAGE:2911315 /UG=Hs.155635 ESTs, Moderately similar to PCAF associated factor 65 beta H.sapiens Consensus includes gb:BE467688 /FEA=EST /DB_XREF=gi:9513463
231259_s_at_HG-U133B	CCND2	cyclin D2	/DB_XREF=est:h267h08.x1 /CLONE=IMAGE:3213087 /UG=Hs.75586 cyclin D2

231269_at_HG-U133B	DJ467N11.1	dJ467N11.1 protein ESTs	Consensus includes gb:AU153330 /FEA=EST /DB_XREF=gi:11014851 /DB_XREF=est:AU153330 /CLONE=NT2RP3002911 /UG=Hs.143917
231277_X_at_HG-U133B			Consensus includes gb:H29590 /FEA=EST /DB_XREF=gi:900500
231310_at_HG-U133B			Consensus includes gb:ym6ta05.s1 /CLONE=IMAGE:52642 /UG=Hs.14822 ESTs
231332_at_HG-U133B			Consensus includes gb:BF057073 /FEA=EST /DB_XREF=gi:10810969 /DB_XREF=est:7k15e01.x1 /CLONE=IMAGE:3444552 /UG=Hs.113170 ESTs
231406_at_HG-U133B			Consensus includes gb:AW295037 /FEA=EST /DB_XREF=gi:6701673 /DB_XREF=est:U1-H-BI2-ahs-g-10-0-U1.s1 /CLONE=IMAGE:2728122
231418_at_HG-U133B	MS4A2		ESTs. Moderately similar to 2109260A B cell growth factor [H.sapiens]
231472_at_HG-U133B			Consensus includes gb:AW205664 /FEA=EST /DB_XREF=gi:6505138 /DB_XREF=est:U1-H-BI1-ahf-h-07-0-U1.s1 /CLONE=IMAGE:2722813
231538_at_HG-U133B	FLJ23499		ESTs
231552_at_HG-U133B			membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for; beta poly peptide)
231567_s_at_HG-U133B	TSP-NY		ESTs

231647_s_at_HG-U133B	IRTA2	immunoglobulin superfamily receptor translocation associated 2	Consensus includes gb:AW241983 /FEA=EST /DB_XREF=gi:65575737 /DB_XREF=est:xn7704.x1 /CLONE=IMAGE:2700511 /UG=Hs.191958 ESTs
231656_x_at_HG-U133B	OSBPL10	oxysterol binding protein-like 10	Consensus includes gb:AW593467 /FEA=EST /DB_XREF=gi:7280725 /DB_XREF=est:hg1607.x1 /CLONE=IMAGE:2945797 /UG=Hs.321622 hypothetical protein FLJ20363
231736_x_at_HG-U133B	MGST1	microsomal glutathione S-transferase 1	Consensus includes gb:NM_020300.1 /DEF=Homo sapiens microsomal glutathione S-transferase 1 (MGST1), mRNA, /FEA=CDS /GEN=MGST1 /PROD=microsomal glutathione S-transferase 1 /DB_XREF=gi:9945305 /UG=Hs.790 microsomal glutathione S-transferase 1 /FL=gb:NM_020300.1
231775_at_HG-U133B	TNFRSF10A	tumor necrosis factor receptor superfamily, member 10a	Consensus includes gb:W65310 /FEA=EST /DB_XREF=gi:1373636 /DB_XREF=est:zd33e01.r1 /CLONE=IMAGE:342456 /UG=Hs.249190 tumor necrosis factor receptor superfamily, member 10a /FL=gb:U90875.1
231793_s_at_HG-U133B	CaMK2D	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	Consensus includes gb:AA448956 /FEA=EST /DB_XREF=gi:2162976 /DB_XREF=est:z07b10.r1 /CLONE=IMAGE:785755 /UG=Hs.111460 Homo sapiens cDNA: FLJ21715 fis, clone COL10287, highly similar to AF071569 Homo sapiens multifunctional calcium/calmodulin-dependent protein kinase II delta2 isoform mRNA /FL=gb:AF071569.1
231794_at_HG-U133B	CTLA4	cytotoxic T-lymphocyte-associated protein 4	Consensus includes gb:BG536887 /FEA=EST /DB_XREF=gi:13528433 /DB_XREF=est:602564631F1 /CLONE=IMAGE:4689582 /UG=Hs.247824
231837_at_HG-U133B	USP28	ubiquitin specific protease 28	Consensus includes gb:AB0404948.1 /DEF=Homo sapiens mRNA for KIAA1515 protein, partial cds. /FEA=mRNA /GEN=KIAA1515 /PROD=KIAA1515 protein /DB_XREF=gi:7959296 /UG=Hs.142856 KIAA1515 protein
231854_at_HG-U133B		Homo sapiens cDNA FLJ11448 fis, clone HEMBA1001391	Consensus includes gb:W63579 /FEA=EST /DB_XREF=gi:1371152 /DB_XREF=est:zb99a10.r1 /CLONE=IMAGE:320922 /UG=Hs.120905 Homo sapiens cDNA FLJ11448 fis, clone HEMBA1001391